M

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 February 2002 (07.02.2002)

PCT

(10) International Publication Number
WO 02/10217 A2

(51) International Patent Classification[7]: C07K 16/00

(21) International Application Number: PCT/US01/24031

(22) International Filing Date: 1 August 2001 (01.08.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/222,599 2 August 2000 (02.08.2000) US
60/224,360 11 August 2000 (11.08.2000) US
60/282,850 11 April 2001 (11.04.2001) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:
US 60/222,599 (CON)
Filed on 2 August 2000 (02.08.2000)
US 60/224,360 (CON)
Filed on 11 August 2000 (11.08.2000)
US 60/282,850 (CON)
Filed on 11 April 2001 (11.04.2001)

(71) Applicant (*for all designated States except US*): THE JOHNS HOPKINS UNIVERSITY [US/US]; 111 Market Place, Baltimore, MD 21202 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): ST. CROIX, Brad [CA/US]; 319 Lord Byron Lane #202, Cockeysville, MD 21020 (US). KINZLER, Kenneth, W. [US/US]; 1403 Halkirk Way, BelAir, MD 21015 (US). VOGELSTEIN, Bert [US/US]; 3700 Brenton Way, Baltimore, MD 21208 (US).

(74) Agents: KAGAN, Sarah, A. et al.; Banner & Witcoff, Ltd., 1001 G Street, N.W., Eleventh Floor, Washington, DC 20001-4597 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/10217 A2

(54) Title: ENDOTHELIAL CELL EXPRESSION PATTERNS

(57) Abstract: To gain a better understanding of tumor angiogenesis, new techniques for isolating endothelial cells (ECs) and evaluating gene expression patterns were developed. When transcripts from ECs derived f rom normal and malignant colorectal tissues were compared with transcripts from non-endothelial cells, over 170 genes predominantly expressed in the endothelium were identified. Comparison between normal- and tumor-derived endothelium revealed 79 differentially expressed genes, including 46 that were specifically elevated in tumor-associated endothelium. Experiments with representative genes from this group demonstrated that most were similarly expressed in teh endothelium of primary lung, breast, brain, and pancreatic cancers as well as in metastatic lesions of the liver. These results demonstrate that neoplastic and normal endothelium in humans are distinct at the molecular level, and have significant implications for the development of anti-angiogenic therapies in the future.

ENDOTHELIAL CELL EXPRESSION PATTERNS

[01] This application claims the benefit of provisional applications serial numbers 60/222,599 filed August 2, 2000, 60/224,360 filed August 11, 2000, and 60/282,850 filed April 11, 2001, the disclosures of which are expressly incorporated herein.

[02] The U.S. government retains certain rights in the invention by virtue of the provisions of National Institutes of Heath grants CA57345 and CA43460, which supported this work.

TECHNICAL FIELD OF THE INVENTION

[03] This invention is related to the area of angiogenesis and anti-angiogenesis. In particular, it relates to genes which are characteristically expressed in tumor endothelial and normal endothelial cells.

BACKGROUND OF THE INVENTION

[04] It is now widely recognized that tumors require a blood supply for expansive growth. This recognition has stimulated a profusion of research on tumor angiogenesis, based on the idea that the vasculature in tumors represents a potential therapeutic target. However, several basic questions about tumor endothelium remain unanswered. For example, are vessels of tumors qualitatively different from normal vessels of the same tissue? What is the relationship of tumor endothelium to endothelium of healing wounds or other physiological or pathological forms of angiogenesis? The answers to these questions critically impact on the potential for new therapeutic approaches to inhibit angiogenesis in a specific manner.

[05] There is a continuing need in the art to characterize the vasculature of tumors relative to normal vasculature so that any differences can be exploited for therapeutic and diagnostic benefits.

[06] One technique which can be used to characterize gene expression, or more precisely gene transcription, is termed serial analysis of gene expression (SAGE). Briefly, the SAGE approach is a method for the rapid quantitative and qualitative analysis of mRNA transcripts based upon the isolation and analysis of short defined sequence tags (SAGE Tags) corresponding to expressed genes. Each Tag is a short nucleotide sequences (9-17 base pairs in length) from a defined position in the transcript. In the SAGE method, the Tags are dimerized to reduce bias inherent in cloning or amplification reactions. (See, US Patent 5,695,937) SAGE is particularly suited to the characterization of genes associated with vasculature stimulation or inhibition because it is capable of detecting rare sequences, evaluating large numbers of sequences at one time, and to provide a basis for the identification of previously unknown genes.

SUMMARY OF THE INVENTION

[07] One embodiment of the invention provides an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, and 271, respectively. The molecule can be, for example, an in tact antibody molecule, a single chain variable region (ScFv), a monoclonal antibody, a humanized antibody, or a human antibody. The molecule can optionally be bound to a cytotoxic moiety, bound to a therapeutic moiety, bound to a detectable moiety, or bound to an anti-tumor agent.

[08] According to another embodiment of the invention a method of inhibiting neoangiogenesis is provided. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, and 271, respectively, is administered to a subject in need thereof. Neoangiogenesis is consequently inhibited. The subject may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, may have psoriasis, for example.

[09] Another aspect of the invention is a method of inhibiting tumor growth. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, and 271, respectively, is administered to a human subject bearing a tumor. The growth of the tumor is consequently inhibited.

[10] Still another aspect of the invention provides an isolated molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 200, 212, 230, 232, and 271 , respectively. The molecule can be, for example, an in tact antibody molecule, a single chain variable region (ScFv), a monoclonal antibody, a humanized antibody, or a human antibody. The molecule can optionally be bound to a cytotoxic moiety, bound to a therapeutic moiety, bound to a detectable moiety, or bound to an anti-tumor agent.

[11] According to still another aspect of the invention an isolated and purified human transmembrane protein is provided. The protein is selected from the group consisting of: TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively.

[12] Yet another aspect of the invention is an isolated and purified nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: : TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively. The isolated and purified nucleic acid molecule may optionally comprise a coding sequence selected from those shown in SEQ ID NO: : 199, 211, 229, and 231.

[13] Still another aspect of the invention is a recombinant host cell which comprises a nucleic acid molecule. The nucleic acid molecule comprises a coding sequence for a transmembrane TEM selected from the group consisting of: : TEM 3, 9, 17, and 19 as shown in SEQ ID NO: 200, 212, 230, and 232, respectively. The recombinant host cell optionally comprises a coding sequence selected from those shown in SEQ ID NO: 199, 211, 229, and 231.

[14] According to one embodiment of the invention a method is provided for inducing an immune response in a mammal. A nucleic acid molecule comprising a coding sequence for a human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: , respectively, is administered to the mammal. An immune response to the human transmembrane protein is thereby induced in the mammal. Optionally the coding sequence is shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250 and 271.

[15] According to yet another embodiment of the invention a method of inducing an immune response in a mammal is provided. A purified human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250 and 271, respectively, is administered to the mammal. An immune response to the human transmembrane protein is thereby induced in the mammal.

[16] Another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with an isolated and purified human trasmembrane protein selected from the group consisting of 1, 3, 9, 13, 17, 30, 19, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 250, and 271. The isolated and purified human trasmembrane protein is also contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 13, 17, 30, 19, and 44 as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 250, and 271 respectively. Binding of the molecule comprising an antibody variable region to the human transmembrane protein is determined. A test compound which diminishes the binding of the molecule comprising an antibody variable region to the human transmembrane protein is identified as a ligand involved in endothelial cell regulation.

[17] Yet another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with a cell comprising a human transmembrane protein selected from the group consisting of 1, 3, 9, 17, and 19 as shown in SEQ ID NO: 196, 200, 212, 230, and 232. The cell is also contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, and 19 as shown in SEQ ID NO: 196, 200, 212, 230, and 232 , respectively. Binding of the molecule comprising an antibody variable region to the cell is determined. A test compound which diminishes the binding of the molecule comprising an antibody variable region to the cell is identified as a ligand involved in endothelial cell regulation.

[18] Yet another aspect of the invention is a method for identification of a ligand involved in endothelial cell regulation. A test compound is contacted with a human transmembrane protein selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27,

28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275. Binding of a test compound to the human transmembrane protein is determined. A test compound which binds to the protein is identified as a ligand involved in endothelial cell regulation.

[19] Another embodiment of the present invention is a soluble form of a human transmembrane protein selected from the group consisting of: TEM 1, 3, 9, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 200, 212, 230, 232, 238, 250, and 271 respectively. The soluble forms lack transmembrane domains. The soluble form may consist of an extracellular domain of the human transmembrane protein.

[20] Also provided by the present invention is a method of inhibiting neoangiogenesis in a patient. A soluble form of a human transmembrane protein is adminstered to the patient. Neoangiogenesis in the patient is consequently inhibited. The patient may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, or may have psoriasis, for example.

[21] Another embodiment of the invention provides a method of inhibiting neoangiogenesis in a patient. A soluble form of a human transmembrane protein is administered to the patient. Neoangiogenesis in the patient is consequently inhibited. The patient may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy, may have rheumatoid arthritis, or may have psoriasis, for example.

[22] According to still another aspect of the invention a method of identifying regions of neoangiogenesis in a patient is provided. A molecule comprising an antibody variable region which specifically binds to an

extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 13, 17, 19, 22, 30, and 44, as shown in SEQ ID NO: 196, 200, 212, 220, 230, 232, 238, 250, and 271, respectively, is administered to a patient. The molecule is bound to a detectable moiety. The detectable moiety is detected in the pateint, thereby identifying neoangiogenesis.

[23] According to another aspect of the invention a method is provided for inducing an immune response to tumor endothelial cells in a patient. A mouse TEM protein selected from the group consisting of: 1, 2, 3, 9, 13, 17, 19, 22, and 30 as shown in SEQ ID NO: 291, 293, 299, 295, 303, 297, 301, 305, and 307, is administered to a patient in need thereof. An immune response to a human TEM protein is consequently induced.

[24] Still another embodiment of the invention is a method of screening for neoangiogenesis in a patient. A body fluid collected from the patient is contacted with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 3, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 200, 212, 230, 232, and 271, respectively. Detection of cross-reactive material in the body fluid with the molecule indicates neo-angiogenesis in the patient.

[25] Still another embodiment of the invention provides a method of inhibiting neoangiogenesis in a patient. A molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40 as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 and 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, is administered to the patient. Neoangiogenesis in the patient consequently inhibited.

[26] Yet another aspect of the invention is a method of screening for neoangiogenesis in a patient. A body fluid collected from the patient is

contacted with a molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, respectively. Detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

[27] Also provided by the present invention is a method of promoting neoangiogenesis in a patient. A TEM protein selected from the group consising of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, is administered to a patient in need of neoangiogenesis. Neoangiogenesis in the patient is consequently stimulated.

[28] One embodiment of the invention provides a method of promoting neoangiogenesis in a patient. A nucleic acid molecule encoding a TEM protein selected from the group consising of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264, is administered to a patient in need of neoangiogenesis. The TEM protein is consequently expressed and neoangiogenesis in the patient is stimulated.

[29] Another embodiment of the invention provides a method of screening for neoangiogenesis in a patient. A TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: : 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244,.252, 257, 259, 261. 263, and 265, respectively, is detected in a body fluid collected from the patient. Detection of the TEM protein indicates neoangiogenesis in the patient.

[30] Another aspect of the invention is a method of screening for neoangiogenesis in a patient. A nucleic acid encoding a TEM protein

selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40 is detected in a body fluid collected from the patient. The nucleic acid is selected from the group consisting of those shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264. Detection of the TEM protein indicates neoangiogenesis in the patient.

[31] Yet another embodiment of the invention is an isolated and purified nucleic acid molecule which encodes a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289. The nucleic acid molecule optionally comprises a coding sequence as shown in SEQ ID NO: 278, 282, 284, and 288. The nucleic acid may be maintained in a recombinant host cell.

[32] The present invention also provides an isolated and purified NEM protein selected from the group consising of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

[33] The present invention further provides an isolated molecule comprising an antibody variable region which specifically binds to a NEM protein selected from the group consisting of: 14, 22, 23, and 33, as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

[34] An additional embodiment of the present invention is a method of inhibiting neoangiogenesis. An effective amount of a NEM protein selected from the group consising of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289 is administered to a subject in need thereof . Neoangiogenesis is thereby inhibited.

[35] A still further embodiment of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more TEM genes selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,

12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: : 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 221 & 222, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 256, 258, 260, 262, 266, 268, 270, 272, and 274, respectively, are contacted with a test compound. Expression of said one or more TEM genes is determined by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA. A test compound is identified as a candidate drug for treating tumors if it decreases expression of said one or more TEM genes. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Test compounds which increase expression can be identified as candidates for promoting wound healing.

[36] Yet another embodiment of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more TEM proteins selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, are contacted with a test compound. The amount of said one or more TEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it decreases the amount of one or more TEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Alternatively, a test compound which increases the amount of one or more TEM proteins in said cells is identified as a candidate drug for treating wound healing.

[37] According to another aspect of the invention a method is provided to identify candidate drugs for treating tumors. Cells which express one or more TEM proteins selected from the group consisting of: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, are contacted with a test compound. Activity of said one or more TEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it decreases the activity of one more TEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs. Optionally the cells are endothelial cells. If a test compound increases the acitivity of one more TEM proteins in said cells it can be identified as a candidate drug for treating wound healing.

[38] An additional aspect of the invention is a method to identify candidate drugs for treating patients bearing tumors. A test compound is contacted with recombinant host cells which are transfected with an expession construct which encodes one or more TEM proteins selected from the group consisting of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively. Proliferation of said cells is determined. A test compound which inhibits proliferation of said cells is identified as a candidate drug for treating patients bearing tumors. A test coumpound which stimulates

proliferation of said cells is identified as a candidate drug for promoting neoangiogenesis, such as for use in wound healing.

[39] Another embodiment of the invention provides a method to identify candidate drugs for treating tumors. Cells which express one or more NEM genes selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 278, 282, 284, and 288, respectively, are contacted with a test compound. Expression of said one or more NEM genes is determined by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA. A test compound is identified as a candidate drug for treating tumors if it increases expression of said one or more NEM genes. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[40] According to another aspect of the invention a method is provided to identify candidate drugs for treating tumors. Cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, are contacted with a test compound. The amount of said one or more NEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating tumors if it increases the amount of one more NEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[41] An additional aspect of the invention is a method to identify candidate drugs for treating tumors. Cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, are contacted with a test compound. Activity of said one or more NEM proteins in said cells is determined. A test compound is identified as a candidate drug for treating

tumors if it increases the activity of said one or more NEM proteins in said cells. Optionally the cells are endothelial cells. Alternatively or additionally, the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

[42] Still another embodiment of the invention provides a method to identify candidate drugs for treating patients bearing tumors. Atest compound is contacted with recombinant host cells which are transfected with an expession construct which encodes one or more NEM proteins selected from the group consisting of 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289. Proliferation of said cells is determined. A test compound which stimulates proliferation of said cells is identified as a candidate drug for treating patients bearing tumors.

[43] Another aspect of the invention is a method for identifying endothelial cells. One or more antibodies which bind specifically to a TEM or NEM protein selected from the group consisting of TEM : 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 and NEM 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, is contacted with a population of cells. Cells in the population which have bound to said antibodies are detected. Cells which are bound to said antibodies are identified as endothelial cells. Optionally cells which have bound to said antibodies are isolated from cells which have not bound.

[44] Still another aspect of the invention is a method for identifying endothelial cells. One or more nucleic acid hybridization probes which are complementary to a TEM or NEM gene nucleic acid sequence selected from the group consisting of of TEM : 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16,

17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 and NEM 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, is contacted with nucleic acids of a population of cells. Nucleic acids which have specifically hybridized to said nucleic acid hybridization probes are detected. Cells whose nucleic acids specifically hybridized are identified as endothelial cells.

[45] Yet another embodiment of the invention is a method of inhibiting neoangiogenesis. An effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a mouse TEM protein selected from the group consisting of: 1, 2, 3, 9, 17, and 19, as shown in SEQ ID NO: 291, 293, 299, 295, 297, and 301, respectively, is administered to a subject in need thereof . Neoangiogenesis is thereby inhibited. The subject may be a mouse, may bear a vascularized tumor, may have polycystic kidney disease, may have diabetic retinopathy. may have rheumatoid arthritis, or may have psoriasis, for example.

[46] These and other embodiments which will be apparent to those of skill in the art upon reading the specification provide the art with reagents and methods for detection, diagnosis, therapy, and drug screening pertaining to neoangiogenesis and pathological processes involving or requiring neoangiogenesis.

BRIEF DESCRIPTION OF THE DRAWINGS

[47] Fig. 1A-1B. vWF expression in colorectal cancers. vWF (red stain) was detected in vessels by in situ hybridization. At low power magnification (Fig. 1.A) vessels were often surrounded by a perivascular cuff of viable cells

(red arrows), with a ring of necrotic cells evident at the periphery (black arrows). At high power magnification (Fig. 1.B) the expression of vWF (red) was clearly localized to the vessels. Sections were counterstained with methyl green.

[48] Fig. 2A-2D. Purification of Endothelial Cells (ECs) from human normal and malignant tissue. (Fig. 2A) Vessels (red) of frozen sections were stained by immunofluorescence with the P1H12 monoclonal antibody (Chemicon, Temecula, CA) and detected using a biotinylated goat anti-mouse IgG secondary antibody followed by rhodamine-linked strepavidin. The region stained is from within the lamina propria of normal colonic mucosa. Note that the larger vessels (arrowheads) and capillaries (arrows) are positive, and staining of hematopoietic cells was undetectable. E-cadherin positive epithelial cells (green) at the edge of the crypt were simultaneously visualized using a rabbit polyclonal antibody (Santa Cruz, Santa Cruz, CA), followed by a goat anti-rabbit IgG secondary antibody labelled with alexa (Molecular Probes, Eugene, OR). Sections were imaged at 60X magnification using confocal microscopy. (Fig. 2.B) To isolate pure populations from collagenase dispersed tissues, the epithelial and hematopoietic cell fractions were sequentially removed by negative selection with magnetic beads. The remaining cells were stained with P1H12 and ECs were isolated by positive selection with magnetic beads. (Fig. 2.C) RT-PCR analysis used to assess the purity of the EC preparations. Semiquantitative PCR analysis was performed on cDNA generated either directly from colorectal cancer tissue (unfractionated tumor) or from purified ECs isolated from normal colonic mucosa (normal EC fraction) or colorectal cancer (tumor EC fraction). PCR amplification of the epithelial specific marker cytokeratin 20 (CK20), demonstrated its expression was limited to the unfractionated tumor. Two endothelial specific markers, vWF and VE-cadherin (VE-Cad) showed robust amplification only in the endothelial fractions, validating the purity and enrichment protocol shown in (Fig. 2.B). The ubiquitous housekeeping enzyme GAPDH was observed in all samples.

No signal was detected in the no-template (NT) control. cDNA templates were diluted 1:10, 1:100, 1:1000, 1:4000, and 1:40,000 as indicated by the declining wedge. (Fig. 2.D) The relative expression level of select genes was determined by measuring the tag abundance from several SAGE libraries combined into four groups. The first was composed of ~193,000 tags from the two in vivo-derived EC preparations (Endothelial Cell Fraction) while the second contained a single library of ~57,000 tags containing macrophages and other leukocytes derived from the negative selection (Hematopoietic Fraction). The fourth library contained ~401,000 tags from cultured HUVEC and HMVEC (Endothelial Cells in Culture), and the fourth consisted of ~748,000 tags from 6 colon cancer cell lines in culture (Epithelial Cells). After normalization, the library with the highest tag number for each marker was given a value of 100%, and the corresponding relative expression levels of the remaining 3 libraries was plotted on the ordinate. Note the high level of CD31 present on hematopoietic cells, the likely cause of the impurity of the initial endothelial selection, compared with the selectivity of P1H12.

[49] Fig. 3A- 3E). Expression of Pan-Endothelial Markers (PEMs) is limited to ECs. The endothelial origin of PEMs identified by SAGE was confirmed using a highly sensitive in situ hybridization assay. Localization of novel PEMs to the ECs was demonstrated by examining two representative PEMs, PEM3 (Fig. 3A) and PEM6 (Fig. 3B) in lung cancer and colon cancer, respectively. Hevin expression was readily detected in the ECs of a colon tumor (Fig. 3C) despite its low level of expression in cultured ECs. Expression of VEGFR2 was readily detectable in the ECs of both normal (Fig. 3D) and malignant colon tissue (Fig. 3E).

[50] Fig. 4A-4J. Expression of Tumor Endothelial Markers (TEMs). (Fig. 4A) RT-PCR analysis confirmed the tumor specific expression of selected novel TEMs. Semiquantitative PCR analysis was performed on cDNA generated either from purified epithelial cells as a negative control (Control) or from purified ECs isolated from normal colonic mucosa (Normal ECs) or

colorectal cancer (Tumor ECs) from two different patients. Two endothelial specific markers, vWF and PEM6 showed robust amplification only in the endothelial fractions whereas the ubiquitous housekeeping enzyme GAPDH was observed in all samples. TEM1 (BSC-TEM1), TEM 17 (BSC-TEM7) and TEM22 (BSC-TEM9) were specifically expressed in tumor compared to normal ECs. The cDNA template was diluted 1:10, 1:100, 1:1000, and 1:10,000 as indicated by the declining wedge. (Fig. 4 B- 4J) The endothelial origin of TEMs identified by SAGE was confirmed using in situ hybridization as in Fig 3. Expression of TEM 1 (BSC-TEM1) (Fig. 4 B) and TEM17 (BSC-TEM7) (Fig. 4 C) was demonstrated to be highly specific to the ECs in colorectal cancers; sections were imaged in the absence of a counterstain to show the complete lack of detectable expression in the non-endothelial cells of the tumor. Expression of TEM17 (BSC-TEM7) in ECs was demonstrated in a metastatic liver lesion from a primary colorectal cancer (Fig. 4 D), a lung (Fig. 4 E), breast (Fig. 4 F), pancreatic (Fig. 4 G) and brain cancer (Fig. 4 H), as well as in a sarcoma (Fig. 4 I). TEM 17 (BSC-TEM7) was also localized to vessels during normal physiological angiogenesis of the corpus luteum (Fig. 4 J).

DETAILED DESCRIPTION OF THE INVENTION

[51] We identified 46 human genes that were expressed at significantly higher levels (> 10-fold) in tumor endothelium than in normal endothelium, and 33 genes that were expressed at significantly lower levels in human tumor versus normal endothelium. See Tables 2 and 4, respectively. Most of these genes were either not expressed or expressed at relatively low levels in Endothelial Cells (ECs) maintained in culture. Moreover, we identified 93 genes which are expressed in both normal and tumor human endothelium. Interestingly, the tumor endothelium genes were expressed in all tumors tested, regardless of its tissue or organ source. Most tumor endothelium genes were also expressed in corpus luteum and wounds.

[52] As the work has progressed, we have refined and classified our original 46 tumor endothelial markers. We have named these markers TEMs and renumbered them consecutively by the prevalence of their tags in our SAGE analysis. Originally we had not used a consecutive numbering system. Our non-consecutive numbering system has been renamed as BSC-TEMs. For most of the original 46 SAGE Tags, we now provide full-length nucleic acid and protein sequence. In some cases, the sequences were obtained through the public databases, in others the sequences were obtained by cloning and through the use of gene prediction tools. In some cases, we found SAGE Tags corresponding to genes having different splice varients or with known polymorphisms. For example, in one case the SAGE Tag BSC-TEM3 has been found to hybridize to an alternatively spliced form of the transcript encoding BSC-TEM7. The proteins encoded by the two transcripts are the same; therefore they are cumulatively called TEM7. A highly related sequence was found via homology searches, BSC-TEM7R. This paralog sequence is now called TEM3. See Table 2, which follows, showing tumor endothelial markers by order of prevalence (except for TEM 3). Column 1 indicates the prevalence number. Column 2 indicates the original nomenclature. Column 3 indicates the short tags. Column 4 indicates the long tags. Column 5 indicates the accession number in GenBank. Column 6 indicates the sequence identifiers for the short tag, the long tag, the full nucleic acid, and the protein. Column 7 provides a functional description, which is expanded below in the text.

TEM1	BSC-TEM1	GGGGCTGCCCA	GGGGCTGCCCAGCTGA	NM020404	SEQ ID NO: 94, 309, 195, 196	tumor endothelial marker 1 precursor
TEM 2	BSC-TEM2	GATCTCCGTGT			SEQ ID NO: 95, 197.198	sapiens tumor endothelial marker 2 (BSC-TEM2) mRNA/mouse Ras, dexamethasone-induced 1 (RASD1), mRNA
TEM 3	BSC-TEM7R				SEQ ID NO:199, 200	human ortholog of mouse paralog of mouse TEM-7
TEM 4		CTTTCTTTGAG	CTTTCTTTGAGTTTTAA	AB034203	SEQ ID NO:97, 311, 201, 202	Homo sapiens dickkopf-3 (DKK-3) mRNA,
TEM 5	BSC-TEM4	TATTAACTCTC	TATTAACTCTCTTTGGA		SEQ ID NO:98, 312, 203, 204	Tumor endothelial marker 4
TEM 6		CAGGAGACCCC	CAGGAGACCCCAGGCCC	X57766	SEQ ID NO:99, 314, 205, 206	Human stromelysin-3 mRNA.
TEM 7		GGAAATGTCAA	GGAAATGTCAGCAAGTA	BC002576	SEQ ID NO:100, 315.207, 208	matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)

TEM 8		CCTGGTTCAGT			SEQ ID NO:101, 316, 209, 210	HeyL transcription factor
TEM 9	BSC-TEM5	TTTTTAAGAAC	TTTTTAAGAACTCGGGT		SEQ ID NO:102, 317, 211, 212	
TEM 10		TTTGGTTTTCC	TTTGGTTTTCCAAAAGA	J03464, M18057, X02488	SEQ ID NO:103, 319, 213, 214	Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1.
TEM 11		ATTTTGTATGA	ATTTTGTATGATTTTTA	NM_002508	SEQ ID NO:104, 321, 215, 216	nidogen/entactin
TEM 12		ACTTTAGATGG	ACTTTAGATGGGAAGCC	X52022	SEQ ID NO:105, 322, 217, 218	H.sapiens RNA for type VI collagen alpha3 chain.
TEM 13		GAGTGAGACCC	GAGTGAGACCCAGGAGC	M11749	SEQ ID NO:106, 324, 219, 220	Human Thy-1 glycoprotein gene, complete cds.
TEM 14		GTACACACACC	GTACACACACCCCCACC		SEQ ID NO:107, 325, 221, 223	Cystatin SN

TEM 14		GTACACACACC	GTACACACACCCCCACC	X54667	SEQ ID NO:107, 325, 222, 224	H.sapiens mRNA for cystatin S.
TEM 15		CCACAGGGGAT	CCACAGGGGATTCTCCT	NM_000090	SEQ ID NO:108, 327, 225, 226	Human mRNA 3' region for pro-alpha1(III) collagen.
TEM 16	BSC-TEM6	TTAAAAGTCAC	TTAAAAGTCACTGTGCA		SEQ ID NO:109, 328, 227, 228	
TEM 17	BSC-TEM7	ACAGACTGTTA	ACAGACTGTTAGCCAAG	AF279144	SEQ ID NO:110, 329, 229, 230	Human Tumor endothelial marker 7
TEM 18		CCACTGCAACC			SEQ ID NO:111	
TEM 19	BSC-TEM8	CTATAGGAGAC			SEQ ID NO:112, 330, 231, 232	
TEM 20		GTTCCACAGAA		NM_000089	SEQ ID NO:113, 233, 234	collagen, type I, alpha 2 (COL1A2

TEM 21		TACCACCTCCC	TACCACCTCCCTTTCCT		SEQ ID NO:114, 331, 235, 236	Homo sapiens mRNA; cDNA DKFZp762B245 (from clone DKFZp762B245);
TEM 22	BSC-TEM9	GCCCTTTCTCT	GCCCTTTCTCTGTAGTT	NM_006039	SEQ ID NO:115, 334, 237, 238	endocytic receptor (macrophage mannose receptor family) (KIAA0709),
TEM 23		TTAAATAGCAC	TTAAATAGCACCTTTAG		SEQ ID NO:116, 335	no match
TEM 24		AGACATACTGA	AGACATACTGACAGAAT	NM_022648	SEQ ID NO:117, 336, 239, 240	Homo sapiens mRNA; cDNA DKFZp434G162 (from clone DKFZp434G162);
TEM 25		TCCCCCAGGAG	TCCCCCAGGAGCCACCG	L35279, NM_006129	SEQ ID NO:118, 338, 241, 242	Homo sapiens (clone KT2) bone morphogenetic protein-1 (BMP-1) mRNA
TEM 26		AGCCCAAAGTG			SEQ ID NO:119	No Match
TEM 27		ACTACCATAAC		NM_003062	SEQ ID NO:120, 243.244	Homo sapiens mRNA for MEGF5, partial cds.
TEM 28		TACAAATCGTT	TACAAATCGTTGTCAAA	NM_014859	SEQ ID NO:121, 339, 245, 246	Homo sapiens mRNA for KIAA0672 protein, complete cds.

TEM 29		TTGGGTGAA AA			SEQ ID NO:122, 247, 248	ESTs (2 unigene clusters)
TEM 30		CATTATCCAA A	CATTATCCAAAAACA AT	THC534029, X68742, AI262158, AI88747, AI394565, AA679721	SEQ ID NO:123, 340, 249, 250	integrin, alpha 1
TEM 31		AGAAACCAC GG	AGAAACCACGGAAA TGG	NM_001845	SEQ ID NO:124, 341, 251, 252	hypothetical protein KIAA1164
TEM 32		ACCAAAACC AC			SEQ ID NO:125	no match
TEM 33		TGAAATAAAC		NM_000255	SEQ ID NO:126, 253, 254	methylmalonyl Coenzyme A mutase
TEM 34		TTTGGTTTCC			SEQ ID NO:127	no match
TEM 35		GTGGAGACG GA	GTGGAGACGGACTC TGT	ESTAI186535	SEQ ID NO:128, 345, 255, 358	est

TEM 36		TTTGTGTTGT A	TTTGTGTTGTATATT TA	NM_00437 0	SEQ ID NO:129, 346, 256, 257	est
TEM 37		TTATGTTTAA T	TTATGTTTAATAGTT GA	NM_00234 5	SEQ ID NO:130, 347, 258, 259	Human lumican mRNA, complete cds.
TEM 38		TGGAAATGA C	TGGAAATGACCCAA AAA	NM_00008 8	SEQ ID NO:131, 348, 260, 261	collagen type1 alpha1
TEM 39		TGCCACACA GT	TGCCACACAGTGAC TTG	NM_00323 9	SEQ ID NO:132, 350, 262, 263	Human transforming growth factor-beta 3 (TGF-beta3) mRNA, complete
TEM 40		GATGAGGAG AC	GATGAGGAGACTGG CAA		SEQ ID NO:133, 351, 264, 265	collagen, type I, alpha 2
TEM 41		ATCAAAGGTT T	ATCAAAGGTTTGATT TA		SEQ ID NO:134, 352, 266, 267	est
TEM 42		AGTCACTAGT	AGTCACATAGTACAT AA	NM_02522 6	SEQ ID NO: 135, 353, 268, 269	ESTs

TEM 43		TTCGGTTGG TC	TTCGGTTGGTCAAA GAT		SEQ ID NO:136, 354	No match
TEM 44		CCCCACACG GG	CCCCACACGGGCAA GCA	NM_01835 4v	SEQ ID NO: 137, 355, 270, 271	Homo sapiens cDNA FLJ11190 fis, clone PLACE1007583.
TEM 45		GGCTTGCCT TT	GGCTTGCCTTTTTGT AT	NM_00036 6	SEQ ID NO:138, 356, 272, 273	est
TEM 46		ATCCCTTCCC G	ATCCCTTCCCGCCA CAC	NM_00268 8	SEQ ID NO:139, 357, 274, 275	Homo sapiens mRNA for peanut-like protein 1, PNUTL1 (hCDCrel-1).

[53] The studies described below provide the first definitive molecular characterization of ECs in an unbiased and general manner. They lead to several important conclusions that have direct bearing on long-standing hypotheses about angiogenesis. First, it is clear that normal and tumor endothelium are highly related, sharing many endothelial cell specific markers. Second, it is equally clear that the endothelium derived from tumors is qualitatively different from that derived from normal tissues of the same type and is also different from primary endothelial cultures. Third, these genes are characteristically expressed in tumors derived from several different tissue types, documenting that tumor endothelium, in general, is different from normal endothelium. Fourth, the genes expressed differentially in tumor endothelium are also expressed during other angiogenic processes such as corpus luteum formation and wound healing. It is therefore more appropriate to regard the formation of new vessels in tumors as "neoangiogenesis" rather than "tumor angiogenesis" *per se*. This distinction is important from a variety of perspectives, and is consistent with the idea that tumors recruit vasculature using much of, or basically the same signals elaborated during other physiologic or pathological processes. That tumors represent "unhealed wounds" is one of the oldest ideas in cancer biology.

[54] The nature and precise biological function of many of the Tumor Endothelial Markers (TEMs) identified here are unknown. Of the previously characterized genes shown in Table 2, it is intriguing that several encode proteins involved in extracellular matrix formation or remodelling (TEM 6, TEM 6, TEM 10, TEM 7, TEM 11, TEM 12, TEM 14, TEM 20, TEM 24, TEM 25, TEM 27, TEM 37, TEM 38, and TEM 40,) Deposition of extracellular matrix is likely critical to the growth of new vessels. Finally, it is perhaps not surprising that so many of the endothelial-specific transcripts identified here, whether expressed only in neovasculature or in endothelium in general, have not been previously characterized, and some are not even represented in EST databases. In part, this may be due to the fact that the EST databases are heavily biased toward certain

tissues, but moreover, may be due to the fact that even in highly vascularized tissues endothelial cells are still a relatively small proportion of the population. Thus, the sensitivity of the SAGE method is a particularly appropriate tool.

[55] Sequence and literature study has permitted the following identifications to be made among the family of TEM proteins. TEM proteins have been identified which contain transmembrane regions. These include TEM 1, TEM 3, TEM 9, TEM 13, TEM 17, TEM 19, TEM 22, TEM 30, and TEM 44. TEM proteins have been identified which are secreted proteins, including TEM 4, TEM 6, TEM 7, TEM 10, TEM 12, TEM 14, TEM 20, TEM 25, TEM 27, TEM 31, TEM 36, TEM 37, TEM 38, and TEM 39. HeyL (TEM 8) is a transcription factor which may be involved in regulating TEMs as one or more groups. The protein corresponding to the tag for TEM44 was found in the public databases, but no biological function has yet been ascribed to it.

[56] TEM 1 has been named endosialin in the literature. It has a signal sequence at amino acids 1-17 and a transmembrare domain at amino acids 686-708. Thus it is a cell surface protein. Its extracellular domain is at resiudes 1-685. Endosialin may be involved in endocytosis. The mouse ortholog is predicte d to have a signal peptide at residues 1-21.

[57] TEM 2 is a dexamethasone induced, ras related protein homolog of 266 amino acids. It has neither a signal sequence nor a transmembrane domain. Thus it is neither a cell surface nor a secreted protein. TEM 2 plays a role in signal transduction. It regulates alterations in cell morphology, proliferation, and cell-extracellular matrix interactions.

[58] TEM 3 (originally termed TEM 7R) has both a signal sequence (at residues 1-24 or 1-30) and a transmembrane domain (at residues 456 – 477). Thus it is a cell surface protein. The portion of the protein which is extracelular is at amino acids 1- 455. TEM 3 has domains with homology to integrins, plexin,

and adhesion molecules. TEM 3 may regulate GTPases that control signal transduction pathways linking plasma membrane receptors to the actin cytoskeleton. In the mouse ortholog, the signal peptide is predicted to be residues 1-30.

[59] TEM 4 is also known as DKK –3. It has a signal sequence (residues1-16), suggesting that is a secreted protein. TEM 4 regulates *wnt* signaling, and it may be involved in vasculogenesis and *wnt*-dependent signaling for endothelial growth. TEM 4 is an inhibitor of Wnt oncogene and such *inhibition* can be determined by assay. Tsuji et al., Biochem.Biophys.Res.Comm. 268:20-4, 2000.

[60] TEM 5 appears to be neither secreted nor a cell surface protein. TEM 5 appears to be a component of a G protein - GTPase signaling pathway.

[61] TEM 6 is also known as stromelysin - 3 /Matrix metalloproteinase 11 (MMP -11). It has a signal sequence at residues 1-31, but no transmembrane domain. It has an alternative signal peptide splice site at residues 108-109. Thus it appears to be a secreted protein. TEM 6 belongs to the zinc metaloprotease family, also known as the matrixin subfamily. TEM 6 is expressed in most invasive carcinomas. Alpha 1 - protease inhibitor is a natural substrate of MMP 11. TEM 6 degrades extracellhular matrix proteins such as collagen and is involved in extracellular matrix remodeling and cell migration. Stromelysin can be assayed using a casein-resorufin substrate, for example. See Tortorella and Arner, Inflammation Research 46 Supp. 2:S122-3, 1997.

[62] TEM 7 is a protein of many names, also being known as matrix metalloproeinase 2, gelatinase A, and 72KD type IV collagenase. TEM 7 has a signal sequence at residues 1- 26 and is a secreted protein. Like TEM 6, TEM 7 belongs to the matrixin subfamily (zinc metalloproteinases). TEM 7 cleaves gelatin type I, collagen type I, IV, V VII and X.. TEM 7 associates with integrin on the surface of endothelial cells and promotes vascular invasion. TEM 7 is

involved in tissue remodeling. TEM 7 can be assayed using zymography or quenched fluorescent substrate hydrolysis, for example. Garbett, et al., Molecular Pathology 53:99-106, 2000. A fluorogenic matrix metalloproteinase substrae assay can also be used which employs methoxycoumarin continaing septapeptide analog of the alpha2(I) collagen cleavage site. See Bhide et al., J. Periodontology 71:690-700, 2000.

[63] TEM 8 is HEYL protein . It has neither a signal sequence nor a transmembrane domain. It is related to the hairy/Enhancer of split genes. TEM 8 is likely a nuclear protein, having a role as a transcription factor. TEM 8 belongs to a new class of Notch signal tranducers and plays a key role in various developmental processes, such as vascular development, somatogenesis and neurogenesis. SNP's at residues 615 and 2201 have Cytosine bases. Notch 3 mutations underlie the CADASIL vascular disorder. See *Mech Dev* 2000 Nov; 98 (1-2):175

[64] TEM 9 is a G- protein coupled receptor homolog, having both a signal sequence at residues 1-26 and 7 transmembrane domains. Thus it is a cell surface protein. Its extracellular region resides in amino acids 1-769. Its transmembrane domains are at residues 817-829 (TM2 and TM3), residues 899-929 (TM4 and TM5), and residues 1034-1040 (TM6 and TM7). TEM 9 acts as a G-protein coupled receptor with extracellular domains characteristic of cell adhesion proteins. One of its splice variants may function as a soluble receptor. TEM 9 may regulate cell polarity and cell migration. It may be involved in exocytosis based on latrophilin function. The mouse ortholog has a predicted signal peptide at residues 1-29.

[65] TEM 10 is collagen type I, alpha2 (COL1A2), which has a signal sequence at residues 1-22. It is an extracellular matrix (ECM) protein which is secreted subsequent to synthesis. TEM 10 interacts with a number of proteins including other ECM proteins, certain growth factors, and matrix metalloproteases. TEM

10 is required for the induction of endothelial tube formation and is involved in tissue remodeling. A variant at nucleotide 3233 which substitutes an A, is associated with osteogenesis imperfecta type IV. A variant at nucleotide 4321 substituting an A retains a wild type phenotype. Nucleotide 715 is a site of a polymorphism. Nucleotides 695-748 are deleted in Ehlers-Danos syndrome. Other mutations are associated with idiopathic osteoporosis, and atypical Marfan syndrome. Variants are known at nucleotides 226(T,C), 314(A,C), 385(T,C), 868 (G,A), 907(C,T), 965(A,G), 970(T,A), 1784 (G,C), 2017(T,G), 2172(C,A), 2284(T,C), 2308(T,C), 2323(T,G), 2344(T,G), 2604(G,A), 2974(A,T), 2903(A,G), 2995(C,T), 3274(C,T), 3581(A,C), 3991(A,C), 4201(G,T), 4434(C,T), 4551(A,C), 4606(C,A), 4947(T,C), 4978(C,T), 4982(G,T), 5051(G,T). PolyA sites are located at nucleotides 4450, 4550, 4885, and 5082. PolyA signals are located at 4420-4424, 4515-4520, 4529-4534, 4866-4871, 5032-5037, 5053-5058. TEM 10, 20, and 40 derive from the same gene but are different isoforms having different lengths.

[66] TEM 11 is Nidogen /Entactin. It is a secreted protein which has a signal sequence at residues 1-28. TEM 11 is an extracellular matrix protein which is a component of a basement membrane. TEM 11 binds to laminin and collagen IV and other extracellular matrix proteins. TEM 11 regulates capillary formation and is involved in tissue remodelling. Variations have been observed at nucleotides 4265(T,C), 4267(G,C,T), and 4738(T,G). Nidogen can be assayed by its effect on the morphology of astrocytes. See Grimpe et al., GLIA 28:138-49, 1999.

[67] TEM 12 is the alpha 3 chain of collagen type VI. It has a signal sequence at residues 1-25. A secreted protein, TEM 12 is an extrallcellular matrix protein. TEM 12 has a splice variant. TEM 12 is a major constituent of vascular subendothelium and is involved in tissue remodeling. It regulates platelet activation and aggregation. Alternatively spliced domains are located at nucleotides 347-964, 965-1567, 2153-3752, and 4541-5041.

[68] TEM 13 is also known as Thy -1 glycoprotein. It has both a signal sequence (at residues 1-19) and a transmembrane domain (at residues 143-159). Residues 131-161 are removed in a matured form of the protein. The extracellular region of the protein is resudes 1- 142 or residues 1-130. TEM 13 has a glycosyl phosphatidylinositol (GPI) anchor at residue 130 anchoring it to the membrane. TEM 13 is detectale in its soluble form in human serum. TEM 13 is reported to be a marker for activated endothelial cells (a marker of adult but not embryonic angiogenesis). TEM 13 on vascular endothelial cells may function as a possible vascular permeability modulator. Antibody to Thy-1 is a mitogenic signal for the CD4+CD45+ and CD8+CD45+ cells, but fails to induce proliferation in the CD45- T cells. Pingel et al., International Immunology 6:169-78, 1994. Thy-1 can be assayed as an inhibitor of such signal.

[69] TEM 14 is also known as cystatin S. It is a secreted protein with a signal sequence at residues 1-20 and an extracelllular region at residues 1-141. It is a cysteine protease inhibitor. TEM 14 may regulate cysteine protease function involved in angiogenesis and tissue remodeling. TEM14 is an inhibitor of the activity of papain and such inhibition can be assayed. Hiltke et al., J. Dental Research 78:1401-9, 1999.

[70] TEM 15 is collagen type III, alpha 1 (COL3A1). It has a signal sequence (residues 1-23) and is secreted. Type III collagen binds to von Willebrand factor. It is involved in cell-cell adhesion, proliferation, and migration activities. Variants at nucleotides 2104(C,A), 2194(G,A), 2346(C,T), 2740(C,T), 3157(T), 3468(G), 3652(T), 3666(C), 3693(C), 3755(G), 3756(T), 3824(C), 4546(A, G), 4661(G), 4591(C,T), 4665(C), 5292(C), 5293(C), and 5451 (A) have been observed.

[71] TEM 16 is a tensin homolog which is apparently an intracellular protein. It may have splice variants or isoforms. One form with 1704 amino acids has a region at the N-terminal domain which is similar to a tumor suppressor protein,

phosphatase and tensin homolog (PTEN). Tensin is a focal adhesion molecule that binds to actins and phosphorylated proteins. It is involved in cell migration linking signal tranduction pathways to the cytoskeleton. PTEN regulates tumor induced angiogenesis.

[72] TEM 17 (BSC-TEM 7) has a signal sequence which includes residues 1-18 and a transmembrane domain at residues 427-445. It is a cell surface marker with an extracellular region comprising residues 1-426. It has homologs in both mouse and *C. elegans*. Residues 137-244 share weak homology with nidogen; residues 280-344 share homology to PSI domains found in plexin, semaphorins and integrin beta subunits. Variants have been observed at nucleotides 1893(A,G), 1950(C,G), 2042(A,G), and 2220(G,A). In mouse TEM 17 the signal sequence includes residues 1-19.

[73] TEM 19 was originally reported to be tumor endothelial marker 8, *i.e.*, BSC-TEM 8. It has a signal sequence at residues 1-27 and a transmembrane domain at residues 322-343. It is a cell surface protein having an extracellular region at residues 1-321.TEM 19 has a von Willebrand Factor (vWF) A domain at residues 44-216; a domain at residues 34-253 which is found in leukointegrin alpha D chain; and a domain at residues 408-560 found in PRAM-1 or adaptor molecule –1 of the vinculin family. TEM 19's function is adhesion related. vonWillibrand Factor domains are typically involved in a variety of functions including vascular processes. TEM 19 may play a role in the migration of vascular endothelial cells. The mouse ortholog has a predicted signal peptide at residues 1-27.

[74] TEM 20 is collagen type I, alpha 2 (COL1A2). It has a signal sequence at residues 1-22 and is a secreted extracellular matrix protein. TEM 20 induces endothelial tube formation *in vitro* and is involved in tissue remodeling. Variants have been observed at nucleotides 226(T,C), 314(A,C), 385(T,C), 868 (G,A), 907(C,T), 965(A,G), 970(T,A), 1784(G,C), 2017(T,G), 2172(C,A), 2284(T,C),

2308(T,C), 2323(T,G), 2344(T,G), 2604(G,A), 2794(A,T), 2903(A,G), 2995(C,T), 3274(C,T), 3581(A,C), 3991(A,C), 4201(G,T), 4434(C,T), 4551(A,C), 4606(C,A), 4895-4901(–, GGACAAC), 4947(T,C), 4978(C,T), 4982(G,T), 5051(G,T).

[75] TEM 21 is a Formin – like protein homolog which is an intracellular protein. Formin related proteins interact with Rho family small GTPases, profilin, and other actin associated proteins. Formin-binding proteins bind to FH1 domains with their WW domains. TEM 21 has a proline rich FH1 domain at residues 221-449. Formin related proteins play crucial roles in morphogenesis, cell polarity , cytokinesis and reorganization of the actin cytoskeleton. They may also regulate apoptosis, cell adhesion and migration.

[76] TEM 22 is an endocytic receptor in the macrophage mannose receptor family. It has both a signal sequence at residues 1-30 and a transmembrane domain at residues 1415-1435, and resides on the cell surface. Its extracellular domain is amino acids 1- 1414. TEM 22 may be present as a soluble (secreted) form and act as an inhibitor. It may bind secreted phopholipase A2 (sPLA2) and mediate biological responses elicited by sPLA2. TEM 22 may have endocytic properties for sPLA2 and mediate endocytosis for endothelial related proteins. It may promote cell adhesion and be involved in cell-cell communication. Variations have been observed at nucleotide 5389 (A, G). TEM 22 mediates uptake of micro-organisms and host-derived glycoproteins. Groger et al., J. Immunology 165:5428-34, 2000.

[77] TEM 24 is tensin, an intracellular protein. It is a focal adhesion molecule that binds to actin filaments and interacts with phosphotyrosine containing proteins. It may mediate kinase signaling activities and regulate cellular transformation. Variations have been observed at nucleotides 2502 (A, G), 2622(A, G), 6027(A, G). TEM24 binds to actin filaments and interacts with phosphotyrosine-containing proteins. Chen et al., Biochem. J. 351 Pt2:403-11,

2000. TEM24 also binds to phosphoinositide3-kinase. Auger et al., J. Bio. Chem. 271:23452-7, 1996 TEM 24 also binds to nuclear protein p130. Lo et al., Bioessays 16:817-23, 1994.

[78] TEM 25 is Bone morphogenic protein 1 (BMP-1) which has a signal sequence at residues 1-22. It is a secreted protein. There are at least 6 isoforms of BMP-1 as well as splice variants which add carboxy terminal CUB domains and an additional EGF domain. TEM 25 is a metalloprotease enzyme. It cleaves the C-terminal propeptide of collagen type I, II and III and laminin 5 gamma 2 , proteins that are important for vascular processes. It is involved in cartilage formation. Variations have been observed at nucleotides 3106(C,T), 3248(G,A), 3369(G,A). TEM 25 cleave probiglycan at a single site, removing the propeptide and producing a biglycan molecule with an NH(2) terminus identical to that of the mature form found in tissues. Sctt et al., J. Biol. Chem. 275:30504-11, 2000. Laminin alpha 3 and gamma2 short chains are substraates of TEM 25. Amano et al., J. Biol. Chem. 275:22728-35, 2000.

[79] TEM 27 is known as Slit homolog 3, a secreted protein with a signal sequence at residues 1-27. TEM 27 is a secreted guide protein involved in migration, repulsion and patterning. It interacts with "round about" receptors (Robo receptors). TEM 27 may interact with extracellular matrix (ECM) proteins and is involved in cell adhesion. Variations have been observed at nucleotides 4772 (C,T)

[80] TEM 28 is similar to mouse nadrin (neuron specific GTPase activiating protein). TEM 28 is an intracellular protein with a RhoGAP domain. The RhoGAP domain activates RhoA, Rac1, and Cdc42 GTPases. It is involved in the reorganization of actin filaments and enhancing exocytosis. It may also be involved in cell signalling. Variations have been observed at nucleotide 3969 (A,C),

[81] TEM 29 is protein tyrosine phosphatase type IVA, member 3, isoform 1, an intracellular protein. It has alternate splice variants. TEM 29 belongs to a small class of prenylated protein tyrosine phosphatases (PTPs). It may be membrane associated by prenylation. PTPs are cell signaling molecules and play regulatory roles in a variety of cellular processes and promote cell proliferation. PTP PRL-3 regulates angiotensin –II induced signaling events.

[82] TEM 30 is integrin alpha 1, a cell surface protein having both a signal sequence (residues 1-28) and a transmembrane domain (residues 1142--1164). Its extracellular region includes amino acids 1-1141. TEM 30 is a receptor for laminin and collagen. It mediates a variety of adhesive interactions. TEM 30 is abundantly expressed on microvascular endothelial cells. It stimulates endothelial cell proliferation and vascularization. TEM 30 may regulate angiostatin production. Variations have been observed at nucleotide 418 (C,T). TEM 30 activates the Ras/Shc/mitogen-activated protein kinase pathway promoting fibroblast cell proliferation. It also acts to inhibit collagen and metalloproteinase synthesis. Pozzi et al., Proc. Nat. Acad. Sci. USA 97:2202-7, 2000,

[83] TEM 31 is Collagen IV alpha 1 (COL4A1) a secreted protein with a at residues 1-27. TEM 31 is a component of the basement membrane. It binds to alpha3 beta 1integrin and promotes integrin mediated cell adhesion. Non-collagenous domains of type IV subunits are involved in tumoral angiogenesis. TEM 31 is involved in tissue remodeling. Variations have been observed at nucleotide 4470 (C,T)

[84] TEM 33 is methylmalonyl Co-A Mutase a protein which is localized in the mitochondrial matrix. It degrades several amino acids, odd-numbered-acid fatty acids, and cholesterol to the tricarboylic acid cycle. A defect in TEM 33 causes a fatal disorder in organic acid metabolism termed methylmalonic acidurea. Variations have been observed at nucleotides 1531(G,A), 1671(G,A), 2028(T,C), 2087(G,A), 2359(A,G), 2437(C,A), 2643(G,C), 2702(G,C). TEM 33

converts L-methylmalonyl CoA to succinyl CoA. This reaction can be assayed as is known in the art. See, e.g., Clin. Chem. 41(8 Pt I):1164-70, 1995.

[85] TEM 36 is collagen type XII, alpha1 (COL12A1), an extracellular matrix protein having a signal sequence at residues 1-23 or 24. TEM 36 has von Willebrand Factor (vWF) type A domains, Fibronectin type III domains, and thrombospondin N-terminal like domain. TEM 36 is expressed in response to stress environment. TEM 36 may organize extracellular matrix architecture and be involved in matrix remodeling. There are two isoforms of the protein, a long form and a short form. The short form is missing amino acids 25-1188, and therefore nucleotides 73 to 3564. Both forms share the signal sequence and are therefore both secreted.

[86] TEM 37 is lumican, an extracellular matrix sulfated proteoglycan having a signal sequence at residues 1-18. Lumican interacts with proteins that are involved in matrix assembly such as collagen type I and type VI; it is involved in cell proliferation and tissue morphogenesis. Lumican plays an important role in the regulation of collagen fiber assembly. Variations have been observed at nucleotides 1021(G,T), 1035(A,G), 1209(A,G), 1259(A,C), 1418(C,A), 1519(T,A). TEM 37 is a binding partner of TGF-β. See FASEB J. 15:559-61, 2000. One assay that can be used to determine TEM 37 activity is a collagen fibril formation/sedimentation assay. Svensson et al., FEBS Letters 470:178-82, 2000.

[87] TEM 38 is collagen type I, alpha 1 (COL1A1), an extracellular matrix protein having a signal sequence at residues 1-22. Type I collagen promotes endothelial cell migration and vascularization and induces tube formation and is involved in tissue remodelling. Telopeptide derivative is used as a marker for malignancy and invasion for certain cancer types. Variations have been observed at nucleotides 296(T,G), 1810(G,A), 1890(G,A), 2204(T,A), 3175(G,C), 3578(C,T), 4298(C,T), 4394(A,T), 4410(A,C), 4415(C.A), 4419 (A,T), 4528(C,A), 4572(G,T), 4602(T,C), 5529(T,C), 5670(C,T), 5985(C,T), 6012(C,T).

[88] TEM 39 is transforming growth factor β –3 (TGF-beta3). It has a signal sequence at residues 1-23. It is a secreted protein. TEM 39 regulates cell growth and differentiation. TGF-beta isoforms play a major role in vascular repair processes and remodeling. Variations have been observed at nucleotide 2020(G,T).

[89] TEM 41 is similar to Olfactomedin like protein. It appears to be an intracellular protein, having no obvious predicted signal sequence. Olfactomedin is the major glycoprotein of the extracellular mucous matrix of olfactory neuroepithelium. TEM 41 shares homology with latrophilin (extracellular regions) which has cell-adhesive type domains. TEM 41 may be involved in adhesive function.

[90] **TEM 42 is MSTP032 protein, a cell surface protein having a trasmembrane domain at residues 42-61. Its function is unknown and it shares little homology with other proteins. Variations have been observed at nucleotides 418(A,T), 724(C,A).**

[91] TEM 44 is a hypothetical protein FLJ11190 (NM_018354) which has two predicted transmembrane domains at residues 121-143 and 176 –1 97. Residues 144-175 may form an extracellular region. TEM 44's function is not known and shares no homology to other known proteins.

[92] TEM 45 is tropomyosin 1 (alpha), a protein which is intracellular. It forms dimers with a beta subunit. It influences actin function. TEM 45 may be involved in endothelial cell cytoskeletal rearrangement. Variations have been observed at nucleotides 509(A,C), 621(A,C), 635(T,G), 642(C,G), 1059(G,T).

[93] TEM 46 is peanut-like 1 protein/septin 5, which belongs to the septin family. Proteins in the septin family bind to GTP and phosphatidylinositol 4,5-bisphosphate. They are involved in the signal tranduction cascades controlling cytokinesis and cell division.

[94] NEM 4 is a member of the small inducible cytokine subfamily A (cys-cys), member 14 (SCYA14). NEM4 is a secreted protein characterized by two adjacent cysteine residues. One isoform lacks internal 16 amino acids compared to isoform 2.

[95] NEM 22 shares homology with guanylate kinase-interacting protein 1Maguin-1. It is a membrane associated protein.

[96] NEM 23 is human signaling lymphocytic acitavation molecule (SLAM). It has a signal sequence at residues 1-20. The extracellular domain may reside at residues 21-237. There is a secreted isoform of the protein.

[97] NEM33 is netrin 4. It induces neurite outgrowth and promotes vascular development. At higher concentration, neurite outgrowth is inhibited.

[98] ECs represent only a minor fraction of the total cells within normal or tumor tissues, and only those EC transcripts expressed at the highest levels would be expected to be represented in libraries constructed from unfractionated tissues. The genes described in the current study should therefore provide a valuable resource for basic and clinical studies of human angiogenesis in the future. Genes which have been identified as tumor endothelial markers (TEMs) correspond to tags shown in SEQ ID NOS: 94-139, 173-176, 180-186. Genes which have been identified as normal endothelial markers (NEMs) correspond to tags shown in SEQ ID NOS: 140-172. Genes which have been identified as pan-endothelial markers (PEMs) *i.e.,* expressed in both tumor and normal endothelial cells correspond to tags shown in SEQ ID NOS: 1-93. Genes which have been previously identified as being expressed predominantly in the endothelium correspond to PEM tags shown in SEQ ID NOS: 1-6, 8, 10-15. Markers in each class can be used interchangeably for some purposes.

[99] Isolated and purified nucleic acids, according to the present invention are those which are not linked to those genes to which they are linked in the human genome. Moreover, they are not present in a mixture such as a library containing a multitude of distinct sequences from distinct genes. They may be, however, linked to other genes such as vector sequences or sequences of other genes to which they are not naturally adjacent. Tags disclosed herein, because of the way that they were made, represent sequences which are 3' of the 3' most restriction enzyme recognition site for the tagging enzyme used to generate the SAGE tags. In this case, the tags are 3' of the most 3' most NlaIII site in the cDNA molecules corresponding to mRNA. Nucleic acids corresponding to tags may be RNA, cDNA, or genomic DNA, for example. Such corresponding nucleic acids can be determined by comparison to sequence databases to determine sequence identities. Sequence comparisons can be done using any available technique, such as BLAST, available from the National Library of Medicine, National Center for Biotechnology Information. Tags can also be used as hybridization probes to libraries of genomic or cDNA to identify the genes from which they derive. Thus, using sequence comparisons or cloning, or combinations of these methods, one skilled in the art can obtain full-length nucleic acid sequences. Genes corresponding to tags will contain the sequence of the tag at the 3' end of the coding sequence or of the 3' untranslated region (UTR), 3' of the 3' most recognition site in the cDNA for the restriction endonuclease which was used to make the tags. The nucleic acids may represent either the sense or the anti-sense strand. Nucleic acids and proteins althought disclosed herein with sequence particularity, may be derived from a single individual. Allelic variants which occur in the population of humans are including within the scope of such nucleic acids and proteins. Those of skill in the art are well able to identify allelic variants as being the same gene or protein Given a nucleic acid, one of ordinary skill in the art can readily determine an open reading frame present, and consequently the sequence of a polypeptide encoded by the open reading frame and, using techniques well known in the art, express such protein in a suitable

host. Proteins comprising such polypeptides can be the naturally occurring proteins, fusion proteins comprising exogenous sequences from other genes from humans or other species, epitope tagged polypeptides, etc. Isolated and purified proteins are not in a cell, and are separated from the normal cellular constituents, such as nucleic acids, lipids, etc. Typically the protein is purified to such an extent that it comprises the predominant species of protein in the composition, such as greater than 50, 60 70, 80, 90, or even 95% of the proteins present.

[100] Using the proteins according to the invention, one of ordinary skill in the art can readily generate antibodies which specifically bind to the proteins. Such antibodies can be monoclonal or polyclonal. They can be chimeric, humanized, or totally human. Any functional fragment or derivative of an antibody can be used including Fab, Fab', Fab2, Fab'2, and single chain variable regions. So long as the fragment or derivative retains specificity of binding for the endothelial marker protein it can be used. Antibodies can be tested for specificity of binding by comparing binding to appropriate antigen to binding to irrelevant antigen or antigen mixture under a given set of conditions. If the antibody binds to the appropriate antigen at least 2, 5, 7, and preferably 10 times more than to irrelevant antigen or antigen mixture then it is considered to be specific.

[101] Techniques for making such partially to fully human antibodies are known in the art and any such techniques can be used. According to one particularly preferred embodiment, fully human antibody sequences are made in a transgenic mouse which has been engineered to express human heavy and light chain antibody genes. Multiple strains of such transgenic mice have been made which can produce different classes of antibodies. B cells from transgenic mice which are producing a desirable antibody can be fused to make hybridoma cell lines for continuous production of the desired antibody. See for example, Nina D. Russel, Jose R. F. Corvalan, Michael L. Gallo, C. Geoffrey Davis, Liise-Anne Pirofski. Production of Protective Human Antipneumococcal Antibodies by Transgenic Mice with Human Immunoglobulin Loci *Infection and Immunity* April 2000, p.

1820-1826; Michael L. Gallo, Vladimir E. Ivanov, Aya Jakobovits, and C. Geoffrey Dåvis. The human immunoglobulin loci introduced into mice: V (D) and J gene segment usage similar to that of adult humans *European Journal of Immunology* 30: 534-540, 2000; Larry L. Green. Antibody engineering via genetic engineering of the mouse: XenoMouse strains are a vehicle for the facile generation of therapeutic human monoclonal antibodies *Journal of Immunological Methods 231* 11-23, 1999; Yang X-D, Corvalan JRF, Wang P, Roy CM-N and Davis CG. Fully Human Anti-interleukin-8 Monoclonal Antibodies: Potential Therapeutics for the Treatment of Inflammatory Disease States. *Journal of Leukocyte Biology* Vol. 66, pp401-410 (1999); Yang X-D, Jia X-C, Corvalan JRF, Wang P, CG Davis and Jakobovits A. Eradication of Established Tumors by a Fully Human Monoclonal Antibody to the Epidermal Growth Factor Receptor without Concomitant Chemotherapy. *Cancer Research* Vol. 59, Number 6, pp1236-1243 (1999) ; Jakobovits A. Production and selection of antigen-specific fully human monoclonal antibodies from mice engineered with human Ig loci. *Advanced Drug Delivery Reviews* Vol. 31, pp: 33-42 (1998); Green L and Jakobovits A. Regulation of B cell development by variable gene complexity in mice reconstituted with human immunoglobulin yeast artificial chromosomes. *J. Exp. Med.* Vol. 188, Number 3, pp: 483-495 (1998); Jakobovits A. The long-awaited magic bullets: therapeutic human monoclonal antibodies from transgenic mice. *Exp. Opin. Invest. Drugs* Vol. 7(4), pp : 607-614 (1998) ; Tsuda H, Maynard-Currie K, Reid L, Yoshida T, Edamura K, Maeda N, Smithies O, Jakobovits A. Inactivation of Mouse HPRT locus by a 203-bp retrotransposon insertion and a 55-kb gene-targeted deletion: establishment of new HPRT-Deficient mouse embryonic stem cell lines. *Genomics* Vol. 42, pp: 413-421 (1997) ; Sherman-Gold, R. Monoclonal Antibodies: The Evolution from '80s Magic Bullets To Mature, Mainstream Applications as Clinical Therapeutics. *Genetic Engineering* News Vol. 17, Number 14 (August 1997); Mendez M, Green L, Corvalan J, Jia X-C, Maynard-Currie C, Yang X-d, Gallo M, Louie D, Lee D, Erickson K, Luna J, Roy C, Abderrahim H, Kirschenbaum F, Noguchi M,

Smith D, Fukushima A, Hales J, Finer M, Davis C, Zsebo K, Jakobovits A. Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice. *Nature Genetics* Vol. 15, pp: 146-156 (1997); Jakobovits A. Mice engineered with human immunoglobulin YACs: A new technology for production of fully human antibodies for autoimmunity therapy. *Weir's Handbook of Experimental Immunology, The Integrated Immune System* Vol. IV, pp: 194.1-194.7 (1996) ; Jakobovits A. Production of fully human antibodies by transgenic mice. *Current Opinion in Biotechnology* Vol. 6, No. 5, pp: 561-566 (1995) ; Mendez M, Abderrahim H, Noguchi M, David N, Hardy M, Green L, Tsuda H, Yoast S, Maynard-Currie C, Garza D, Gemmill R, Jakobovits A, Klapholz S. Analysis of the structural integrity of YACs comprising human immunoglobulin genes in yeast and in embryonic stem cells. *Genomics* Vol. 26, pp: 294-307 (1995); Jakobovits A. YAC Vectors: Humanizing the mouse genome. *Current Biology* Vol. 4, No. 8, pp: 761-763 (1994); Arbones M, Ord D, Ley K, Ratech H, Maynard-Curry K, Otten G, Capon D, Tedder T. Lymphocyte homing and leukocyte rolling and migration are impaired in L-selectin-deficient mice. *Immunity* Vol. 1, No. 4, pp: 247-260 (1994); Green L, Hardy M, Maynard-Curry K, Tsuda H, Louie D, Mendez M, Abderrahim H, Noguchi M, Smith D, Zeng Y, et. al. Antigen-specific human monoclonal antibodies from mice engineered with human Ig heavy and light chain YACs. *Nature Genetics* Vol. 7, No. 1, pp: 13-21 (1994); Jakobovits A, Moore A, Green L, Vergara G, Maynard-Curry K, Austin H, Klapholz S. Germ-line transmission and expression of a human-derived yeast artificial chromosome. *Nature* Vol. 362, No. 6417, pp: 255-258 (1993) ; Jakobovits A, Vergara G, Kennedy J, Hales J, McGuinness R, Casentini-Borocz D, Brenner D, Otten G. Analysis of homozygous mutant chimeric mice: deletion of the immunoglobulin heavy-chain joining region blocks B-cell development and antibody production. *Proceedings of the National Academy of Sciences USA* Vol. 90, No. 6, pp: 2551-2555 (1993); Kucherlapati et al., U.S. 6,1075,181.

[102] Antibodies can also be made using phage display techniques. Such techniques can be used to isolate an initial antibody or to generate variants with altered specificity or avidity characteristics. Single chain Fv can also be used as is convenient. They can be made from vaccinated transgenic mice, if desired. Antibodies can be produced in cell culture, in phage, or in various animals, including but not limited to cows, rabbits, goats, mice, rats, hamsters, guinea pigs, sheep, dogs, cats, monkeys, chimpanzees, apes.

[103] Antibodies can be labeled with a detectable moiety such as a radioactive atom, a chromophore, a fluorophore, or the like. Such labeled antibodies can be used for diagnostic techniques, either *in vivo*, or in an isolated test sample. Antibodies can also be conjugated, for example, to a pharmaceutical agent, such as chemotherapeutic drug or a toxin. They can be linked to a cytokine, to a ligand, to another antibody. Suitable agents for coupling to antibodies to achieve an anti-tumor effect include cytokines, such as interleukin 2 (IL-2) and Tumor Necrosis *Factor* (TNF); photosensitizers, for use in photodynamic therapy, including aluminum (III) phthalocyanine tetrasulfonate, hematoporphyrin, and phthalocyanine; radionuclides, such as iodine-131 (^{131}I), yttrium-90 (^{90}Y), bismuth-212 (^{212}Bi), bismuth-213 (^{213}Bi), technetium-99m (^{99m}Tc), rhenium-186 (^{186}Re), and rhenium-188 (^{188}Re); antibiotics, such as doxorubicin, adriamycin, daunorubicin, methotrexate, daunomycin, neocarzinostatin, and carboplatin; bacterial, plant, and other toxins, such as diphtheria toxin, pseudomonas exotoxin A, staphylococcal enterotoxin A, abrin-A toxin, ricin A (deglycosylated ricin A and native ricin A), TGF-alpha toxin, cytotoxin from chinese cobra (naja naja atra), and gelonin (a plant toxin); ribosome inactivating proteins from plants, bacteria and fungi, such as restrictocin (a ribosome inactivating protein produced by *Aspergillus restrictus*), saporin (a ribosome inactivating protein from *Saponaria officinalis*), and RNase; tyrosine kinase inhibitors; ly207702 (a difluorinated purine nucleoside); liposomes containing antitumor agents (*e.g.*,

antisense oligonucleotides, plasmids which encode for toxins, methotrexate, etc.); and other antibodies or antibody fragments, such as F(ab).

[104] Those of skill in the art will readily understand and be able to make such antibody derivatives, as they are well known in the art. The antibodies may be cytotoxic on their own, or they may be used to deliver cytotoxic agents to particular locations in the body. The antibodies can be administered to individuals in need thereof as a form of passive immunization.

[105] Characterization of extracellular regions for the cell surface and secreted proteins from the protein sequence is based on the prediction of signal sequence, transmembrane domains and functional domains. Antibodies are preferably specifically immunoreactive with membrane associated proteins, particularly to extracellular domains of such proteins or to secreted proteins. Such targets are readily accessible to antibodies, which typically do not have access to the interior of cells or nuclei. However, in some applications, antibodies directed to intracellular proteins may be useful as well. Moreover, for diagnostic purposes, an intracellular protein may be an equally good target since cell lysates may be used rather than a whole cell assay.

[106] Computer programs can be used to identify extracellular domains of proteins whose sequences are known. Such programs include SMART software (Schultz et al., Proc. Natl. Acad. Sci. USA *95:* 5857-5864, 1998) and Pfam software (Bateman et al., Nucleic acids Res. *28:* 263-266, 2000) as well as PSORTII. Typically such programs identify transmembrane domains; the extracellular domains are identified as immediately adjacent to the transmembrane domains. Prediction of extracellular regions and the signal cleavage sites are only approximate. It may have a margin of error + or – 5 residues. Signal sequence can be predicted using three different methods (Nielsen et al, *Protein Engineering* 10: 1-6 ,1997, Jagla et. al, Bioinformatics 16: 245-250 , 2000, Nakai, K and Horton, P. Trends in Biochem. Sci. 24:34-35, 1999) for greater accuracy.

Similarly transmembrane (TM) domains can be identified by multiple prediction methods. (Pasquier, et. al, Protein Eng. 12:381-385, 1999, Sonnhammer et al., In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p. 175-182 , Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998 , Klein, et.al, Biochim. Biophys. Acta, 815:468, 1985, Nakai and Kanehisa Genomics, 14: 897-911 , 1992). In ambiguous cases, locations of functional domains in well characterized proteins are used as a guide to assign a cellular localization.

[107] Putative functions or functional domains of novel proteins can be inferred from homologous regions in the database identified by BLAST searches (Altschul et. al. Nucleic Acid Res. 25: 3389-3402, 1997) and/or from a conserved domain database such as Pfam (Bateman et.al, Nucleic Acids Res. 27:260-262 1999) BLOCKS (Henikoff, et. al, Nucl. Acids Res. 28:228-230, 2000) and SMART (Ponting, et. al, Nucleic Acid Res. 27,229-232, 1999). Extracellular domains include regions adjacent to a transmembrane domain in a single transmembrane domain protein (out-in or type I class). For multiple transmembrane domains proteins, the extracellular domain also includes those regions between two adjacent transmembrane domains (in-out and out-in). For type II transmembrane domain proteins, for which the N-terminal region is cytoplasmic, regions following the transmembrane domain is generally extracellular. Secreted proteins on the other hand do not have a transmembrane domain and hence the whole protein is considered as extracellular.

[108] Membrane associated proteins can be engineered to delete the transmembrane domains, thus leaving the extracellular portions which can bind to ligands. Such soluble forms of transmembrane receptor proteins can be used to compete with natural forms for binding to ligand. Thus such soluble forms act as inhibitors. and can be used therapeutically as anti-angiogenic agents, as diagnostic tools for the quantification of natural ligands, and in assays for the identification of small molecules which modulate or mimic the activity of a TEM:ligand complex.

[109] Alternatively, the endothelial markers themselves can be used as vaccines to raise an immune response in the vaccinated animal or human. For such uses, a protein, or immunogenic fragment of such protein, corresponding to the intracellular, extracellular or secreted TEM of interest is administered to a subject. The immogenic agent may be provided as a purified preparation or in an appropriately expressing cell. The administration may be direct, by the delivery of the immunogenic agent to the subject, or indirect, through the delivery of a nucleic acid encoding the immunogenic agent under conditions resulting in the expression of the immunogenic agent of interest in the subject. The TEM of interest may be delivered in an expressing cell, such as a purified population of tumor endothelial cells or a populations of fused tumor endothelial and dendritic cells. Nucleic acids encoding the TEM of interest may be delivered in a viral or non-viral delivery vector or vehicle. Non-human sequences encoding the human TEM of interest or other mammalian homolog can be used to induce the desired immunologic response in a human subject. For several of the TEMs of the present invention, mouse, rat or other ortholog sequences are described herein or can be obtained from the literature or using techniques well within the skill of the art.

[110] Endothelial cells can be identified using the markers which are disclosed herein as being endothelial cell specific. These include the human markers identified by SEQ ID NOS: 1-172, *i.e.*, the normal, pan-endothelial, and the tumor endothelial markers. Homologous mouse markers include tumor endothelial markers of SEQ ID NO: 182-186 and 190-194. Antibodies specific for such markers can be used to identify such cells, by contacting the antibodies with a population of cells containing some endothelial cells. The presence of cross-reactive material with the antibodies identifies particular cells as endothelial. Similarly, lysates of cells can be tested for the presence of cross-reactive material. Any known format or technique for detecting cross-reactive material can be used including, immunoblots, radioimmunoassay, ELISA, immunoprecipitation, and

immunohistochemistry. In addition, nucleic acid probes for these markers can also be used to identify endothelial cells. Any hybridization technique known in the art including Northern blotting, RT-PCR, microarray hybridization, and in situ hybridization can be used.

[111] One can identify tumor endothelial cells for diagnostic purposes, testing cells suspected of containing one or more TEMs. One can test both tissues and bodily fluids of a subject. For example, one can test a patient's blood for evidence of intracellular and membrane associated TEMs, as well as for secreted TEMs. Intracellular and/or membrane associated TEMs may be present in bodily fluids as the result of high levels of expression of these factors and/or through lysis of cells expressing the TEMs.

[112] Populations of various types of endothelial cells can also be made using the antibodies to endothelial markers of the invention. The antibodies can be used to purify cell populations according to any technique known in the art, including but not limited to fluorescence activated cell sorting. Such techniques permit the isolation of populations which are at least 50, 60, 70, 80, 90, 92, 94, 95, 96, 97, 98, and even 99 % the type of endothelial cell desired, whether normal, tumor, or pan-endothelial. Antibodies can be used to both positively select and negatively select such populations. Preferably at least 1, 5, 10, 15, 20, or 25 of the appropriate markers are expressed by the endothelial cell population.

[113] Populations of endothelial cells made as described herein, can be used for screening drugs to identify those suitable for inhibiting the growth of tumors by virtue of inhibiting the growth of the tumor vasculature.

[114] Populations of endothelial cells made as described herein, can be used for screening candidate drugs to identify those suitable for modulating angiogenesis, such as for inhibiting the growth of tumors by virtue of inhibiting the growth of endothelial cells, such as inhibiting the growth of the tumor or other undesired

vasculature, or alternatively, to promote the growth of endothelial cells and thus stimulate the growth of new or additional large vessel or microvasculature.

[115] Inhibiting the growth of endothelial cells means either regression of vasculature which is already present, or the slowing or the absence of the development of new vascularization in a treated system as compared with a control system. By stimulating the growth of endothelial cells, one can influence development of new (neovascularization) or additional vasculature development (revascularization). A variety of model screen systems are available in which to test the angiogenic and/or anti-angiogenic properties of a given candidate drug. Typical tests involve assays measuring the endothelial cell response, such as proliferation, migration, differentiation and/or intracellular interaction of a given candidate drug. By such tests, one can study the signals and effects of the test stimuli. Some common screens involve measurement of the inhibition of heparanase, endothelial tube formation on Matrigel, scratch induced motility of endothelial cells, platelet-derived growth factor driven proliferation of vascular smooth muscle cells, and the rat aortic ring assay (which provides an advantage of capillary formation rather than just one cell type).

[116] Drugs can be screened for the ability to mimic or modulate, inhibit or stimulate, growth of tumor endothelium cells and/or normal endothelial cells. Drugs can be screened for the ability to inhibit tumor endothelium growth but not normal endothelium growth or survival. Similarly, human cell populations, such as normal endothelium populations or tumor endothelial cell populations, can be contacted with test substances and the expression of tumor endothelial markers and/or normal endothelial markers determined. Test substances which decrease the expression of tumor endothelial markers (TEMs) are candidates for inhibiting angiogenesis and the growth of tumors. Conversely, markers which are only expressed in normal endothelium but not in tumor endothelium (NEMs) can be monitored. Test substances which increase the expression of such NEMs in tumor endothelium and other human cells can be identified as candidate antitumor or

anti-angiogenic drugs In cases where the activity of a TEM or NEM is known, agents can be screened for their ability to decrease or increase the activity.

[117] For those tumor endothelial markers identified as containing transmembrane regions, it is desirable to identify drug candidates capable of binding to the TEM receptors found at the cell surface. For some applications, the identification of drug candidates capable of blocking the TEM receptor from its native ligand will be desired. For some applications, the identification of a drug candidate capable of binding to the TEM receptor may be used as a means to deliver a therapeutic or diagnostic agent. For other applications, the identification of drug candidates capable of mimicing the activity of the native ligand will be desired. Thus, by manipulating the binding of a transmembrane TEM receptor:ligand complex, one may be able to promote or inhibit further development of endothelial cells and hence, vascularization.

[118] For those tumor endothelial markers identified as being secreted proteins, it is desirable to identify drug candidates capable of binding to the secreted TEM protein. For some applications, the identification of drug candidates capable of interfering with the binding of the secreted TEM it is native receptor. For other applications, the identification of drug candidates capable of mimicing the activity of the native receptor will be desired. Thus, by manipulating the binding of the secreted TEM:receptor complex, one may be able to promote or inhibit futher development of endothelial cells, and hence, vascularization.

[119] Expression can be monitored according to any convenient method. Protein or mRNA can be monitored. Any technique known in the art for monitoring specific genes' expression can be used, including but not limited to ELISAs, SAGE, microarray hybridization, Western blots. Changes in expression of a single marker may be used as a criterion for significant effect as a potential pro-angiogenic, anti-angiogenic or anti-tumor agent. However, it also may be desirable to screen for test substances which are able to modulate the expression

of at least 5, 10, 15, or 20 of the relevant markers, such as the tumor or normal endothelial markers. Inhibition of TEM protein activity can also be used as a drug screen. Human and mouse TEMS can be used for this purpose.

[120] Test substances for screening can come from any source. They can be libraries of natural products, combinatorial chemical libraries, biological products made by recombinant libraries, etc. The source of the test substances is not critical to the invention. The present invention provides means for screening compounds and compositions which may previously have been overlooked in other screening schemes. Nucleic acids and the corresponding encoded proteins of the markers of the present invention can be used therapeutically in a variety of modes. NEMs, can be used to restrict, diminish, reduce, or inhibit proliferation of tumor or other abnormal or undesirable vasculature. TEMs can be used to stimulate the growth of vasculature, such as for wound healing or to circumvent a blocked vessel. The nucleic acids and encoded proteins can be administered by any means known in the art. Such methods include, using liposomes, nanospheres, viral vectors, non-viral vectors comprising polycations, etc. Suitable viral vectors include adenovirus, retroviruses, and sindbis virus. Administration modes can be any known in the art, including parenteral, intravenous, intramuscular, intraperitoneal, topical, intranasal, intrarectal, intrabronchial, etc.

[121] Specific biological antagonists of TEMs can also be used to therapeutic benefit. For example, antibodies, T cells specific for a TEM, antisense to a TEM, and ribozymes specific for a TEM can be used to restrict, inhibit, reduce, and/or diminish tumor or other abnormal or undesirable vasculature growth. Such antagonists can be administered as is known in the art for these classes of antagonists generally. Anti-angiogenic drugs and agents can be used to inhibit tumor growth, as well as to treat diabetic retinopathy, rheumatoid arthritis, psoriasis, polycystic kidney disease (PKD), and other diseases requiring angiogenesis for their pathologies.

[122] Mouse counterparts to human TEMS can be used in mouse cancer models or in cell lines or *in vitro* to evaluate potential anti-angiogenic or anti-tumor compounds or therapies. Their expression can be monitored as an indication of effect. Mouse TEMs are disclosed in SEQ ID NO: 182-186 and 190-194. Mouse TEMs can be used as antigens for raising antibodies which can be tested in mouse tumor models. Mouse TEMs with transmembrane domains are particularly preferred for this purpose. Mouse TEMs can also be ued as vaccines to raise an immunological response in a human to the human ortholog.

[123] The above disclosure generally describes the present invention. All references disclosed herein are expressly incorporated by reference. A more complete understanding can be obtained by reference to the following specific examples which are provided herein for purposes of illustration only, and are not intended to limit the scope of the invention.

EXAMPLE 1

Visualization of vasculature of colorectal cancers

[124] The endothelium of human colorectal cancer was chosen to address the issues of tumor angiogenesis, based on the high incidence, relatively slow growth, and resistance to anti-neoplastic agents of these cancers. While certain less common tumor types, such as glioblastomas, are highly vascularized and are regarded as good targets for anti-angiogenic therapy, the importance of angiogenesis for the growth of human colorectal cancers and other common solid tumor types is less well documented.

[125] We began by staining vessels in colorectal cancers using von Willebrand Factor (vWF) as a marker. In each of 6 colorectal tumors, this examination revealed a high density of vessels throughout the tumor parenchyma (Examples in Fig. 1 A and B). Interestingly, these analyses also substantiated the importance of these

vessels for tumor growth, as endothelium was often surrounded by a perivascular cuff of viable cells, with a ring of necrotic cells evident at the periphery (Example in Fig. 1A). Although these preliminary studies suggested that colon tumors are angiogenesis-dependent, reliable markers that could distinguish vessels in colon cancers from the vessels in normal colon are currently lacking. One way to determine if such markers exist is by analyzing gene expression profiles in endothelium derived from normal and neoplastic tissue.

EXAMPLE 2

Purification of endothelial cells

[126] Global systematic analysis of gene expression in tumor and normal endothelium has been hampered by at least three experimental obstacles. First, endothelium is enmeshed in a complex tissue consisting of vessel wall components, stromal cells, and neoplastic cells, requiring highly selective means of purifying ECs for analysis. Second, techniques for defining global gene expression profiles were not available until recently. And third, only a small fraction of the cells within a tumor are endothelial, mandating the development of methods that are suitable for the analysis of global expression profiles from relatively few cells.

[127] To overcome the first obstacle, we initially attempted to purify ECs from dispersed human colorectal tissue using CD31, an endothelial marker commonly used for this purpose. This resulted in a substantial enrichment of ECs but also resulted in contamination of the preparations by hematopoietic cells, most likely due to expression of CD31 by macrophages. We therefore developed a new method for purifying ECs from human tissues using P1H12, a recently described marker for ECs. Unlike CD31, P1H12 was specifically expressed on the ECs of both colorectal tumors and normal colorectal mucosa. Moreover, immunofluorescence staining of normal and cancerous colon with a panel of known cell surface endothelial markers (e.g. VE-cadherin, CD31 and CD34)

revealed that P1H12 was unique in that it stained all vessels including microvessels (see Fig. 2A and data not shown). In addition to selection with P1H12, it was necessary to optimize the detachment of ECs from their neighbors without destroying their cell surface proteins as well as to employ positive and negative affinity purifications using a cocktail of antibodies (Fig. 2B). The ECs purified from normal colorectal mucosa and colorectal cancers were essentially free of epithelial and hematopoietic cells as judged by RT-PCR (Fig. 2C) and subsequent gene expression analysis (see below).

EXAMPLE 3

Comparison of tumor and normal endothelial cell expression patterns

[128] To overcome the remaining obstacles, a modification of the Serial Analysis of Gene Expression (SAGE) technique was used. SAGE associates individual mRNA transcripts with 14 base pair tags derived from a specific position near their 3' termini. The abundance of each tag provides a quantitative measure of the transcript level present within the mRNA population studied. SAGE is not dependent on pre-existing databases of expressed genes, and therefore provides an unbiased view of gene expression profiles. This feature is particularly important in the analysis of cells that constitute only a small fraction of the tissue under study, as transcripts from these cells are unlikely to be well represented in extant EST databases. We adapted the SAGE protocol so that it could be used on small numbers of purified ECs obtained from the procedure outlined in Fig. 2B. A library of ~100,000 tags from the purified ECs of a colorectal cancer, and a similar library from the ECs of normal colonic mucosa from the same patient were generated. These ~193,000 tags corresponded to over 32,500 unique transcripts. Examination of the expression pattern of hematopoietic, epithelial and endothelial markers confirmed the purity of the preparations (Fig. 2D).

EXAMPLE 4

Markers of normal and tumor endothelium

[129] We next sought to identify Pan Endothelial Markers (PEMs), that is, transcripts that were expressed at significantly higher levels in both normal and tumor associated endothelium compared to other tissues. To identify such PEMs, tags expressed at similar levels in both tumor and normal ECs were compared to ~ 1.8 million tags from a variety of cell lines derived from tumors of non-endothelial origin. This simple comparison identified 93 transcripts that were strikingly EC-specific, i.e. expressed at levels at least 20-fold higher in ECs in vivo compared to non-endothelial cells in culture. The 15 tags corresponding to characterized genes which were most highly and specifically expressed in endothelium are shown in Table 1A. Twelve of these 15 most abundant endothelial transcripts had been previously shown to be preferentially expressed in endothelium , while the other 3 genes had not been associated with endothelium in the past (Table 1A). These data sets also revealed many novel PEMs, which became increasingly prevalent as tag expression levels decreased (Table 1B). For many of the transcripts, their endothelial origin was confirmed by SAGE analysis of ~401,000 transcripts derived from primary cultures of human umbilical vein endothelial cells (HUVEC) and human dermal microvascular endothelial cells (HMVEC) (Table 1 A and B). To further validate the expression of these PEMs in vivo, we developed a highly sensitive non-radioactive in situ hybridization method that allowed the detection of transcripts expressed at relatively low levels in frozen sections of human tissues. Two uncharacterized markers, PEM3 and PEM6, were chosen for this analysis. In each case, highly specific expression was clearly limited to vascular ECs in both normal and neoplastic tissues (Fig. 3 A and B and data not shown). These data also suggest that ECs maintained in culture do not completely recapitulate expression patterns observed in vivo. For example, Hevin and several other PEM's were expressed at high levels in both tumor and normal

ECs in vivo, but few or no transcripts were detected in cultured HUVEC or HMVEC (Table 1). The source of the Hevin transcripts was confirmed to be endothelium by in situ hybridization in normal and malignant colorectal tissue (Fig. 3C).

[130] Many of the markers reported in Table 1 were expressed at significantly higher levels than previously characterized genes commonly associated with ECs. For example, the top 25 markers were all expressed at greater than 200 copies per cell. In contrast, the receptors for VEGF (VEGFR-1 and VEGFR-2) were expressed at less than 20 copies per cell. Interestingly, VEGFR2 (KDR), which had previously been reported to be up-regulated in vessels during colon cancer progression , was found to be expressed in both normal and neoplastic colorectal tissue (Fig. 3 D and E). The lack of specificity of this gene was in accord with the SAGE data, which indicated that the VEGFR was expressed at 12 copies per cell in both normal and tumor endothelium.

EXAMPLE 5

Tumor *versus* normal endothelium

[131] We next attempted to identify transcripts that were differentially expressed in endothelium derived from normal or neoplastic tissues. This comparison revealed 33 tags that were preferentially expressed in normal-derived endothelium at levels at least 10-fold higher than in tumor-derived endothelium. Conversely, 46 tags were expressed at 10-fold or higher levels in tumor vessels. Because those transcripts expressed at higher levels in tumor endothelium are most likely to be useful in the future for diagnostic and therapeutic purposes, our subsequent studies focussed on this class. Of the top 25 tags most differentially expressed, 12 tags corresponded to 11 previously identified genes, one with an alternative polyadenylation site (see Table 2). Of these 10 genes, 6 have been recognized as markers associated with angiogenic vessels. The remaining 14 tags corresponded

to uncharacterised genes, most of which have only been deposited as ESTs (Table 2).

[132] To validate the expression patterns of these genes, we chose to focus on 9 Tumor Endothelial Markers (BSC-TEM 1-9; TEM 1, 2, 5, 9, 16, 17, 19, and 22) for which EST sequences but no other information was available (Table 2). These tags were chosen simply because they were among the most differentially expressed on the list and because we were able to obtain suitable probes. In many cases, this required obtaining near full-length sequences through multiple rounds of sequencing and cDNA walking (See accession numbers in Table 2). RT-PCR analysis was then used to evaluate the expression of the corresponding transcripts in purified ECs derived from normal and tumor tissues of two patients different from the one used to construct the SAGE libraries. As shown in Fig. 4 A, the vWF gene, expected to be expressed in both normal and tumor endothelium on the basis of the SAGE data as well as previous studies, was expressed at similar levels in normal and tumor ECs from both patients, but was not expressed in purified tumor epithelial cells. As expected, PEM2 displayed a pattern similar to vWF. In contrast, all 9 TEMs chosen for this analysis were prominently expressed in tumor ECs, but were absent or barely detectable in normal ECs (Table 3 and examples in Fig. 4A). It is important to note that these RT-PCR assays were extremely sensitive indicators of expression, and the absence of detectable transcripts in the normal endothelium, combined with their presence in tumor endothelial RNAs even when diluted 100-fold, provides compelling confirmatory evidence for their differential expression. These results also show that these transcripts were not simply expressed differentially in the ECs of the original patient, but were characteristic of colorectal cancer endothelium in general.

[133] It could be argued that the results noted above were compromised by the possibility that a small number of non-endothelial cells contaminated the cell populations used for SAGE and RT-PCR analyses, and that these non-endothelial

cells were responsible for the striking differences in expression of the noted transcripts. To exclude this possibility, we performed in situ hybridization on normal and neoplastic colon tissue. In every case where transcripts could be detected (BSC-TEM 1, 3, 4, 5, 7, 8, and 9; TEM 1, 5, 9, 17, and 19), they were specifically localized to ECs (Table 3 and examples in Fig. 4 B and C). Although caution must be used when interpreting negative in situ hybridization results, none of the TEMs were expressed in vascular ECs associated with normal colorectal tissue even though vWF and Hevin were clearly expressed (Table 3).

EXAMPLE 6

Tumor endothelium markers are expressed in multiple tumor types

[134] Were these transcripts specifically expressed in the endothelium within primary colorectal cancers, or were they characteristic of tumor endothelium in general? To address this question, we studied the expression of a representative TEM (BSC-TEM7; TEM 17) in a liver metastasis from a colorectal cancer, a sarcoma, and in primary cancers of the lung, pancreas, breast and brain. As shown in Fig. 4, the transcript was found to be expressed specifically in the endothelium of each of these cancers, whether metastatic (Fig. 4D) or primary (Fig. 4E-I). Analysis of the other six TEMs, (BSC-TEM 1, 3,4,5, 7, 8 and 9; TEM 1, 5, 9, 17, and 19) revealed a similar pattern in lung tumors, brain tumors, and metastatic lesions of the liver (see Table 3).

EXAMPLE 7

Tumor endothelium markers are neo-angiogenic

[135] Finally, we asked whether these transcripts were expressed in angiogenic states other than that associated with tumorigenesis. We thus performed in situ hybridizations on corpus luteum tissue as well as healing wounds. Although there

were exceptions, we found that these transcripts were generally expressed both in the corpus luteum and in the granulation tissue of healing wounds (Table 3 and example in Fig. 4J). In all tissues studied, expression of the genes was either absent or exclusively confined to the EC compartment.

References and Notes

The disclosure of each reference cited is expressly incorporated herein.

1. J. Folkman, in *Cancer Medicine* J. Holland, Bast Jr, RC, Morton DL, Frei III, E, Kufe, DW, Weichselbaum, RR, Ed. (Williams & Wilkins, Baltimore, 1997) pp. 181.

2. R. S. Kerbel, *Carcinogenesis* 21, 505 (2000).

3. P. Wesseling, D. J. Ruiter, P. C. Burger, *J Neurooncol* 32, 253 (1997).

4. Q. G. Dong, et al., *Arterioscler Thromb Vasc Biol* 17, 1599 (1997).

5. P. W. Hewett, J. C. Murray, *In Vitro Cell Dev Biol Anim* 32, 462 (1996).

6. M. A. Hull, P. W. Hewett, J. L. Brough, C. J. Hawkey, *Gastroenterology* 111, 1230 (1996).

7. G. Haraldsen, et al., *Gut* 37, 225 (1995).

8. The original EC isolation protocol was the same as that shown in Fig. 2B except that dispersed cells were stained with anti-CD31 antibodies instead of anti-P1H12, and magnetic beads against CD64 and CD14 were not included in the negative selection. After generating 120,000 SAGE tags from these two EC preparations, careful analysis of the SAGE data revealed that, in addition to endothelial-specific markers, several macrophage-specific markers were also present.

9. A. Solovey, et al., *N Engl J Med* 337, 1584 (1997).

10. V. E. Velculescu, L. Zhang, B. Vogelstein, K. W. Kinzler, *Science* 270 , 484-487 (1995).

11. In order to reduce the minimum amount of starting material required from ~50 million cells to ~50,000 cells (i.e. ~1000-fold less) we and others (38) have introduced

several modifications to the original SAGE protocol. A detailed version of our modified "MicroSAGE" protocol is available from the authors upon request.

12. 96,694 and 96,588 SAGE tags were analyzed from normal and tumor derived ECs, respectively, and represented 50,298 unique tags. A conservative estimate of 32,703 unique transcripts was derived by considering only those tags observed more than once in the current data set or in the 134,000 transcripts previously identified in human transcriptomes (39).

13. To identify endothelial specific transcripts, we normalized the number of tags analyzed in each group to 100,000, and limited our analysis to transcripts that were expressed at levels at least 20-fold higher in ECs than in non-endothelial cell lines in culture and present at fewer than 5 copies per 100,000 transcripts in non-endothelial cell lines and the hematopoietic fraction (~57,000 tags)(41). Non-endothelial cell lines consisted of 1.8x106 tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. A complete list of PEMs is available at www.sagenet.org\angio\table1.htm.

14. M. Tucci, et al., *J Endocrinol* 157, 13 (1998).

15. T. Oono, et al., *J Invest Dermatol* 100 , 329 (1993).

16. K. Motamed, *Int J Biochem Cell Biol* 31, 1363 (1999).

17. N. Bardin, et al., *Tissue Antigens* 48, 531 (1996).

18. D. M. Bradham, A. Igarashi, R. L. Potter, G. R. Grotendorst, *J Cell Biol* 114, 1285 (1991).

19. K. Akaogi, et al., *Proc Natl Acad Sci U S A* 93, 8384 (1996).

20. Y. Muragaki, et al., *Proc Natl Acad Sci U S A* 92, 8763 (1995).

21. M. L. Iruela-Arispe, C. A. Diglio, E. H. Sage, *Arterioscler Thromb* 11 , 805 (1991).

22. J. P. Girard, T. A. Springer, *Immunity* 2, 113 (1995).

23. E. A. Jaffe, et al., *J Immunol* 143, 3961 (1989).

24. J. P. Girard, et al., *Am J Pathol* 155, 2043 (1999).

25. H. Ohtani, N. Sasano, *J Electron Microsc* 36, 204 (1987).

26. For non-radioactive in situ hybridization, digoxigenin (DIG)-labelled sense and anti-sense riboprobes were generated through PCR by amplifying 500-600 bp products and incorporating a T7 promoter into the anti-sense primer. In vitro transcription was performed using DIG RNA labelling reagents and T7 RNA polymerase (Roche, Indianapolis, IN). Frozen tissue sections were fixed with 4 % paraformaldehyde, permeabilized with pepsin, and incubated with 200 ng/ml of riboprobe overnight at 55oC. For signal amplification, a horseradish peroxidase (HRP) rabbit anti-DIG antibody (DAKO, Carpinteria, CA) was used to catalyse the deposition of Biotin-Tyramide (from GenPoint kit, DAKO). Further amplification was achieved by adding HRP rabbit anti-biotin (DAKO), biotin-tyramide, and then alkaline-phosphatase (AP) rabbit anti-biotin (DAKO). Signal was detected using the AP substrate Fast Red TR/Napthol AS-MX (Sigma, St. Louis, MO), and cells were counterstained with hematoxylin unless otherwise indicated. A detailed protocol including the list of primers used to generate the probes can be obtained from the authors upon request.

27. Transcript copies per cell were calculated assuming an average cell contains 300,000 transcripts.

28. R. S. Warren, H. Yuan, M. R. Matli, N. A. Gillett, N. Ferrara, *J Clin Invest* 95, 1789 (1995).

29. Y. Takahashi, Y. Kitadai, C. D. Bucana, K. R. Cleary, L. M. Ellis, *Cancer Res* 55, 3964 (1995).

30. L. F. Brown, et al., *Cancer Res* 53, 4727 (1993).

31. Endothelial-specific transcripts were defined as those expressed at levels at least 5-fold higher in ECs in vivo than in non-endothelial cell lines in culture (13), and present at no more than 5 copies per 100,000 transcripts in non-endothelial cell lines and the hematopoietic cell fraction (41). Transcripts showing statistically different levels of expression (P <0.05) were then identified using Monte Carlo analysis as previously described (40). Transcripts preferentially expressed in normal endothelium were then defined as those expressed at levels at least 10-fold higher in normal endothelium than in tumor endothelium. Conversely, tumor endothelial transcripts were at least 10-fold higher in tumor versus normal endothelium. See www.sagenet.org\angio\table2.htm and www.sagenet.org\angio\table3.htm for a complete list of differentially expressed genes.

32. M. Iurlaro, et al., *Eur J Clin Invest* 29 , 793 (1999).

33. W. S. Lee, et al., *Circ Res* 82, 845 (1998).

34. J. Niquet, A. Represa, *Brain Res Dev Brain Res* 95, 227 (1996).

35. L. Fouser, L. Iruela-Arispe, P. Bornstein, E. H. Sage, *J Biol Chem* 266 , 18345 (1991).

36. M. L. Iruela-Arispe, P. Hasselaar, H. Sage, *Lab Invest* 64, 174 (1991).

37. H. F. Dvorak, *N Engl J Med* 315, 1650 (1986).

38. B. Virlon, et al., *Proc Natl Acad Sci U S A* 96, 15286 (1999).

39. V. E. Velculescu, et al., *Nat Genet* 23, 387 (1999).

40. L. Zhang, et al., *Science* 276, 1268 (1997).

41. Human colon tissues were obtained within ½ hour after surgical removal from patients. Sheets of epithelial cells were peeled away from normal tissues with a glass slide following treatment with 5 mM DDT, then 10 mM EDTA, leaving the lamina propria intact. After a 2h incubation in collagenase at 37 oC, cells were filtered sequentially through 400 um, 100 um, 50 um and 25 um mesh, and spun through a 30 % pre-formed Percoll gradient to pellet RBCs. Epithelial cells (Epithelial Fraction), which were found to non-specifically bind magnetic beads, were removed using Dynabeads coupled to BerEP4 (Dynal, Lake Success, NY). Subsequently, macrophages and other leukocytes (Hematopoietic Fraction) were removed using a cocktail of beads coupled to anti-CD45, anti-CD14 and anti-CD64 (Dynal). The remaining cells were stained with P1H12 antibody, purified with anti-mouse IgG-coupled magnetic beads, and lysed in mRNA lysis buffer. A detailed protocol can be obtained from the authors upon request.

42. H. Sheikh, H. Yarwood, A. Ashworth, C. M. Isacke, J Cell Sci 113, 1021-32 (2000).

Sequence name	SEQ ID NO:
PEM 1	1
PEM 2	2
PEM 3	3
PEM 4	4
PEM 5	5
PEM 6	6
PEM 7	7
PEM 8	8
PEM 9	9
PEM 10	10
PEM 11	11
PEM 12	12
PEM 13	13
PEM 14	14
PEM 15	15
PEM 16	16
PEM 17	17
PEM 18	18
PEM 19	19
PEM 20	20
PEM 21	21
PEM 22	22
PEM 23	23
PEM 24	24
PEM 25	25
PEM 26	26
PEM 27	27
PEM 28	28
PEM 29	29
PEM 30	30
PEM 31	31
PEM 32	32
PEM 33	33
PEM 34	34
PEM 35	35

SEQ ID NO:	Sequence name
1	PEM 1
2	PEM 2
3	PEM 3
4	PEM 4
5	PEM 5
6	PEM 6
7	PEM 7
8	PEM 8
9	PEM 9
10	PEM 10
11	PEM 11
12	PEM 12
13	PEM 13
14	PEM 14
15	PEM 15
16	PEM 16
17	PEM 17
18	PEM 18
19	PEM 19
20	PEM 20
21	PEM 21
22	PEM 22
23	PEM 23
24	PEM 24
25	PEM 25
26	PEM 26
27	PEM 27
28	PEM 28
29	PEM 29
30	PEM 30
31	PEM 31
32	PEM 32
33	PEM 33
34	PEM 34
35	PEM 35

PEM 36	36
PEM 37	37
PEM 38	38
PEM 39	39
PEM 40	40
PEM 41	41
PEM 42	42
PEM 43	43
PEM 44	44
PEM 45	45
PEM 46	46
PEM 47	47
PEM 48	48
PEM 49	49
PEM 50	50
PEM 51	51
PEM 52	52
PEM 53	53
PEM 54	54
PEM 55	55
PEM 56	56
PEM 57	57
PEM 58	58
PEM 59	59
PEM 60	60
PEM 61	61
PEM 62	62
PEM 63	63
PEM 64	64
PEM 65	65
PEM 66	66
PEM 67	67
PEM 68	68
PEM 69	69
PEM 70	70
PEM 71	71
PEM 72	72
PEM 73	73
PEM 74	74

36	PEM 36
37	PEM 37
38	PEM 38
39	PEM 39
40	PEM 40
41	PEM 41
42	PEM 42
43	PEM 43
44	PEM 44
45	PEM 45
46	PEM 46
47	PEM 47
48	PEM 48
49	PEM 49
50	PEM 50
51	PEM 51
52	PEM 52
53	PEM 53
54	PEM 54
55	PEM 55
56	PEM 56
57	PEM 57
58	PEM 58
59	PEM 59
60	PEM 60
61	PEM 61
62	PEM 62
63	PEM 63
64	PEM 64
65	PEM 65
66	PEM 66
67	PEM 67
68	PEM 68
69	PEM 69
70	PEM 70
71	PEM 71
72	PEM 72
73	PEM 73
74	PEM 74

PEM 75	75
PEM 76	76
PEM 77	77
PEM 78	78
PEM 79	79
PEM 80	80
PEM 81	81
PEM 82	82
PEM 83	83
PEM 84	84
PEM 85	85
PEM 86	86
PEM 87	87
PEM 88	88
PEM 89	89
PEM 90	90
PEM 91	91
PEM 92	92
PEM 93	93
TEM 1	94
TEM 2	95
TEM 3	96
TEM 4	97
TEM 5	98
TEM 6	99
TEM 7	100
TEM 8	101
TEM 9	102
TEM 10	103
TEM 11	104
TEM 12	105
TEM 13	106
TEM 14	107
TEM 15	108
TEM 16	109
TEM 17	110
TEM 18	111
TEM 19	112
TEM 20	113

75	PEM 75
76	PEM 76
77	PEM 77
78	PEM 78
79	PEM 79
80	PEM 80
81	PEM 81
82	PEM 82
83	PEM 83
84	PEM 84
85	PEM 85
86	PEM 86
87	PEM 87
88	PEM 88
89	PEM 89
90	PEM 90
91	PEM 91
92	PEM 92
93	PEM 93
94	TEM 1
95	TEM 2
96	TEM 3
97	TEM 4
98	TEM 5
99	TEM 6
100	TEM 7
101	TEM 8
102	TEM 9
103	TEM 10
104	TEM 11
105	TEM 12
106	TEM 13
107	TEM 14
108	TEM 15
109	TEM 16
110	TEM 17
111	TEM 18
112	TEM 19
113	TEM 20

TEM 21	114
TEM 22	115
TEM 23	116
TEM 24	117
TEM 25	118
TEM 26	119
TEM 27	120
TEM 28	121
TEM 29	122
TEM 30	123
TEM 31	124
TEM 32	125
TEM 33	126
TEM 34	127
TEM 35	128
TEM 36	129
TEM 37	130
TEM 38	131
TEM 39	132
TEM 40	133
TEM 41	134
TEM 42	135
TEM 43	136
TEM 44	137
TEM 45	138
TEM 46	139
NEM 1	140
NEM 2	141
NEM 3	142
NEM 4	143
NEM 5	144
NEM 6	145
NEM 7	146
NEM 8	147
NEM 9	148
NEM 10	149
NEM 11	150
NEM 12	151
NEM 13	152

114	TEM 21
115	TEM 22
116	TEM 23
117	TEM 24
118	TEM 25
119	TEM 26
120	TEM 27
121	TEM 28
122	TEM 29
123	TEM 30
124	TEM 31
125	TEM 32
126	TEM 33
127	TEM 34
128	TEM 35
129	TEM 36
130	TEM 37
131	TEM 38
132	TEM 39
133	TEM 40
134	TEM 41
135	TEM 42
136	TEM 43
137	TEM 44
138	TEM 45
139	TEM 46
140	NEM 1
141	NEM 2
142	NEM 3
143	NEM 4
144	NEM 5
145	NEM 6
146	NEM 7
147	NEM 8
148	NEM 9
149	NEM 10
150	NEM 11
151	NEM 12
152	NEM 13

NEM 14	153
NEM 15	154
NEM 16	155
NEM 17	156
NEM 18	157
NEM 19	158
NEM 20	159
NEM 21	160
NEM 22	161
NEM 23	162
NEM 24	163
NEM 25	164
NEM 26	165
NEM 27	166
NEM 28	167
NEM 29	168
NEM 30	169
NEM 31	170
NEM 32	171
NEM 33	172
TEM 1 DNA	173
TEM 2 DNA	174
TEM 7 DNA	175
TEM 8 DNA	176
TEM 1 Protein	177
TEM 2 Protein	178
TEM 8 Protein	179
TEM 5 DNA	180
TEM 7B DNA	181
mTEM 1 DNA	182
mTEM 5 DNA	183
mTEM 7 DNA	184
mTEM 7B DNA	185
mTEM 8 DNA	186
TEM 8 Protein	187
TEM 5 Protein	188
TEM 7B Protein	189
mTEM 1 Protein	190
mTEM 5 Protein	191

153	NEM 14
154	NEM 15
155	NEM 16
156	NEM 17
157	NEM 18
158	NEM 19
159	NEM 20
160	NEM 21
161	NEM 22
162	NEM 23
163	NEM 24
164	NEM 25
165	NEM 26
166	NEM 27
167	NEM 28
168	NEM 29
169	NEM 30
170	NEM 31
171	NEM 32
172	NEM 33
173	TEM 1 DNA
174	TEM 2 DNA
175	TEM 7 DNA
176	TEM 8 DNA
177	TEM 1 Protein
178	TEM 2 Protein
179	TEM 8 Protein
180	TEM 5 DNA
181	TEM 7B DNA
182	mTEM 1 DNA
183	mTEM 5 DNA
184	mTEM 7 DNA
185	mTEM 7B DNA
186	mTEM 8 DNA
187	TEM 8 Protein
188	TEM 5 Protein
189	TEM 7B Protein
190	mTEM 1 Protein
191	mTEM 5 Protein

mTEM 7 Protein	192
mTEM 7b Protein	193
mTEM 8 Protein	194
TEM 1 DNA	195
TEM 1 Protein	196
TEM 2 DNA	197
TEM 2 Protein	198
TEM 3 DNA	199
TEM 3 Protein	200
TEM 4 DNA	201
TEM 4 Protein	202
TEM 5 DNA	203
TEM 5 Protein	204
TEM 6 DNA	205
TEM 6 Protein	206
TEM 7 DNA	207
TEM 7 Protein	208
TEM 8 DNA	209
TEM 8 Protein	210
TEM 9 DNA	211
TEM 9 Protein	212
TEM 10 DNA	213
TEM 10 Protein	214
TEM 11 DNA	215
TEM 11 Protein	216
TEM 12 DNA	217
TEM 12 Protein	218
TEM 13 DNA	219
TEM 13 Protein	220
TEM 14a DNA	221
TEM 14b DNA	222
TEM 14a Protein	223
TEM 14b Protein	224
TEM 15 DNA	225
TEM 15 Protein	226
TEM 16 DNA	227
TEM 16 Protein	228
TEM 17 DNA	229
TEM 17 Protein	230

192	mTEM 7 Protein
193	mTEM 7b Protein
194	mTEM 8 Protein
195	TEM 1 DNA
196	TEM 1 Protein
197	TEM 2 DNA
198	TEM 2 Protein
199	TEM 3 DNA
200	TEM 3 Protein
201	TEM 4 DNA
202	TEM 4 Protein
203	TEM 5 DNA
204	TEM 5 Protein
205	TEM 6 DNA
206	TEM 6 Protein
207	TEM 7 DNA
208	TEM 7 Protein
209	TEM 8 DNA
210	TEM 8 Protein
211	TEM 9 DNA
212	TEM 9 Protein
213	TEM 10 DNA
214	TEM 10 Protein
215	TEM 11 DNA
216	TEM 11 Protein
217	TEM 12 DNA
218	TEM 12 Protein
219	TEM 13 DNA
220	TEM 13 Protein
221	TEM 14a DNA
222	TEM 14b DNA
223	TEM 14a Protein
224	TEM 14b Protein
225	TEM 15 DNA
226	TEM 15 Protein
227	TEM 16 DNA
228	TEM 16 Protein
229	TEM 17 DNA
230	TEM 17 Protein

TEM 19 DNA	231
TEM 19 Protein	232
TEM 20 DNA	233
TEM 20 Protein	234
TEM 21 DNA	235
TEM 21 Protein	236
TEM 22 DNA	237
TEM 22 Protein	238
TEM 24 DNA	239
TEM 24 Protein	240
TEM 25 DNA	241
TEM 25 Protein	242
TEM 27 DNA	243
TEM 27 Protein	244
TEM 28 DNA	245
TEM 28 Protein	246
TEM 29 DNA	247
TEM 29 Protein	248
TEM 30 DNA	249
TEM 30 Protein	250
TEM 31 DNA	251
TEM 31 Protein	252
TEM 33 DNA	253
TEM 33 Protein	254
TEM 35 DNA	255
TEM 35 Protein	358
TEM 36 DNA	256
TEM 36 Protein	257
TEM 37 DNA	258
TEM 37 Protein	259
TEM 38 DNA	260
TEM 38 Protein	261
TEM 39 DNA	262
TEM 39 Protein	263
TEM 40 DNA	264
TEM 40 Protein	265
TEM 41 DNA	266
TEM 41 Protein	267
TEM 42 DNA	268

231	TEM 19 DNA
232	TEM 19 Protein
233	TEM 20 DNA
234	TEM 20 Protein
235	TEM 21 DNA
236	TEM 21 Protein
237	TEM 22 DNA
238	TEM 22 Protein
239	TEM 24 DNA
240	TEM 24 Protein
241	TEM 25 DNA
242	TEM 25 Protein
243	TEM 27 DNA
244	TEM 27 Protein
245	TEM 28 DNA
246	TEM 28 Protein
247	TEM 29 DNA
248	TEM 29 Protein
249	TEM 30 DNA
250	TEM 30 Protein
251	TEM 31 DNA
252	TEM 31 Protein
253	TEM 33 DNA
254	TEM 33 Protein
255	TEM 35 DNA
256	TEM 36 DNA
257	TEM 36 Protein
258	TEM 37 DNA
259	TEM 37 Protein
260	TEM 38 DNA
261	TEM 38 Protein
262	TEM 39 DNA
263	TEM 39 Protein
264	TEM 40 DNA
265	TEM 40 Protein
266	TEM 41 DNA
267	TEM 41 Protein
268	TEM 42 DNA
269	TEM 42 Protein

TEM 42 Protein	269
TEM 44 DNA	270
TEM 44 Protein	271
TEM 45 DNA	272
TEM 45 Protein	273
TEM 46 DNA	274
TEM 46 Protein	275
NEM 4 DNA	276
NEM 4 Protein	277
NEM 14 DNA	278
NEM 14 Protein	279
NEM 17 DNA	280
NEM 17 Protein	281
NEM 22 DNA	282
NEM 22 Protein	283
NEM 23 DNA	284
NEM 23 Protein	285
NEM 23 Secreted	286
NEM 23 Short	287
NEM 33 DNA	288
NEM 33 Protein	289
mTEM 1 DNA	290
mTEM 1 Protein	291
mTEM 2 DNA	292
mTEM 2 Protein	293
mTEM 3 DNA	298
mTEM 3 Protein	299
mTEM 9 DNA	294
mTEM 9 Protein	295
mTEM 13 DNA	302
mTEM 13 Protein	303
mTEM 17 DNA	296
mTEM 17 Protein	297
mTEM 19 DNA	300
mTEM 19 Protein	301
mTEM 22 DNA	304
mTEM 22 Protein	305
mTEM 30 DNA	306
mTEM 30 Protein	307

270	TEM 44 DNA
271	TEM 44 Protein
272	TEM 45 DNA
273	TEM 45 Protein
274	TEM 46 DNA
275	TEM 46 Protein
276	NEM 4 DNA
277	NEM 4 Protein
278	NEM 14 DNA
279	NEM 14 Protein
280	NEM 17 DNA
281	NEM 17 Protein
282	NEM 22 DNA
283	NEM 22 Protein
284	NEM 23 DNA
285	NEM 23 Protein
286	NEM 23 Secreted
287	NEM 23 Short
288	NEM 33 DNA
289	NEM 33 Protein
290	mTEM 1 DNA
291	mTEM 1 Protein
292	mTEM 2 DNA
293	mTEM 2 Protein
294	mTEM 9 DNA
295	mTEM 9 Protein
296	mTEM 17 DNA
297	mTEM 17 Protein
298	mTEM 3 DNA
299	mTEM 3 Protein
300	mTEM 19 DNA
301	mTEM 19 Protein
302	mTEM 13 DNA
303	mTEM 13 Protein
304	mTEM 22 DNA
305	mTEM 22 Protein
306	mTEM 30 DNA
307	mTEM 30 Protein
308	TEM 2 tag

TEM 2 tag	308
TEM 1 long tag	309
TEM 3 long tag	310
TEM 4 long tag	311
TEM 5 long tag	312
TEM 5 long tag	313
TEM 6 long tag	314
TEM 7 long tag	315
TEM 8 long tag	316
TEM 9 long tag	317
TEM 10 long tag	318
TEM 10 long tag	319
TEM 10 long tag	320
TEM 11 long tag	321
TEM 12 long tag	322
TEM 13 long tag	323
TEM 13 long tag	324
TEM 14 long tag	325
TEM 15 long tag	326
TEM 15 long tag	327
TEM 16 long tag	328
TEM 17 long tag	329
TEM 19 long tag	330
TEM 21 long tag	331
TEM 21 long tag	332
TEM 22 long tag	333
TEM 22 long tag	334
TEM 23 long tag	335
TEM 24 long tag	336
TEM 25 long tag	337
TEM 25 long tag	338
TEM 28 long tag	339
TEM 30 long tag	340
TEM 31 long tag	341
TEM 32 long tag	342
TEM 33 long tag	343
TEM 33 long tag	344
TEM 35 long tag	345
TEM 36 long tag	346

309	TEM 1 long tag
310	TEM 3 long tag
311	TEM 4 long tag
312	TEM 5 long tag
313	TEM 5 long tag
314	TEM 6 long tag
315	TEM 7 long tag
316	TEM 8 long tag
317	TEM 9 long tag
318	TEM 10 long tag
319	TEM 10 long tag
320	TEM 10 long tag
321	TEM 11 long tag
322	TEM 12 long tag
323	TEM 13 long tag
324	TEM 13 long tag
325	TEM 14 long tag
326	TEM 15 long tag
327	TEM 15 long tag
328	TEM 16 long tag
329	TEM 17 long tag
330	TEM 19 long tag
331	TEM 21 long tag
332	TEM 21 long tag
333	TEM 22 long tag
334	TEM 22 long tag
335	TEM 23 long tag
336	TEM 24 long tag
337	TEM 25 long tag
338	TEM 25 long tag
339	TEM 28 long tag
340	TEM 30 long tag
341	TEM 31 long tag
342	TEM 32 long tag
343	TEM 33 long tag
344	TEM 33 long tag
345	TEM 35 long tag
346	TEM 36 long tag
347	TEM 37 long tag

TEM 37 long tag	347
TEM 38 long tag	348
TEM 38 long tag	349
TEM 39 long tag	350
TEM 40 long tag	351
TEM 41 long tag	352
TEM 42 long tag	353
TEM 43 long tag	354
TEM 44 long tag	355
TEM 45 long tag	356
TEM 46 long tag	357

348	TEM 38 long tag
349	TEM 38 long tag
350	TEM 39 long tag
351	TEM 40 long tag
352	TEM 41 long tag
353	TEM 42 long tag
354	TEM 43 long tag
355	TEM 44 long tag
356	TEM 45 long tag
357	TEM 46 long tag
358	TEM 35 Protein

CLAIMS

1. An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, and 271, respectively.
2. The isolated molecule of claim 1 which is an in tact antibody molecule.
3. The isolated molecule of claim 1 which is a single chain variable region (ScFv).
4. The isolated molecule of claim 1 which is a monoclonal antibody.
5. The isolated molecule of claim 1 which is a humanized antibody.
6. The isolated molecule of claim 1 which is a human antibody.
7. The isolated molecule of claim 1 which is bound to a cytotoxic moiety.
8. The isolated molecule of claim 1 which is bound to a therapeutic moiety.
9. The isolated molecule of claim 1 which is bound to a detectable moiety.
10. The isolated molecule of claim 1 which is bound to an anti-tumor agent.

11. A method of inhibiting neoangiogenesis, comprising:
administering to a subject in need thereof an effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, 238, and 271, respectively, whereby neoangiogenesis is inhibited.
12. The method of claim 11 wherein the subject bears a vascularized tumor.
13. The method of claim 11 wherein the subject has polycystic kidney disease.
14. The method of claim 11 wherein the subject has diabetic retinopathy.
15. The method of claim 11 wherein the subject has rheumatoid arthritis.
16. The method of claim 11 wherein the subject has psoriasis.

17. A method of inhibiting tumor growth, comprising:

administering to a human subject bearing a tumor an effective amount of an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, 22, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, 238, and 271, respectively, whereby growth of the tumor is inhibited.

18. An isolated molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 9, 17, 19, and 44, as shown in SEQ ID NO: 212, 230, 232, and 271, respectively.
19. The isolated molecule of claim 18 which is a single chain variable region (ScFv).
20. The isolated molecule of claim 18 which is a monoclonal antibody.
21. The isolated molecule of claim 18 which is a humanized antibody.
22. The isolated molecule of claim 18 which is a human antibody.
23. The isolated molecule of claim 18 which is bound to a cytotoxic moiety.
24. The isolated molecule of claim 18 which is bound to a therapeutic moiety.
25. The isolated molecule of claim 18 which is bound to a detectable

moiety.

26. The isolated molecule of claim 18 which is bound to an anti-tumor agent.
27. The isolated molecule of claim 18 which is an in tact antibody molecule.
28. An isolated and purified human transmembrane protein selected from the group consisting of: TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, and 232, respectively.
29. An isolated and purified nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: : TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, 232, respectively.
30. The isolated and purified nucleic acid molecule of claim 29 which comprises a coding sequence selected from those shown in SEQ ID NO: 211, 229, and 231,.
31. A recombinant host cell which comprises a nucleic acid molecule comprising a coding sequence for a transmembrane TEM selected from the group consisting of: TEM 9, 17, and 19 as shown in SEQ ID NO: 212, 230, and 232, respectively.
32. The recombinant host cell of claim 31 which comprises a coding sequence selected from those shown in SEQ ID NO: 211, 229, and 231.
33. A method of inducing an immune response in a mammal, comprising:

administering to the mammal a nucleic acid molecule comprising a coding sequence for a human transmembrane protein selected from the group consisting of: TEM 1, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250 and 271, respectively, whereby an immune response to the human transmembrane protein is induced in the mammal.

34. The method of claim 33 wherein the coding sequence is shown in SEQ ID NO: 195, 211, 219, 229, 231, 237, 249, 270.

35. A method of inducing an immune response in a mammal, comprising:

administering to the mammal a purified human transmembrane protein selected from the group consisting of: TEM 1, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250 and 271 , respectively, whereby an immune response to the human transmembrane protein is induced in the mammal.

36. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with an isolated and purified human trasmembrane protein selected from the group consisting of 1, 9, 13, 17, 19, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 250, 232 and 271;

contacting the isolated and purified human trasmembrane protein with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 13, 17, 19, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 250, 232 and 271, respectively;

determining binding of the molecule comprising an antibody variable region to the human transmembrane protein, wherein a test compound which diminishes the binding of the molecule comprising an antibody variable region to the human transmembrane protein is identified as a ligand involved in endothelial cell regulation.

37. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with a cell comprising a human transmembrane protein selected from the group consisting of 1, 9, 17, and 19 as shown in SEQ ID NO: 196, 212, 230, and 232;

contacting the cell with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, and 19 as shown in SEQ ID NO: 196, 212, 230, and 232, respectively;

determining binding of the molecule comprising an antibody variable region to the cell, wherein a test compound which diminishes the binding of the molecule comprising an antibody variable region to the cell is identified as a ligand involved in endothelial cell regulation.

38. A soluble form of a human transmembrane protein selected from the group consisting of: TEM 1, 9, 17, 19, 22, 30 and 44 as shown in SEQ ID NO: 196, 212, 230, 232, 238, 250, and 271, respectively, wherein the soluble forms lack transmembrane domains.

39. The soluble form of claim 38 wherein the soluble form consists of an extracellular domain of the human transmembrane protein.

40. A method of inhibiting neoangiogenesis in a patient, comprising: administering to the patient a soluble form of a human transmembrane protein according to claim 38, whereby neoangiogenesis in the patient is inhibited.

41. A method of inhibiting neoangiogenesis in a patient, comprising: administering to the patient a soluble form of a human transmembrane protein according to claim 39, whereby neoangiogenesis in the patient is inhibited.

42. The method of claim 40 wherein the patient bears a vascularized tumor.

43. The method of claim 41 wherein the patient bears a vascularized tumor.

44. The method of claim 40 wherein the patient has polycystic kidney disease.

45. The method of claim 40 wherein the patient has diabetic retinopathy.

46. The method of claim 40 wherein the patient has rheumatoid arthritis.

47. The method of claim 40 wherein the patient has psoriasis.

48. The method of claim 41 wherein the patient has polycystic kidney disease.

49. The method of claim 41 wherein the patient has diabetic retinopathy.

50. The method of claim 41 wherein the patient has rheumatoid arthritis.

51. The method of claim 41 wherein the patient has psoriasis.

52. A method of identifying regions of neoangiogenesis in a patient, comprising:

administering to a patient a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 13, 17, 19, 22, 30, and 44, as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250, and 271, respectively, wherein the molecule is bound to a detectable moiety; and

detecting the detectable moiety in the pateint, thereby identifying neoangiogenesis.

53. A method of screening for neoangiogenesis in a patient, comprising:

contacting a body fluid collected from the patient with a molecule comprising an antibody variable region which specifically binds to an extracellular domain of a TEM protein selected from the group consisting of: 1, 9, 17, 19, and 44, as shown in SEQ ID NO: 196, 212, 230, 232, and 271, respectively, wherein detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

54. A method of screening for neoangiogenesis in a patient, comprising:

contacting a body fluid collected from the patient with a molecule comprising an antibody variable region which specifically binds to a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 25, 27, 31, 36, 37, 38, 39, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 242, 244, 252, 257, 259, 261, and 263, respectively, wherein detection of cross-reactive material in the body fluid with the molecule indicates neoangiogenesis in the patient.

55. A method of promoting neoangiogenesis in a patient, comprising:

administering to a patient in need of neoangiogenesis a TEM protein selected from the group consising of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, whereby neoangiogenesis in the patient is stimulated.

56. A method of promoting neoangiogenesis in a patient, comprising:

administering to a patient in need of neoangiogenesis a nucleic acid molecule encoding a TEM protein selected from the group consising of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, whereby the TEM protein is expressed and neoangiogenesis in the patient is stimulated.

57. A method of screening for neoangiogenesis in a patient, comprising:

detecting a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, as shown in SEQ ID NO: 202, 206, 208, 214, 218, 223 & 224, 234, 242, 244, 252, 257, 259, 261. 263, and 265, respectively, in a body fluid collected from the patient, wherein detection of the TEM protein indicates neoangiogenesis in the patient.

58. A method of screening for neoangiogenesis in a patient, comprising:

detecting in a body fluid collected from the patient a nucleic acid encoding a TEM protein selected from the group consisting of: 4, 6, 7, 10, 12, 14, 20, 25, 27, 31, 36, 37, 38, 39, and 40, wherein the nucleic acid is selected from the group consisting of those shown in SEQ ID NO: 201, 205, 207, 213, 217, 221 & 222, 233, 241, 243, 251, 256, 258, 260, 262, and 264, respectively, wherein detection of the TEM protein indicates neoangiogenesis in the patient.

59. An isolated and purified nucleic acid molecule which encodes a NEM protein selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

60. The nucleic acid molecule of claim 60 wherein the nucleic acid molecule comprises a coding sequence as shown in SEQ ID NO: 278, 282, 284, and 288 .

61. A recombinant host cell which comprises a nucleic acid according to claim 60.

62. An isolated and purified NEM protein selected from the group consising of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, respectively.

63. An isolated molecule comprising an antibody variable region which specifically binds to a NEM protein selected from the group

consisting of: 14, 22, 23, and 33, as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289.

64. A method of inhibiting neoangiogenesis, comprising:

administering to a subject in need thereof an effective amount of a NEM protein selected from the group consising of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, whereby neoangiogenesis is inhibited.

65. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM genes selected from the group consisting of: 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 195, 197, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221 & 222, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 256, 258, 260, 262, 266, 268, 270, 272, and 274, respectively, with a test compound;

determining expression of said one or more TEM genes by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA; and

identifying a test compound as a candidate drug for treating tumors if it decreases expression of said one or more TEM genes.

66. The method of claim 66 wherein the cells are endothelial cells.

67. The method of claim 66 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

68. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM proteins selected from the group consisting of: 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 30, 31, 33, 35, 36, 37, 38, 39, 41,

42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively, with a test compound;

determining amount of said one or more TEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it decreases the amount of one more TEM proteins in said cells.

69. The method of claim 69 wherein the cells are endothelial cells.

70. The method of claim 69 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

71. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more TEM proteins selected from the group consisting of: 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275 respectively, with a test compound;

determining activity of said one or more TEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it decreases the activity of of one more TEM proteins in said cells.

72. The method of claim 72 wherein the cells are endothelial cells.

73. The method of claim 72 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more TEMs.

74. A method to identify candidate drugs for treating patients bearing tumors, comprising:

contacting a test compound with recombinant host cells which are transfected with an expession construct which encodes one or more TEM proteins selected from the group consisting of 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275, respectively;

determining proliferation of said cells; and

identifying a test compound which inhibits proliferation of said cells as a candidate drug for treating patients bearing tumors.

75. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more NEM genes selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 278, 282, 284, and 288, respectively, with a test compound;

determining expression of said one or more NEM genes by hybridization of mRNA of said cells to a nucleic acid probe which is complementary to said mRNA; and

identifying a test compound as a candidate drug for treating tumors if it increases expression of said one or more NEM genes.

76. The method of claim 76 wherein the cells are endothelial cells.

77. The method of claim 76 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

78. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, with a test compound;

determining amount of said one or more NEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it increases the amount of one more NEM proteins in said cells.

79. The method of claim 79 wherein the cells are endothelial cells.

80. The method of claim 79 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

81. A method to identify candidate drugs for treating tumors, comprising:

contacting cells which express one or more NEM proteins selected from the group consisting of: 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289, with a test compound;

determining activity of said one or more NEM proteins in said cells; and

identifying a test compound as a candidate drug for treating tumors if it increases the activity of one more NEM proteins in said cells.

82. The method of claim 82 wherein the cells are endothelial cells.

83. The method of claim 82 wherein the cells are recombinant host cells which are transfected with an expression construct which encodes said one or more NEMs.

84. A method to identify candidate drugs for treating patients bearing tumors, comprising:

contacting a test compound with recombinant host cells which are transfected with an expession construct which encodes one or more NEM proteins selected from the group consisting of 14, 22, 23, and 33 as shown in SEQ ID NO: 279, 283, 285, 286, 287, and 289;

determining proliferation of said cells; and

identifying a test compound which stimulates proliferation of said cells as a candidate drug for treating patients bearing tumors.

85. A method for identification of a ligand involved in endothelial cell regulation, comprising:

contacting a test compound with a human transmembrane TEM protein selected from the group consisting of 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 17, 19, 20, 21, 22, 24, 25, 27, 28, 29, 40, 31, 33, 35, 36, 37, 38, 39, 41, 42, 44, 45, and 46 as shown in SEQ ID NO: 196,

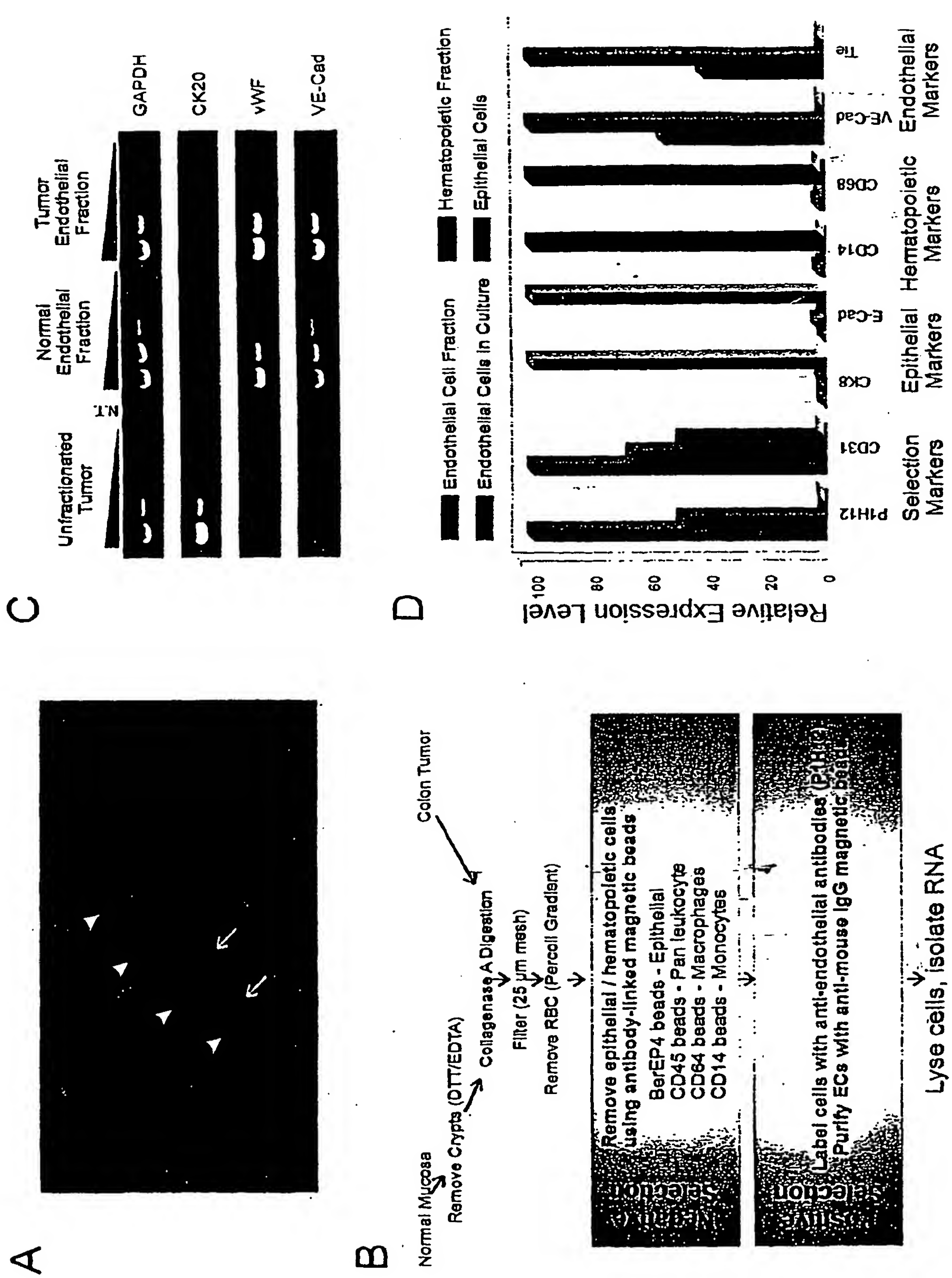
198, 202, 204, 206, 208, 210, 212, 214, 216, 218, 223 & 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 358, 257, 259, 261, 263, 267, 269, 271, 273, and 275;

determining binding of a test compound to the human transmembrane protein, wherein a test compound which binds to the protein is identified as a ligand involved in endothelial cell regulation.

86. A method of inducing an immune response in a mammal, comprising:

administering to the mammal a cell which expresses a transmembrane protein selected from the group consisting of: TEM 1, 9, 13, 17, 19, 22, 30, and 44 as shown in SEQ ID NO: 196, 212, 220, 230, 232, 238, 250 and 271 , respectively, wherein the cell is a recombinant cell which comprises a vector econding said transmembrane protein, or the cell is a fusion of a dendritic cell and a tumor endothelium cell, whereby an immune response to the human transmembrane protein is induced in the mammal.

Figure 1



A
B
Normal Mucosa
Remove Crypts (DTT/EDTA)
Colon Tumor
Collagenase A Digestion
Filter (25 μm mesh)
Remove RBC (Percoll Gradient)
Negative Selection
Remove epithelial / hematopoietic cells using antibody-linked magnetic beads
BerEP4 beads - Epithelial
CD45 beads - Pan leukocyte
CD64 beads - Macrophages
CD14 beads - Monocytes
Positive Selection
Label cells with anti-endothelial antibodies (P1H12)
Purify ECs with anti-mouse IgG magnetic beads
Lyse cells, isolate RNA
C
Unfractionated Tumor
N.T.
Normal Endothelial Fraction
Tumor Endothelial Fraction
GAPDH
CK20
vWF
VE-Cad
D
Endothelial Cell Fraction
Endothelial Cells in Culture
Hematopoietic Fraction
Epithelial Cells
Relative Expression Level
0
20
40
60
80
100
P1H12
CD31
CK8
E-Cad
CD14
CD68
VE-Cad
Tie
Selection Markers
Epithelial Markers
Hematopoietic Markers
Endothelial Markers

Figure 2

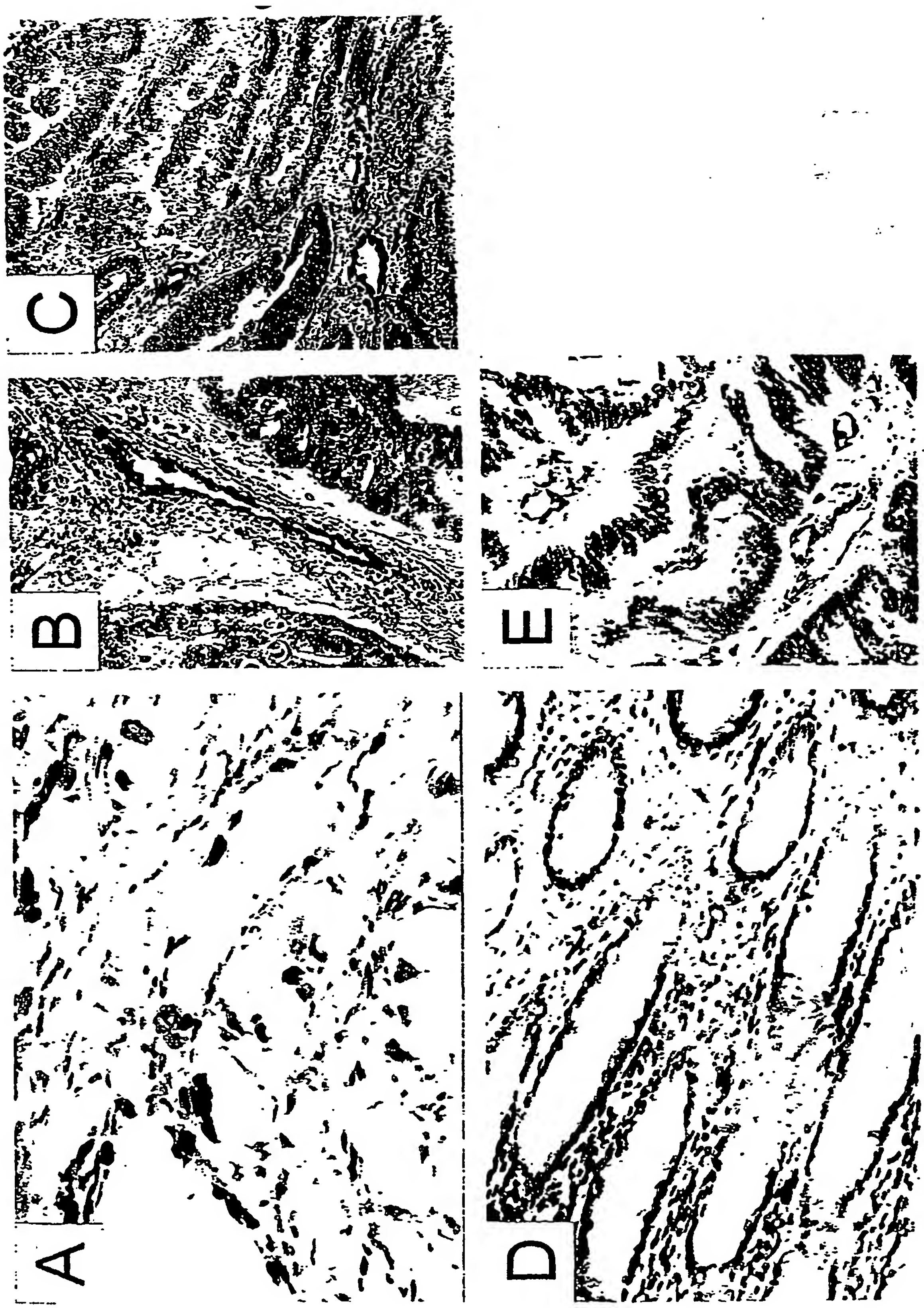


Figure 3

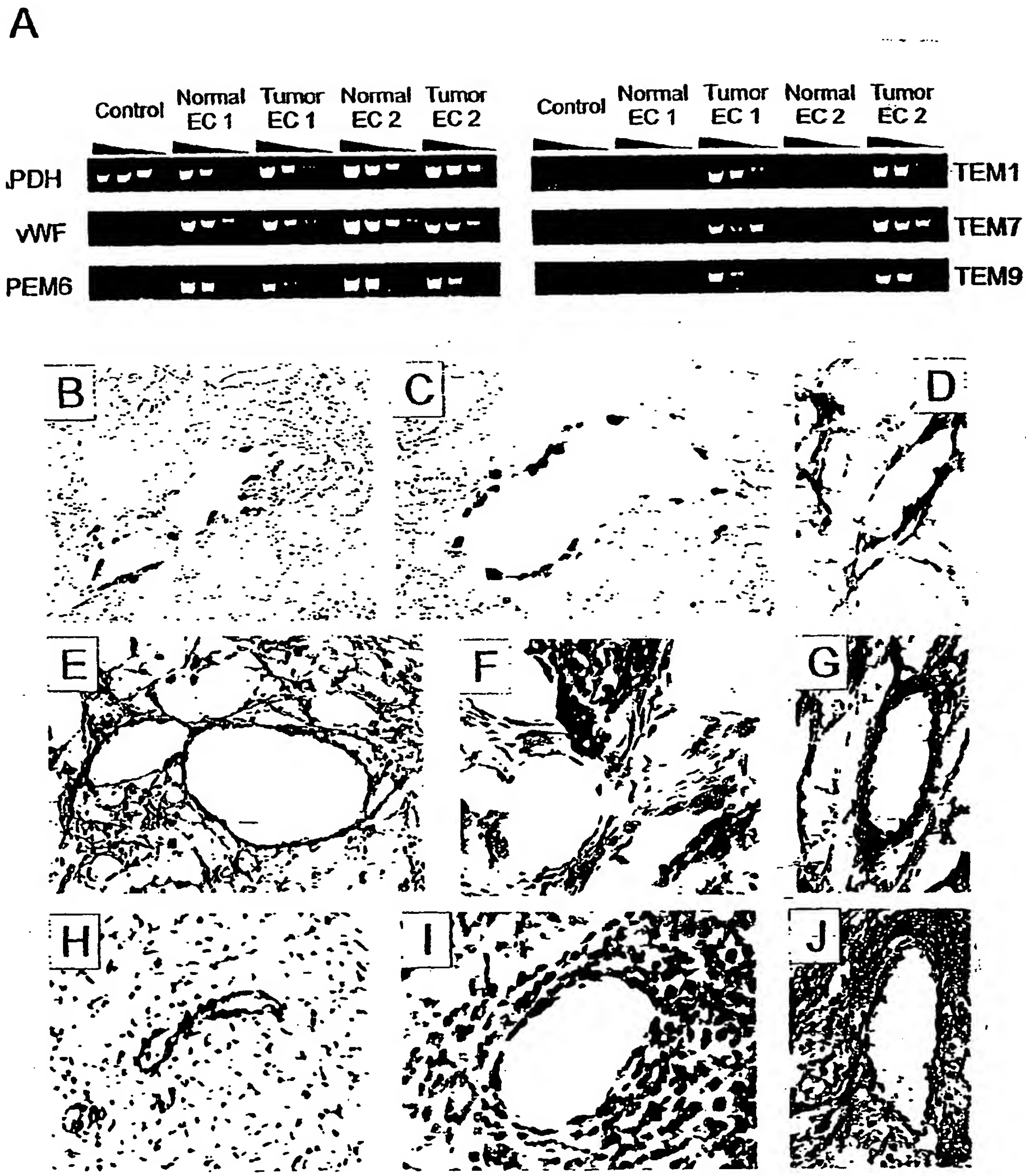

A
Control
Normal EC 1
Tumor EC 1
Normal EC 2
Tumor EC 2
PDH
vWF
PEM6
Control
Normal EC 1
Tumor EC 1
Normal EC 2
Tumor EC 2
TEM1
TEM7
TEM9
B
C
D
E
F
G
H
I
J

Figure 4

SEQUENCE LISTING

<110> Brad St. Croix
Bert Vogelstein
Kenneth Kinzler

<120> ENDOTHELIAL CELL EXPRESSION PATTERNS

<130> 1107.00134

<150> 60/222,599
<151> 2000-08-02

<150> 60/224,360

<151> 2000-08-11

<150> 60/282,850
<151> 2000-04-11

<160> 358

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 11
<212> DNA
<213> Homo sapiens

<400> 1
catatcatta a 11

<210> 2
<211> 11
<212> DNA
<213> Homo sapiens

<400> 2
tgcacttcaa g 11

<210> 3
<211> 11
<212> DNA
<213> Homo sapiens

<400> 3
tttgcacctt t 11

<210> 4
<211> 10
<212> DNA
<213> Homo sapiens

<400> 4
cccttgtccg 10

<210> 5
<211> 11
<212> DNA
<213> Homo sapiens

<400> 5
ttgctgactt t 11

<210> 6
<211> 11
<212> DNA
<213> Homo sapiens

<400> 6
accattggat t 11

<210> 7
<211> 11
<212> DNA
<213> Homo sapiens

<400> 7
acacttcttt c 11

<210> 8
<211> 11
<212> DNA
<213> Homo sapiens

<400> 8
ttctgctctt g 11

<210> 9
<211> 11
<212> DNA
<213> Homo sapiens

<400> 9
tccctggcag a 11

<210> 10
<211> 11
<212> DNA
<213> Homo sapiens

<400> 10
taatcctcaa g 11

<210> 11
<211> 11
<212> DNA
<213> Homo sapiens

<400> 11
atgtcttttc t 11

<210> 12
<211> 11
<212> DNA
<213> Homo sapiens

<400> 12
gggattaaag c 11

<210> 13
<211> 11
<212> DNA
<213> Homo sapiens

<400> 13
ttagtgtcgt a 11

<210> 14
<211> 11
<212> DNA
<213> Homo sapiens

<400> 14
ttctcccaaa t 11

<210> 15

<211> 11
<212> DNA
<213> Homo sapiens

<400> 15
gtgctaagcg g 11

<210> 16
<211> 11
<212> DNA
<213> Homo sapiens

<400> 16
gtttatggat a 11

<210> 17
<211> 11
<212> DNA
<213> Homo sapiens

<400> 17
ccctttcaca c 11

<210> 18
<211> 11
<212> DNA
<213> Homo sapiens

<400> 18
tgttctggag a 11

<210> 19
<211> 11
<212> DNA
<213> Homo sapiens

<400> 19
aagatcaaga t 11

<210> 20
<211> 11
<212> DNA
<213> Homo sapiens

<400> 20
tctctgagca t 11

<210> 21
<211> 11
<212> DNA
<213> Homo sapiens

<400> 21
caggtttcat a 11

<210> 22
<211> 11
<212> DNA
<213> Homo sapiens

<400> 22

gcacaagttc t 11

<210> 23
<211> 11
<212> DNA
<213> Homo sapiens

<400> 23
agcttgtggc c 11

<210> 24
<211> 11
<212> DNA
<213> Homo sapiens

<400> 24
cttctggata a 11

<210> 25
<211> 11
<212> DNA
<213> Homo sapiens

<400> 25
caacaataat a 11

<210> 26
<211> 11
<212> DNA
<213> Homo sapiens

<400> 26
accggcgccc g 11

<210> 27
<211> 11
<212> DNA
<213> Homo sapiens

<400> 27
ggaagctaag t 11

<210> 28
<211> 11
<212> DNA
<213> Homo sapiens

<400> 28
gcaatttaac c 11

<210> 29
<211> 11
<212> DNA
<213> Homo sapiens

<400> 29
gataactaca t 11

<210> 30
<211> 11
<212> DNA

<213> Homo sapiens

<400> 30
tatgagggta a 11

<210> 31
<211> 11
<212> DNA
<213> Homo sapiens

<400> 31
ccacgggatt c 11

<210> 32
<211> 11
<212> DNA
<213> Homo sapiens

<400> 32
tttacaaaga g 11

<210> 33
<211> 11
<212> DNA
<213> Homo sapiens

<400> 33
cccagtaaga t 11

<210> 34
<211> 11
<212> DNA
<213> Homo sapiens

<400> 34
acaaagcatt t 11

<210> 35
<211> 11
<212> DNA
<213> Homo sapiens

<400> 35
gcctgtccct c 11

<210> 36
<211> 11
<212> DNA
<213> Homo sapiens

<400> 36
tactttataa g 11

<210> 37
<211> 11
<212> DNA
<213> Homo sapiens

<400> 37
tgtttaatac a 11

<210> 38
<211> 11
<212> DNA
<213> Homo sapiens

<400> 38
gtccctgcct t 11

<210> 39
<211> 11
<212> DNA
<213> Homo sapiens

<400> 39
gagccatcat a 11

<210> 40
<211> 11
<212> DNA
<213> Homo sapiens

<400> 40
ggccctacag t 11

<210> 41
<211> 11
<212> DNA
<213> Homo sapiens

<400> 41
gctaacccct g 11

<210> 42
<211> 11
<212> DNA
<213> Homo sapiens

<400> 42
atcacacagc t 11

<210> 43
<211> 11
<212> DNA
<213> Homo sapiens

<400> 43
acaagtactg t 11

<210> 44
<211> 11
<212> DNA
<213> Homo sapiens

<400> 44
tcaccgtgga c 11

<210> 45
<211> 11
<212> DNA
<213> Homo sapiens

<400> 45
acattccaag t 11

<210> 46
<211> 11
<212> DNA
<213> Homo sapiens

<400> 46
gagcctggat a 11

<210> 47
<211> 11
<212> DNA
<213> Homo sapiens

<400> 47
ggcactcctg t 11

<210> 48
<211> 11
<212> DNA
<213> Homo sapiens

<400> 48
tcacagcccc c 11

<210> 49
<211> 11
<212> DNA
<213> Homo sapiens

<400> 49
tgccaggtgc a 11

<210> 50
<211> 11
<212> DNA
<213> Homo sapiens

<400> 50
tgggaaacct g 11

<210> 51
<211> 11
<212> DNA
<213> Homo sapiens

<400> 51
tttcatccac t 11

<210> 52
<211> 11
<212> DNA
<213> Homo sapiens

<400> 52
aacaggggcc a 11

<210> 53
<211> 11

<212> DNA
<213> Homo sapiens

<400> 53
actgaaagaa g 11

<210> 54
<211> 11
<212> DNA
<213> Homo sapiens

<400> 54
accgttctgt a 11

<210> 55
<211> 11
<212> DNA
<213> Homo sapiens

<400> 55
atactataat t 11

<210> 56
<211> 11
<212> DNA
<213> Homo sapiens

<400> 56
tttgtataga a 11

<210> 57
<211> 11
<212> DNA
<213> Homo sapiens

<400> 57
gtaatgacag a 11

<210> 58
<211> 11
<212> DNA
<213> Homo sapiens

<400> 58
aataggggaa a 11

<210> 59
<211> 11
<212> DNA
<213> Homo sapiens

<400> 59
gtgctacttc t 11

<210> 60
<211> 11
<212> DNA
<213> Homo sapiens

<400> 60
ccggcccctc c 11

<210> 61
<211> 11
<212> DNA
<213> Homo sapiens

<400> 61
ttgaatttgt t 11

<210> 62
<211> 11
<212> DNA
<213> Homo sapiens

<400> 62
cgagagtgtg a 11

<210> 63
<211> 11
<212> DNA
<213> Homo sapiens

<400> 63
ccctgttcag c 11

<210> 64
<211> 11
<212> DNA
<213> Homo sapiens

<400> 64
cagatggagg c 11

<210> 65
<211> 11
<212> DNA
<213> Homo sapiens

<400> 65
aggctcctgg c 11

<210> 66
<211> 11
<212> DNA
<213> Homo sapiens

<400> 66
tctgcttcta g 11

<210> 67
<211> 11
<212> DNA
<213> Homo sapiens

<400> 67
ggcttaggat g 11

<210> 68
<211> 11
<212> DNA
<213> Homo sapiens

<400> 68
ggttgttgcg g 11

<210> 69
<211> 11
<212> DNA
<213> Homo sapiens

<400> 69
acaagtaccc a 11

<210> 70
<211> 11
<212> DNA
<213> Homo sapiens

<400> 70
cttctcttga g 11

<210> 71
<211> 11
<212> DNA
<213> Homo sapiens

<400> 71
gctaataatg t 11

<210> 72
<211> 11
<212> DNA
<213> Homo sapiens

<400> 72
tgtgcttttt t 11

<210> 73
<211> 11
<212> DNA
<213> Homo sapiens

<400> 73
catcacggat c 11

<210> 74
<211> 11
<212> DNA
<213> Homo sapiens

<400> 74
gcagcagcag c 11

<210> 75
<211> 11
<212> DNA
<213> Homo sapiens

<400> 75
tgactgtatt a 11

<210> 76

<211> 11
<212> DNA
<213> Homo sapiens

<400> 76
gaatgctctt g 11

<210> 77
<211> 11
<212> DNA
<213> Homo sapiens

<400> 77
gtagttctgg a 11

<210> 78
<211> 11
<212> DNA
<213> Homo sapiens

<400> 78
tcccctctct c 11

<210> 79
<211> 11
<212> DNA
<213> Homo sapiens

<400> 79
gggcagtggc t 11

<210> 80
<211> 11
<212> DNA
<213> Homo sapiens

<400> 80
aaatatgtgt t 11

<210> 81
<211> 11
<212> DNA
<213> Homo sapiens

<400> 81
gtcattttct a 11

<210> 82
<211> 11
<212> DNA
<213> Homo sapiens

<400> 82
ctctccaaac c 11

<210> 83
<211> 11
<212> DNA
<213> Homo sapiens

<400> 83

ttaatgtgta a 11

<210> 84
<211> 11
<212> DNA
<213> Homo sapiens

<400> 84
tcaagcaatc a 11

<210> 85
<211> 11
<212> DNA
<213> Homo sapiens

<400> 85
gaagacactt g 11

<210> 86
<211> 11
<212> DNA
<213> Homo sapiens

<400> 86
gggtagggtg a 11

<210> 87
<211> 11
<212> DNA
<213> Homo sapiens

<400> 87
tggaacagtg a 11

<210> 88
<211> 11
<212> DNA
<213> Homo sapiens

<400> 88
gagtggctac c 11

<210> 89
<211> 11
<212> DNA
<213> Homo sapiens

<400> 89
gtcagggtcc c 11

<210> 90
<211> 11
<212> DNA
<213> Homo sapiens

<400> 90
gtcagtcact t 11

<210> 91
<211> 11
<212> DNA

<213> Homo sapiens

<400> 91
agcagagaca a 11

<210> 92
<211> 11
<212> DNA
<213> Homo sapiens

<400> 92
agcgatggag a 11

<210> 93
<211> 11
<212> DNA
<213> Homo sapiens

<400> 93
cgtggggtgt a 11

<210> 94
<211> 11
<212> DNA
<213> Homo sapiens

<400> 94
ggggctgccc a 11

<210> 95
<211> 11
<212> DNA
<213> Homo sapiens

<400> 95
gatctccgtg t 11

<210> 96
<211> 11
<212> DNA
<213> Homo sapiens

<400> 96
catttttatc t 11

<210> 97
<211> 11
<212> DNA
<213> Homo sapiens

<400> 97
ctttctttga g 11

<210> 98
<211> 11
<212> DNA
<213> Homo sapiens

<400> 98
tattaactct c 11

<210> 99
<211> 11
<212> DNA
<213> Homo sapiens

<400> 99
caggagaccc c 11

<210> 100
<211> 11
<212> DNA
<213> Homo sapiens

<400> 100
ggaaatgtca a 11

<210> 101
<211> 11
<212> DNA
<213> Homo sapiens

<400> 101
cctggttcag t 11

<210> 102
<211> 11
<212> DNA
<213> Homo sapiens

<400> 102
tttttaagaa c 11

<210> 103
<211> 11
<212> DNA
<213> Homo sapiens

<400> 103
tttggttttc c 11

<210> 104
<211> 11
<212> DNA
<213> Homo sapiens

<400> 104
attttgtatg a 11

<210> 105
<211> 11
<212> DNA
<213> Homo sapiens

<400> 105
actttagatg g 11

<210> 106
<211> 11
<212> DNA
<213> Homo sapiens

<400> 106
gagtgagacc c 11

<210> 107
<211> 11
<212> DNA
<213> Homo sapiens

<400> 107
gtacacacac c 11

<210> 108
<211> 11
<212> DNA
<213> Homo sapiens

<400> 108
ccacagggga t 11

<210> 109
<211> 11
<212> DNA
<213> Homo sapiens

<400> 109
ttaaaagtca c 11

<210> 110
<211> 11
<212> DNA
<213> Homo sapiens

<400> 110
acagactgtt a 11

<210> 111
<211> 11
<212> DNA
<213> Homo sapiens

<400> 111
ccactgcaac c 11

<210> 112
<211> 11
<212> DNA
<213> Homo sapiens

<400> 112
ctataggaga c 11

<210> 113
<211> 11
<212> DNA
<213> Homo sapiens

<400> 113
gttccacaga a 11

<210> 114
<211> 11

<212> DNA
<213> Homo sapiens

<400> 114
taccacctcc c 11

<210> 115
<211> 11
<212> DNA
<213> Homo sapiens

<400> 115
gccctttctc t 11

<210> 116
<211> 11
<212> DNA
<213> Homo sapiens

<400> 116
ttaaatagca c 11

<210> 117
<211> 11
<212> DNA
<213> Homo sapiens

<400> 117
agacatactg a 11

<210> 118
<211> 11
<212> DNA
<213> Homo sapiens

<400> 118
tcccccagga g 11

<210> 119
<211> 11
<212> DNA
<213> Homo sapiens

<400> 119
agcccaaagt g 11

<210> 120
<211> 11
<212> DNA
<213> Homo sapiens

<400> 120
actaccataa c 11

<210> 121
<211> 11
<212> DNA
<213> Homo sapiens

<400> 121
tacaaatcgt t 11

<210> 122
<211> 11
<212> DNA
<213> Homo sapiens

<400> 122
ttgggtgaaa a 11

<210> 123
<211> 11
<212> DNA
<213> Homo sapiens

<400> 123
cattatccaa a 11

<210> 124
<211> 11
<212> DNA
<213> Homo sapiens

<400> 124
agaaaccacg g 11

<210> 125
<211> 11
<212> DNA
<213> Homo sapiens

<400> 125
accaaaacca c 11

<210> 126
<211> 10
<212> DNA
<213> Homo sapiens

<400> 126
tgaaataaac 10

<210> 127
<211> 10
<212> DNA
<213> Homo sapiens

<400> 127
tttggtttcc 10

<210> 128
<211> 11
<212> DNA
<213> Homo sapiens

<400> 128
gtggagacgg a 11

<210> 129
<211> 11
<212> DNA
<213> Homo sapiens

<400> 129
tttgtgttgt a 11

<210> 130
<211> 11
<212> DNA
<213> Homo sapiens

<400> 130
ttatgtttaa t 11

<210> 131
<211> 11
<212> DNA
<213> Homo sapiens

<400> 131
tggaaatgac c 11

<210> 132
<211> 11
<212> DNA
<213> Homo sapiens

<400> 132
tgccacacag t 11

<210> 133
<211> 11
<212> DNA
<213> Homo sapiens

<400> 133
gatgaggaga c 11

<210> 134
<211> 11
<212> DNA
<213> Homo sapiens

<400> 134
atcaaaggtt t 11

<210> 135
<211> 11
<212> DNA
<213> Homo sapiens

<400> 135
agtcacatag t 11

<210> 136
<211> 11
<212> DNA
<213> Homo sapiens

<400> 136
ttcggttggt c 11

<210> 137

<211> 11
<212> DNA
<213> Homo sapiens

<400> 137
ccccacacgg g 11

<210> 138
<211> 11
<212> DNA
<213> Homo sapiens

<400> 138
ggcttgcctt t 11

<210> 139
<211> 11
<212> DNA
<213> Homo sapiens

<400> 139
atcccttccc g 11

<210> 140
<211> 11
<212> DNA
<213> Homo sapiens

<400> 140
tctcacgtct c 11

<210> 141
<211> 11
<212> DNA
<213> Homo sapiens

<400> 141
ctagcgtttt a 11

<210> 142
<211> 11
<212> DNA
<213> Homo sapiens

<400> 142
gtggctgacg c 11

<210> 143
<211> 11
<212> DNA
<213> Homo sapiens

<400> 143
ctcttaaaaa a 11

<210> 144
<211> 11
<212> DNA
<213> Homo sapiens

<400> 144

tgggaagagg g 11

<210> 145
<211> 11
<212> DNA
<213> Homo sapiens

<400> 145
gtttaaggat g 11

<210> 146
<211> 11
<212> DNA
<213> Homo sapiens

<400> 146
ctttgttttg c 11

<210> 147
<211> 11
<212> DNA
<213> Homo sapiens

<400> 147
attgccaatc t 11

<210> 148
<211> 11
<212> DNA
<213> Homo sapiens

<400> 148
tgttgaaaaa a 11

<210> 149
<211> 11
<212> DNA
<213> Homo sapiens

<400> 149
acaaaaaggc c 11

<210> 150
<211> 11
<212> DNA
<213> Homo sapiens

<400> 150
aagatgcaca c 11

<210> 151
<211> 11
<212> DNA
<213> Homo sapiens

<400> 151
gtagaggaaa a 11

<210> 152
<211> 11
<212> DNA

<213> Homo sapiens

<400> 152
ttgttcaagg g 11

<210> 153
<211> 11
<212> DNA
<213> Homo sapiens

<400> 153
ctcttcaaaa a 11

<210> 154
<211> 11
<212> DNA
<213> Homo sapiens

<400> 154
tattaaaata g 11

<210> 155
<211> 11
<212> DNA
<213> Homo sapiens

<400> 155
gaattcacca g 11

<210> 156
<211> 11
<212> DNA
<213> Homo sapiens

<400> 156
aaggagaact g 11

<210> 157
<211> 11
<212> DNA
<213> Homo sapiens

<400> 157
aatatctgac t 11

<210> 158
<211> 11
<212> DNA
<213> Homo sapiens

<400> 158
tcagtgacca g 11

<210> 159
<211> 11
<212> DNA
<213> Homo sapiens

<400> 159
gcaaagtgcc c 11

<210> 160
<211> 11
<212> DNA
<213> Homo sapiens

<400> 160
taaatacttg t 11

<210> 161
<211> 11
<212> DNA
<213> Homo sapiens

<400> 161
gtcactaatt t 11

<210> 162
<211> 11
<212> DNA
<213> Homo sapiens

<400> 162
ataacctgca g 11

<210> 163
<211> 11
<212> DNA
<213> Homo sapiens

<400> 163
tgcatctgtg c 11

<210> 164
<211> 11
<212> DNA
<213> Homo sapiens

<400> 164
taaaggcaca g 11

<210> 165
<211> 11
<212> DNA
<213> Homo sapiens

<400> 165
gaccgcggct t 11

<210> 166
<211> 11
<212> DNA
<213> Homo sapiens

<400> 166
actccggtgt g 11

<210> 167
<211> 11
<212> DNA
<213> Homo sapiens

<400> 167
cttctcacct a 11

<210> 168
<211> 11
<212> DNA
<213> Homo sapiens

<400> 168
tcgtgctttg t 11

<210> 169
<211> 11
<212> DNA
<213> Homo sapiens

<400> 169
gagcagtgct g 11

<210> 170
<211> 11
<212> DNA
<213> Homo sapiens

<400> 170
ctctaaaaaa a 11

<210> 171
<211> 11
<212> DNA
<213> Homo sapiens

<400> 171
gaaacccggt a 11

<210> 172
<211> 11
<212> DNA
<213> Homo sapiens

<400> 172
aacacagtgc c 11

<210> 173
<211> 2565
<212> DNA
<213> Homo sapiens

<400> 173
tcgcgatgct gctgcgcctg ttgctggcct gggcggccgc agggcccaca ctgggccagg 60
acccctgggc tgctgagccc cgtgccgcct gcggccccag cagctgctac gctctcttcc 120
cacggcgccg caccttcctg gaggcctggc gggcctgccg cgagctgggg ggcgacctgg 180
ccactcctcg gacccccgag gaggcccagc gtgtggacag cctggtgggt gcgggcccag 240
ccagccggct gctgtggatc gggctgcagc ggcaggcccg gcaatgccag ctgcagcgcc 300
cactgcgcgg cttcacgtgg accacagggg accaggacac ggctttcacc aactgggccc 360
agccagcctc tggaggcccc tgcccggccc agcgctgtgt ggccctggag gcaagtggcg 420
agcaccgctg gctggagggc tcgtgcacgc tggctgtcga cggctacctg tgccagtttg 480
gcttcgaggg cgcctgcccg gcgctgcaag atgaggcggg ccaggccggc ccagccgtgt 540
ataccacgcc cttccacctg gtctccacag agtttgagtg gctgcccttc ggctctgtgg 600
ccgctgtgca gtgccaggct ggcaggggag cctctctgct ctgcgtgaag cagcctgagg 660
gaggtgtggg ctggtcacgg gctgggcccc tgtgcctggg gactggctgc agccctgaca 720

acgggggctg cgaacacgaa tgtgtggagg aggtggatgg tcacgtgtcc tgccgctgca 780
ctgagggctt ccggctggca gcagacgggc gcagttgcga ggacccctgt gcccaggctc 840
cgtgcgagca gcagtgtgag cccggtgggc cacaaggcta cagctgccac tgtcgcctgg 900
gtttccggcc agcggaggat gatccgcacc gctgtgtgga cacagatgag tgccagattg 960
ccggtgtgtg ccagcagatg tgtgtcaact acgttggtgg cttcgagtgt tattgtagcg 1020
agggacatga gctggaggct gatggcatca gctgcagccc tgcaggggcc atgggtgccc 1080
aggcttccca ggacctcgga gatgagttgc tggatgacgg ggaggatgag gaagatgaag 1140
acgaggcctg gaaggccttc aacggtggct ggacggagat gcctgggatc ctgtggatgg 1200
agcctacgca gccgcctgac tttgccctgg cctatagacc gagcttccca gaggacagag 1260
agccacagat accctacccg gagcccacct ggccaccccc gctcagtgcc cccagggtcc 1320
cctaccactc ctcagtgctc tccgtcaccc ggcctgtggt ggtctctgcc acgcatccca 1380
cactgccttc tgcccaccag cctcctgtga tccctgccac acacccagct ttgtcccgtg 1440
accaccagat ccccgtgatc gcagccaact atccagatct gccttctgcc taccaacccg 1500
gtattctctc tgtctctcat tcagcacagc ctcctgccca ccagccccct atgatctcaa 1560
ccaaatatcc ggagctcttc cctgcccacc agtcccccat gtttccagac acccgggtcg 1620
ctggcaccca gaccaccact catttgcctg gaatcccacc taaccatgcc cctctggtca 1680
ccaccctcgg tgcccagcta cccctcaag ccccagatgc ccttgtcctc agaacccagg 1740
ccacccagct tcccattatc ccaactgccc agccctctct gaccaccacc tccaggtccc 1800
ctgtgtctcc tgcccatcaa atctctgtgc ctgctgccac ccagcccgca gccctcccca 1860
ccctcctgcc ctctcagagc ccactaacc agacctcacc catcagccct acacatcccc 1920
attccaaagc cccccaaatc ccaagggaag atggccccag tcccaagttg gccctgtggc 1980
tgccctcacc agctcccaca gcagccccaa cagccctggg ggaggctggt cttgccgagc 2040
acagccagag ggatgaccgg tggctgctgg tggcactcct ggtgccaacg tgtgtctttt 2100
tggtggtcct gcttgcactg ggcatcgtgt actgcacccg ctgtggcccc catgcaccca 2160
acaagcgcat cactgactgc tatcgctggg tcatccatgc tgggagcaag agcccaacag 2220
aacccatgcc ccccaggggc agcctcacag ggtgcagac ctgcagaacc agcgtgtgat 2280
ggggtgcaga ccccccctcat ggagtatggg gcgctggaca catggccggg gctgcaccag 2340
ggacccatgg gggctgccca gctggacaga tggcttcctg ctccccaggc ccagccaggg 2400
tcctctctca accactagac ttggctctca ggaactctgc ttcctggccc agcgctcgtg 2460
accaaggata caccaaagcc cttaagacct caggggcgg gtgctggggt cttctccaat 2520
aaatggggtg tcaaccttaa aaaaaaaaaa aaaaaaaaaa aaaaa 2565

<210> 174
<211> 2832
<212> DNA
<213> Homo sapiens

<400> 174
atgcctgctt ctctcgcttt gttgcagccc cgagccatga tgaagacttt gtccagcggg 60
aactgcacgc tcagtgtgcc cgccaaaaac tcataccgca tggtggtgct gggtgcctct 120
cgggtgggca agagctccat cgtgtctcgc ttcctcaatg gccgctttga ggaccagtac 180
acacccacca tcgaggactt ccaccgtaag gtatacaaca tccgcggcga catgtaccag 240
ctcgacatcc tggatacctc tggcaaccac cccttccccg ccatgcgcag gctgtccatc 300
ctcacagggg atgtcttcat cctggtgttc agcctggata accgggagtc cttcgatgag 360
gtcaagcgcc ttcagaagca gatcctggag gtcaagtcct gcctgaagaa caagaccaag 420
gaggcggcgg agctgcccat ggtcatctgt ggcaacaaga acgaccacgg cgagctgtgc 480
cgccaggtgc ccaccaccga ggccgagctg ctggtgtcgg gcgacgagaa ctgcgcctac 540
ttcgaggtgt cggccaagaa gaacaccaac gtggacgaga tgttctacgt gctcttcagc 600
atggccaagc tgccacacga gatgagcccc gccctgcatc gcaagatctc cgtgcagtac 660
ggtgacgcct tccaccccag gcccttctgc atgcgccgcg tcaaggagat ggacgcctat 720
ggcatggtct cgcccttcgc ccgccgcccc agcgtcaaca gtgacctcaa gtacatcaag 780
gccaaggtcc ttcgggaagg ccaggcccgt gagagggaca agtgcaccat ccagtgagcg 840
agggatgctg ggcggggct tggccagtgc cttcagggag gtggccccag atgcccactg 900
tgcgcatctc cccaccgagg ccccggcagc agtcttgttc acagacctta ggcaccagac 960
tggaggcccc cgggcgctgg cctccgcaca ttcgtctgcc ttctcacagc tttcctgagt 1020
ccgcttgtcc acagctcctt ggtggtttca tctcctctgt gggaggacac atctctgcag 1080
cctcaagagt taggcagaga ctcaagttac accttcctct cctggggttg gaagaaatgt 1140
tgatgccaga ggggtgagga ttgctgcgtc atatggagcc tcctgggaca agcctcagga 1200
tgaaaaggac acagaaggcc agatgagaaa ggtctcctct ctcctggcat aacacccagc 1260
ttggtttggg tggcagctgg gagaacttct ctcccagccc tgcaactctt acgctctggt 1320
tcagctgcct ctgcaccccc tcccaccccc agcacacaca caagttggcc cccagctgcg 1380

```
cctgacattg agccagtgga ctctgtgtct gaagggggcg tggccacacc tcctagacca   1440
cgcccaccac ttagaccacg cccacctcct gaccgcgttc ctcagcctcc tctcctaggt   1500
ccctccgccc gacagttgtg ctttgttgtg gttgcagctg ttttcgtgtc atgtatagta   1560
gtagaaatgg aaatcattgt actgtaaaag cctagtgact ccctccttgg ccaggccctc   1620
acccagttca gatccacggc ctccacccgg gacgccttcc tcctctgctc ccaaacaggg   1680
tttccgtggc ctgtttgcag ctagacattg acctccgcca ttgagctcca cggtttacag   1740
acaattgcac aagcgtgggg tgggcaggcc aggactgctt tttttaatg ctcccatttc   1800
acagaggata ccaccgagac tcggaggga cacgatgagc accaggcccc acctttgtcc   1860
cctagcaaat tcagggtaca gctccaccta gaaccaggct gccctctact gtgctcgttc   1920
ctcaagcatt tattaagcac ctactgggtg ctgggttcac tgtgtcctag gaaaccaaga   1980
gggtccccag tcctggcctc tgcccgcccc tgctgcccca ccaccttctg cacacacagc   2040
ggtggggagg cggggaggag cagctgggac ccagaactga gcctgggagg gatccgacag   2100
aaaagctcag ggcgggtctt ctccttgtgc ccgggattgg gctatgctgg gtaccaccat   2160
gtactcaggc atggtgggtt ttgaacccat aaaccaaagg cccttgtcat cagctcttaa   2220
caagtatatt ttgtatttta atctctctaa acatattgaa gttttagggc cctaaggaac   2280
cttagtgatc ttctattggg tctttctgag gttcagagag ggtaagtaac ttcctccagg   2340
tcacacagca agtctgtggg tggcagaagc aagctagcgc tgggcattca gtacatacca   2400
cgatgtgctc cctctcttga tgcttggccc ctggggcctt cagggctttg ggacatcttg   2460
tcctcaaccc tctccctaga tcagtctgtg agggtccctg tagatattgt gtacaccatg   2520
cccatgtata tacaagtaca cacagatgta cacacagatg tacacatgct ccagccccag   2580
ctctgcatac ctgcacctgc accccagcct tggcccctgc ctgcgtctgt gctcaaagca   2640
gcagctccaa ccctgcctct gtccccttcc ccacccactg cctgagcctt ctgagcagac   2700
caggtacctt ggctgcaccg gtgtgtggcc cgctctcacc caggcacagc cccgccacca   2760
tggatctccg tgtacactat caataaaagt gggtttgtta caaaaaaaaa aaaaaaaaaa   2820
aaaaaaaaaa aa                                                      2832
```

<210> 175
<211> 4640
<212> DNA
<213> Homo sapiens

<400> 175

```
gcggccgcag cctgagccag ggccccctcc ctcgtcagga ccggggcagc aagcaggccg     60
ggggcaggtc cgggcaccca ccatgcgagg cgagctctgg ctcctggtgc tggtgctcag    120
ggaggctgcc cgggcgctga gcccccagcc cggagcaggt cacgatgagg gcccaggctc    180
tggatgggct gccaaaggga ccgtgcgggg ctggaaccgg agagcccgag agagccctgg    240
gcatgtgtca gagccggaca ggacccagct gagccaggac ctgggtgggg gcaccctggc    300
catggacacg ctgccagata acaggaccag ggtggtggag gacaaccaca gctattatgt    360
gtcccgtctc tatggcccca gcgagcccca cagccgggaa ctgtgggtag atgtggccga    420
ggccaaccgg agccaagtga agatccacac aatactctcc aacacccacc ggcaggcttc    480
gagagtggtc ttgtcctttg atttcccttt ctacgggcat cctctgcggc agatcaccat    540
agcaactgga ggcttcatct tcatggggga cgtgatccat cggatgctca cagctactca    600
gtatgtggcg cccctgatgg ccaacttcaa ccctggctac tccgacaact ccacagttgt    660
ttactttgac aatgggacag tctttgtggt tcagtgggac cacgtttatc tccaaggctg    720
ggaagacaag ggcagtttca ccttccaggc agctctgcac catgacggcc gcattgtctt    780
tgcctataaa gagatcccta tgtctgtccc ggaaatcagc tcctcccagc atcctgtcaa    840
aaccggccta tcggatgcct tcatgattct caatccatcc ccggatgtgc cagaatctcg    900
gcgaaggagc atctttgaat accaccgcat agagctggac cccagcaagg tcaccagcat    960
gtcggccgtg gagttcaccc cattgccgac ctgcctgcag cataggagct gtgacgcctg   1020
catgtcctca gacctgacct tcaactgcag ctggtgccat gtcctccaga gatgctccag   1080
tggctttgac cgctatcgcc aggagtggga tgggactatg ggctgtgcac aggaggcaga   1140
ggggcaggat gtgcgaggac ttccagggat gaggaccacg acttcagcct cccctgacac   1200
ttccttcagc ccctatgatg gagacctcac cactacctcc tcctccctct tcatcgacag   1260
cctcaccaca gaagatgaca ccaagttgaa tccctatgca ggaggagacg gccttcagaa   1320
caacctgtcc cccaagacaa agggcactcc tgtgcacctg ggcaccatcg tgggcatcgt   1380
gctggcagtc ctcctcgtgg cggccatcat cctggctgga atttacatca atggccaccc   1440
cacatccaat gctgcgctct tcttcatcga gcgtagacct caccactggc cagccatgaa   1500
gtttcgcagc caccctgacc attccaccta tgcggaggtg gagccctcgg gccatgagaa   1560
ggagggcttc atggaggctg agcagtgctg agaacaccaa gtctcccctt tgaagacttt   1620
gaggccacag aaaagacagt taaagcaaag aagagaagtg acttttcctg gcctctccca   1680
gcatgccctg ggctgagatg agatggtggt ttatggctcc agagctgctg ttcgcttcgt   1740
```

cagcacaccc cgaatattga agagggggcc aaaaaacaac cacatggatt ttttatagga 1800
acaacaacct aatctcatcc tgttttgatg caagggttct cttctgtgtc ttgtaaccat 1860
gaaacagcag aagaactaac ataactaact ccatttttgt ttaaggggcc tttacctatt 1920
cctgcaccta ggctaggata actttagagc actgacataa aacgcaaaaa caggaatcat 1980
gccgtttgca aaactaactc tgggattaaa ggggaagcat gtaaacagct aactgttttt 2040
gttaaagatt tataggaatg aggaggtttg gctattgtca catgacagac tgttagccaa 2100
ggacaaagaa gttctgcaaa cctcccctgg acccttgctg gtgtccagat gtctgcggtt 2160
gtcagcccct tcctttcccc cgacctaaac ataaaagaca aggcaaagcc cgcataattt 2220
taagacggtt ctttaggaca ttagtccacc atcttcttgg tttgctggct ctccgaaata 2280
aagtcccttt ccttgctcca aaaaaaaaaa aaaaaaaaaa gcggccgcag cctgagccag 2340
ggccccctcc ctcgtcagga ccggggcagc aagcaggccg ggggcaggtc cgggcaccca 2400
ccatgcgagg cgagctctgg ctcctggtgc tggtgctcag ggaggctgcc cgggcgctga 2460
gcccccagcc cggagcaggt cacgatgagg gcccaggctc tggatgggct gccaaaggga 2520
ccgtgcgggg ctggaaccgg agagcccgag agagccctgg gcatgtgtca gagccggaca 2580
ggacccagct gagccaggac ctgggtgggg gcaccctggc catggacacg ctgccagata 2640
acaggaccag ggtggtggag gacaaccaca gctattatgt gtcccgtctc tatggcccca 2700
gcgagcccca cagccgggaa ctgtgggtag atgtggccga ggccaaccgg agccaagtga 2760
agatccacac aatactctcc aacacccacc ggcaggcttc gagagtggtc ttgtcctttg 2820
atttcccttt ctacgggcat cctctgcggc agatcaccat agcaactgga ggcttcatct 2880
tcatggggga cgtgatccat cggatgctca cagctactca gtatgtggcg cccctgatgg 2940
ccaacttcaa ccctggctac tccgacaact ccacagttgt ttactttgac aatgggacag 3000
tctttgtggt tcagtgggac cacgtttatc tccaaggctg ggaagacaag ggcagtttca 3060
ccttccaggc agctctgcac catgacggcc gcattgtctt tgcctataaa gagatcccta 3120
tgtctgtccc ggaaatcagc tcctcccagc atcctgtcaa aaccggccta tcggatgcct 3180
tcatgattct caatccatcc ccggatgtgc cagaatctcg gcgaaggagc atctttgaat 3240
accaccgcat agagctggac cccagcaagg tcaccagcat gtcggccgtg gagttcaccc 3300
cattgccgac ctgcctgcag cataggagct gtgacgcctg catgtcctca gacctgacct 3360
tcaactgcag ctggtgccat gtcctccaga gatgctccag tggctttgac cgctatcgcc 3420
aggagtggat ggactatggc tgtgcacagg aggcagaggg caggatgtgc gaggacttcc 3480
aggatgagga ccacgactca gcctcccctg acacttcctt cagcccctat gatggagacc 3540
tcaccactac ctcctcctcc ctcttcatcg acagcctcac cacagaagat gacaccaagt 3600
tgaatcccta tgcaggagga gacggccttc agaacaacct gtcccccaag acaaagggca 3660
ctcctgtgca cctgggcacc atcgtgggca tcgtgctggc agtcctcctc gtggcggcca 3720
tcatcctggc tggaatttac atcaatggcc accccacatc caatgctgcg ctcttcttca 3780
tcgagcgtag acctcaccac tggccagcca tgaagtttcg cagccaccct gaccattcca 3840
cctatgcgga ggtggagccc tcgggccatg agaaggaggg cttcatggag gctgagcagt 3900
gctgagaaca ccaagtctcc cctttgaaga ctttgaggcc acagaaaaga cagttaaagc 3960
aaagaagaga agtgactttt cctggcctct cccagcatgc cctgggctga gatgagatgg 4020
tggtttatgg ctccagagct gctgctcgct tcgtcagcac accccgaata ttgaagaggg 4080
ggccaaaaaa caaccacatg gattttttat aggaacaaca acctaatctc atcctgtttt 4140
gatgcaaggg ttctcttctg tgtcttgtaa ccatgaaaca gcagaagaac taacataact 4200
aactccattt ttrtttaagg ggcctttacc tattcctgca cctaggctag gataacttta 4260
gagcactgas ataaaacgca aaaacaggaa tcatgccgtt tgcaaaacta actctgggat 4320
taaaggggaa gcatgtaaac agctaactgt ttttgttaaa gatttatagg aatgaggagg 4380
tttggctatt gtcacatgac agactgttag ccaaggacaa agaagttctg caaacctccc 4440
ctggaccctt gctggtgtcc agatgtctgc ggttgtcagc cccttccttt cccccgacct 4500
aaacataaaa gacaaggcaa agcccgcata atttaagac ggttctttag gacattagtc 4560
caccatcttc ttggtttgct ggctctccga aataaagtcc ctttccttgc tccaaaaaaa 4620
aaaaaaaaaa aaaaaaaaaa 4640

<210> 176
<211> 5540
<212> DNA
<213> Homo sapiens

<400> 176
aattgcttcc ggggagttgc gagggagcga gggggaataa aggacccgcg aggaagggcc 60
cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtgggaa ggagcggacc 120
ctgctctccc cgggctgcgg gccatggcca cggcggagcg gagagccctc ggcatcggct 180
tccagtggct ctctttggcc actctggtgc tcatctgcgc cgggcaaggg ggacgcaggg 240
aggatggggg tccagcctgc tacggcggat ttgacctgta cttcattttg gacaaatcag 300

gaagtgtgct gcaccactgg aatgaaatct attactttgt ggaacagttg gctcacaaat 360
tcatcagccc acagttgaga atgtccttta ttgttttctc cacccgagga acaaccttaa 420
tgaaactgac agaagacaga gaacaaatcc gtcaaggcct agaagaactc cagaaagttc 480
tgccaggagg agacacttac atgcatgaag gatttgaaag ggccagtgag cagatttatt 540
atgaaaacag acaagggtac aggacagcca gcgtcatcat tgctttgact gatggagaac 600
tccatgaaga tctctttttc tattcagaga gggaggctaa taggtctcga gatcttggtg 660
caattgttta ctgtgttggt gtgaaagatt tcaatgagac acagctggcc cggattgcgg 720
acagtaagga tcatgtgttt cccgtgaatg acggctttca ggctctgcaa ggcatcatcc 780
actcaatttt gaagaagtcc tgcatcgaaa ttctagcagc tgaaccatcc accatatgtg 840
caggagagtc atttcaagtt gtcgtgagag gaaacggctt ccgacatgcc cgcaacgtgg 900
acagggtcct ctgcagcttc aagatcaatg actcggtcac actcaatgag aagccctttt 960
ctgtggaaga tacttattta ctgtgtccag cgcctatctt aaaagaagtt ggcatgaaag 1020
ctgcactcca ggtcagcatg aacgatggcc tctcttttat ctccagttct gtcatcatca 1080
ccaccacaca ctgttctgac ggttccatcc tggccatcgc cctgctgatc ctgttcctgc 1140
tcctagccct ggctctcctc tggtggttct ggcccctctg ctgcactgtg attatcaagg 1200
aggtccctcc accccctgcc gaggagagtg aggaagaaga tgatgatggt ctgcctaaga 1260
aaaagtggcc aacggtagac gcctcttatt atggtgggag aggcgttgga ggcattaaaa 1320
gaatggaggt tcgttgggga gaaaagggct ccacagaaga aggtgctaag ttggaaaagg 1380
caaagaatgc aagagtcaag atgccggagc aggaatatga attccctgag ccgcgaaatc 1440
tcaacaacaa tatgcgtcgg ccttcttccc cccggaagtg gtactctcca atcaagggaa 1500
aactcgatgc cttgtgggtc ctactgagga aaggatatga tcgtgtgtct gtgatgcgtc 1560
cacagccagg agacacgggg cgctgcatca acttcaccag ggtcaagaac aaccagccag 1620
ccaagtaccc actcaacaac gcctaccaca cctcctcgcc gcctcctgcc cccatctaca 1680
ctcccccacc tcctgcgccc cactgccctc ccccgccccc cagcgcccct acccctccca 1740
tcccgtcccc accttccacc cttccccctc ctccccaggc tccacctccc aacagggcac 1800
ctcctccctc ccgccctcct ccaaggcctt ctgtctagag cccaaagttc ctgctctggg 1860
ctctctcaga aacttcagga gatgttagaa caagtctttc cagttagaga agaggagtgg 1920
tgataaagcc cactgacctt cacacattct aaaaattggt tggcaatgcc agtataccaa 1980
caatcatgat cagctgaaag aaacagatat tttaaattgc cagaaaacaa atgatgaggc 2040
aactacagtc agatttatag ccagccatct atcacctcta gaaggttcca gagacagtga 2100
aactgcaaga tgctctcaac aggattatgt ctcatggaga ccagtaagaa aatcatttat 2160
ctgaaggtga aatgcagagt tggataagaa atacattgct gggtttctaa aatgctgcct 2220
tcctgcctct actccacctc catccctgga ctttggaccc ttggcctagg agcctaagga 2280
ccttcacccc tgtgcaccac ccaagaaaga ggaaaacttt gcctacaact ttggaaatgc 2340
tggggtccct ggtgtggtaa gaaactcaac atcagacggg tatgcagaag gatgttcttc 2400
tgggatttgc aggtacataa aaaatgtatg gcatcttttc cttgcaaatt cttccagttt 2460
ccaagtgaga aggggagcag gtgtttactg atggaaaagg tatgttgcta tgttgatgtg 2520
taagtgaaat cagttgtgtg caatagacag ggcgtattc atgggagcat cagccagttt 2580
ctaaaaccca caggccatca gcagctagag gtggctggct ttggccagac atggacccta 2640
aatcaacaga caatggcatt gtcgaagagc aacctgttaa tgaatcatgt taaaaatcaa 2700
ggtttggctt cagtttaaat cacttgaggt atgaagttta tcctgttttc cagagataaa 2760
cataagttga tcttcccaaa ataccatcat taggacctat cacacaatat cactagtttt 2820
ttttgtttgt ttgtttttttg tttttttttct tggtaaagcc atgcaccaca gacttctggg 2880
cagagctgag agacaatggt cctgacataa taaggatctt tgattaaccc ccataaggca 2940
tgtgtgtgta tacaaatata cttctctttg gcttttcgac atagaacctc agctgttaac 3000
caaggggaaa tacatcagat ctgcaacaca gaaatgctct gcctgaaatt tccaccatgc 3060
ctaggactca ccccatttat ccaggtcttt ctggatctgt ttaatcaata agccctataa 3120
tcacttgcta aacactgggc ttcatcaccc agggataaaa acagagatca ttgtcttgga 3180
cctcctgcat cagcctattc aaaattatct ctctctctag ctttccacaa atcctaaaat 3240
tcctgtccca agccacccaa attctcagat cttttctgga acaaggcaga atataaaata 3300
aatatacatt tagtggcttg ggctatggtc tccaaagatc cttcaaaaat acatcaagcc 3360
agcttcattc actcacttta cttagaacag agatataagg gcctgggatg catttatttt 3420
atcaatacca atttttgtgg ccatggcaga cattgctaat caatcacagc actatttcct 3480
attaagccca ctgatttctt cacaatcctt ctcaaattac aattccaaag agccgccact 3540
caacagtcag atgaacccaa cagtcagatg agagaaatga accctacttg ctatctctat 3600
cttagaaagc aaaaacaaac aggagtttcc agggagaatg ggaaagccag ggggcataaa 3660
aggtacagtc aggggaaaat agatctaggc agagtgcctt agtcagggac cacgggcgct 3720
gaatctgcag tgccaacacc aaactgacac atctccaggt gtacctccaa ccctagcctt 3780
ctcccacagc tgcctacaac agagtctccc agccttctca gagagctaaa accagaaatt 3840
tccagactca tgaaagcaac cccccagcct ctccccaacc ctgccgcatt gtctaatttt 3900
tagaacacta ggcttcttct ttcatgtagt tcctcataag caggggccag aatatctcag 3960

ccacctgcag tgacattgct ggacccctga aaaccattcc ataggagaat gggttcccca 4020
ggctcacagt gtagagacat tgagcccatc acaactgttt tgactgctgg cagtctaaaa 4080
cagtccaccc accccatggc actgccgcgt gattcccgcg gccattcaga agttcaagcc 4140
gagatgctga cgttgctgag caacgagatg gtgagcatca gtgcaaatgc accattcagc 4200
acatcagtca tatgcccagt gcagttacaa gatgttgttt cggcaaagca ttttgatgga 4260
atagggaact gcaaatgtat gatgattttg aaaaggctca gcaggatttg ttcttaaacc 4320
gactcagtgt gtcatccccg gttatttaga attacagtta agaaggagaa acttctataa 4380
gactgtatga acaaggtgat atcttcatag tgggctatta caggcaggaa aatgttttaa 4440
ctggtttaca aaatccatca atacttgtgt cattccctgt aaaaggcagg agacatgtga 4500
ttatgatcag gaaactgcac aaaattattg ttttcagccc ccgtgttatt gtccttttga 4560
actgtttttt ttttattaaa gccaaatttg tgttgtatat attcgtattc catgtgttag 4620
atggaagcat ttcctatcca gtgtgaataa aaagaacagt tgtagtaaat tattataaag 4680
ccgatgatat ttcatggcag gttattctac caagctgtgc ttgttggttt ttcccatgac 4740
tgtattgctt ttataaatgt acaaatagtt actgaaatga cgagaccctt gtttgcacag 4800
cattaataag aaccttgata agaaccatat tctgttgaca gccagctcac agtttcttgc 4860
ctgaagcttg gtgcaccctc cagtgagaca caagatctct cttttaccaa agttgagaac 4920
agagctggtg gattaattaa tagtcttcga tatctggcca tgggtaacct cattgtaact 4980
atcatcagaa tgggcagaga tgatcttgaa gtgtcacata cactaaagtc caaacactat 5040
gtcagatggg ggtaaaatcc attaaagaac aggaaaaaat aattataaga tgataagcaa 5100
atgtttcagc ccaatgtcaa cccagttaaa aaaaaaatta atgctgtgta aaatggttga 5160
attagtttgc aaactatata aagacatatg cagtaaaaag tctgttaatg cacatcctgt 5220
gggaatggag tgttctaacc aattgccttt tcttgttatc tgagctctcc tatattatca 5280
tactcagata accaaattaa aagaattaga atatgatttt taatacactt aacattaaac 5340
tcttctaact ttcttctttc tgtgataatt cagaagatag ttatggatct tcaatgcctc 5400
tgagtcattg ttataaaaaa tcagttatca ctataccatg ctataggaga ctgggcaaaa 5460
cctgtacaat gacaaccctg gaagttgctt tttttaaaaa aataataaat ttcttaaatc 5520
aaaaaaaaaa aaaaaaaaaa 5540

<210> 177
<211> 757
<212> PRT
<213> Homo sapiens

<400> 177
Met Leu Leu Arg Leu Leu Leu Ala Trp Ala Ala Ala Gly Pro Thr Leu
1 5 10 15
Gly Gln Asp Pro Trp Ala Ala Glu Pro Arg Ala Ala Cys Gly Pro Ser
20 25 30
Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp
35 40 45
Arg Ala Cys Arg Glu Leu Gly Gly Asp Leu Ala Thr Pro Arg Thr Pro
50 55 60
Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Ala Gly Pro Ala Ser
65 70 75 80
Arg Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu
85 90 95
Gln Arg Pro Leu Arg Gly Phe Thr Trp Thr Thr Gly Asp Gln Asp Thr
100 105 110
Ala Phe Thr Asn Trp Ala Gln Pro Ala Ser Gly Gly Pro Cys Pro Ala
115 120 125
Gln Arg Cys Val Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
130 135 140
Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe
145 150 155 160
Glu Gly Ala Cys Pro Ala Leu Gln Asp Glu Ala Gly Gln Ala Gly Pro
165 170 175
Ala Val Tyr Thr Thr Pro Phe His Leu Val Ser Thr Glu Phe Glu Trp
180 185 190
Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly

```
        195                 200                 205
Ala Ser Leu Leu Cys Val Lys Gln Pro Glu Gly Gly Val Gly Trp Ser
    210                 215                 220
Arg Ala Gly Pro Leu Cys Leu Gly Thr Gly Cys Ser Pro Asp Asn Gly
225                 230                 235                 240
Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly His Val Ser Cys
                245                 250                 255
Arg Cys Thr Glu Gly Phe Arg Leu Ala Ala Asp Gly Arg Ser Cys Glu
            260                 265                 270
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly
        275                 280                 285
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu
    290                 295                 300
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly
305                 310                 315                 320
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr
                325                 330                 335
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro
            340                 345                 350
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Gly Asp Glu Leu
        355                 360                 365
Leu Asp Asp Gly Glu Asp Glu Glu Asp Glu Asp Glu Ala Trp Lys Ala
    370                 375                 380
Phe Asn Gly Gly Trp Thr Glu Met Pro Gly Ile Leu Trp Met Glu Pro
385                 390                 395                 400
Thr Gln Pro Pro Asp Phe Ala Leu Ala Tyr Arg Pro Ser Phe Pro Glu
                405                 410                 415
Asp Arg Glu Pro Gln Ile Pro Tyr Pro Glu Pro Thr Trp Pro Pro Pro
            420                 425                 430
Leu Ser Ala Pro Arg Val Pro Tyr His Ser Ser Val Leu Ser Val Thr
        435                 440                 445
Arg Pro Val Val Val Ser Ala Thr His Pro Thr Leu Pro Ser Ala His
    450                 455                 460
Gln Pro Pro Val Ile Pro Ala Thr His Pro Ala Leu Ser Arg Asp His
465                 470                 475                 480
Gln Ile Pro Val Ile Ala Ala Asn Tyr Pro Asp Leu Pro Ser Ala Tyr
                485                 490                 495
Gln Pro Gly Ile Leu Ser Val Ser His Ser Ala Gln Pro Pro Ala His
            500                 505                 510
Gln Pro Pro Met Ile Ser Thr Lys Tyr Pro Glu Leu Phe Pro Ala His
        515                 520                 525
Gln Ser Pro Met Phe Pro Asp Thr Arg Val Ala Gly Thr Gln Thr Thr
    530                 535                 540
Thr His Leu Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr
545                 550                 555                 560
Leu Gly Ala Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg
                565                 570                 575
Thr Gln Ala Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu
            580                 585                 590
Thr Thr Thr Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val
        595                 600                 605
Pro Ala Ala Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln
    610                 615                 620
Ser Pro Thr Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser
625                 630                 635                 640
Lys Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala
                645                 650                 655
Leu Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly
            660                 665                 670
Glu Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu
        675                 680                 685
```

Val Ala Leu Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala
690 695 700
Leu Gly Ile Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys
705 710 715 720
Arg Ile Thr Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser
725 730 735
Pro Thr Glu Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr
740 745 750
Cys Arg Thr Ser Val
755

<210> 178
<211> 278
<212> PRT
<213> Homo sapiens

<400> 178
Met Pro Ala Ser Leu Ala Leu Leu Gln Pro Arg Ala Met Met Lys Thr
1 5 10 15
Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala Lys Asn Ser Tyr
20 25 30
Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys Ser Ser Ile Val
35 40 45
Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr Thr Pro Thr Ile
50 55 60
Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly Asp Met Tyr Gln
65 70 75 80
Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe Pro Ala Met Arg
85 90 95
Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu Val Phe Ser Leu
100 105 110
Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu Gln Lys Gln Ile
115 120 125
Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys Glu Ala Ala Glu
130 135 140
Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His Gly Glu Leu Cys
145 150 155 160
Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val Ser Gly Asp Glu
165 170 175
Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn Thr Asn Val Asp
180 185 190
Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu Pro His Glu Met
195 200 205
Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr Gly Asp Ala Phe
210 215 220
His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu Met Asp Ala Tyr
225 230 235 240
Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val Asn Ser Asp Leu
245 250 255
Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln Ala Arg Glu Arg
260 265 270
Asp Lys Cys Thr Ile Gln
275

<210> 179
<211> 1002
<212> PRT
<213> Homo sapiens

<400> 179
Met Arg Gly Glu Leu Trp Leu Leu Val Leu Val Leu Arg Glu Ala Ala

```
1               5                   10                  15
Arg Ala Leu Ser Pro Gln Pro Gly Ala Gly His Asp Glu Gly Pro Gly
            20                  25                  30
Ser Gly Trp Ala Ala Lys Gly Thr Val Arg Gly Trp Asn Arg Arg Ala
        35                  40                  45
Arg Glu Ser Pro Gly His Val Ser Glu Pro Asp Arg Thr Gln Leu Ser
    50                  55                  60
Gln Asp Leu Gly Gly Gly Thr Leu Ala Met Asp Thr Leu Pro Asp Asn
65                  70                  75                  80
Arg Thr Arg Val Val Glu Asp Asn His Ser Tyr Tyr Val Ser Arg Leu
                85                  90                  95
Tyr Gly Pro Ser Glu Pro His Ser Arg Glu Leu Trp Val Asp Val Ala
            100                 105                 110
Glu Ala Asn Arg Ser Gln Val Lys Ile His Thr Ile Leu Ser Asn Thr
        115                 120                 125
His Arg Gln Ala Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe Tyr
    130                 135                 140
Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile Phe
145                 150                 155                 160
Met Gly Asp Val Ile His Arg Met Leu Thr Ala Thr Gln Tyr Val Ala
                165                 170                 175
Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr Val
            180                 185                 190
Val Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His Val
        195                 200                 205
Tyr Leu Gln Gly Trp Glu Asp Lys Gly Ser Phe Thr Phe Gln Ala Ala
    210                 215                 220
Leu His His Asp Gly Arg Ile Val Phe Ala Tyr Lys Glu Ile Pro Met
225                 230                 235                 240
Ser Val Pro Glu Ile Ser Ser Ser Gln His Pro Val Lys Thr Gly Leu
                245                 250                 255
Ser Asp Ala Phe Met Ile Leu Asn Pro Ser Pro Asp Val Pro Glu Ser
            260                 265                 270
Arg Arg Arg Ser Ile Phe Glu Tyr His Arg Ile Glu Leu Asp Pro Ser
        275                 280                 285
Lys Val Thr Ser Met Ser Ala Val Glu Phe Thr Pro Leu Pro Thr Cys
    290                 295                 300
Leu Gln His Arg Ser Cys Asp Ala Cys Met Ser Ser Asp Leu Thr Phe
305                 310                 315                 320
Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe Asp
                325                 330                 335
Arg Tyr Arg Gln Glu Trp Asp Gly Thr Met Gly Cys Ala Gln Glu Ala
            340                 345                 350
Glu Gly Gln Asp Val Arg Gly Leu Pro Gly Met Arg Thr Thr Thr Ser
        355                 360                 365
Ala Ser Pro Asp Thr Ser Phe Ser Pro Tyr Asp Gly Asp Leu Thr Thr
    370                 375                 380
Thr Ser Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr
385                 390                 395                 400
Lys Leu Asn Pro Tyr Ala Gly Gly Asp Gly Leu Gln Asn Asn Leu Ser
                405                 410                 415
Pro Lys Thr Lys Gly Thr Pro Val His Leu Gly Thr Ile Val Gly Ile
            420                 425                 430
Val Leu Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr
        435                 440                 445
Ile Asn Gly His Pro Thr Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg
    450                 455                 460
Arg Pro His His Trp Pro Ala Met Lys Phe Arg Ser His Pro Asp His
465                 470                 475                 480
Ser Thr Tyr Ala Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe
                485                 490                 495
```

Met Glu Ala Glu Gln Cys Met Arg Gly Glu Leu Trp Leu Leu Val Leu
500 505 510
Val Leu Arg Glu Ala Ala Arg Ala Leu Ser Pro Gln Pro Gly Ala Gly
515 520 525
His Asp Glu Gly Pro Gly Ser Gly Trp Ala Ala Lys Gly Thr Val Arg
530 535 540
Gly Trp Asn Arg Arg Ala Arg Glu Ser Pro Gly His Val Ser Glu Pro
545 550 555 560
Asp Arg Thr Gln Leu Ser Gln Asp Leu Gly Gly Gly Thr Leu Ala Met
565 570 575
Asp Thr Leu Pro Asp Asn Arg Thr Arg Val Val Glu Asp Asn His Ser
580 585 590
Tyr Tyr Val Ser Arg Leu Tyr Gly Pro Ser Glu Pro His Ser Arg Glu
595 600 605
Leu Trp Val Asp Val Ala Glu Ala Asn Arg Ser Gln Val Lys Ile His
610 615 620
Thr Ile Leu Ser Asn Thr His Arg Gln Ala Ser Arg Val Val Leu Ser
625 630 635 640
Phe Asp Phe Pro Phe Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala
645 650 655
Thr Gly Gly Phe Ile Phe Met Gly Asp Val Ile His Arg Met Leu Thr
660 665 670
Ala Thr Gln Tyr Val Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr
675 680 685
Ser Asp Asn Ser Thr Val Val Tyr Phe Asp Asn Gly Thr Val Phe Val
690 695 700
Val Gln Trp Asp His Val Tyr Leu Gln Gly Trp Glu Asp Lys Gly Ser
705 710 715 720
Phe Thr Phe Gln Ala Ala Leu His His Asp Gly Arg Ile Val Phe Ala
725 730 735
Tyr Lys Glu Ile Pro Met Ser Val Pro Glu Ile Ser Ser Ser Gln His
740 745 750
Pro Val Lys Thr Gly Leu Ser Asp Ala Phe Met Ile Leu Asn Pro Ser
755 760 765
Pro Asp Val Pro Glu Ser Arg Arg Arg Ser Ile Phe Glu Tyr His Arg
770 775 780
Ile Glu Leu Asp Pro Ser Lys Val Thr Ser Met Ser Ala Val Glu Phe
785 790 795 800
Thr Pro Leu Pro Thr Cys Leu Gln His Arg Ser Cys Asp Ala Cys Met
805 810 815
Ser Ser Asp Leu Thr Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg
820 825 830
Cys Ser Ser Gly Phe Asp Arg Tyr Arg Gln Glu Trp Met Asp Tyr Gly
835 840 845
Cys Ala Gln Glu Ala Glu Gly Arg Met Cys Glu Asp Phe Gln Asp Glu
850 855 860
Asp His Asp Ser Ala Ser Pro Asp Thr Ser Phe Ser Pro Tyr Asp Gly
865 870 875 880
Asp Leu Thr Thr Thr Ser Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr
885 890 895
Glu Asp Asp Thr Lys Leu Asn Pro Tyr Ala Gly Gly Asp Gly Leu Gln
900 905 910
Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val His Leu Gly Thr
915 920 925
Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala Ala Ile Ile Leu
930 935 940
Ala Gly Ile Tyr Ile Asn Gly His Pro Thr Ser Asn Ala Ala Leu Phe
945 950 955 960
Phe Ile Glu Arg Arg Pro His His Trp Pro Ala Met Lys Phe Arg Ser
965 970 975
His Pro Asp His Ser Thr Tyr Ala Glu Val Glu Pro Ser Gly His Glu

```
        980                 985                 990
Lys Glu Gly Phe Met Glu Ala Glu Gln Cys
    995                 1000

      <210> 180
      <211> 5680
      <212> DNA
      <213> Homo sapiens

      <400> 180
gggcgatggg ttgatgggcg ccgggggacg caggatgcgg ggggcgcccg cgcgcctgct      60
gctgccgctg ctgccgtggc tcctgctgct cctggcgccc gaggctcggg gcgcgcccgg     120
ctgcccgcta tccatccgca gctgcaagtg ctcgggggag cggcccaagg ggctgagcgg     180
cggcgtccct ggcccggctc ggcggagggt ggtgtgcagc ggcggggacc tcccggagcc     240
tcccgagccc ggccttctgc ctaacggcac cgttaccctg ctcttgagca ataacaagat     300
cacggggctc cgcaatggct ccttcctggg actgtcactg ctggagaagc tggacctgag     360
gaacaacatc atcagcacag tgcagccggg cgccttcctg ggcctggggg agctgaagcg     420
tttagatctc tccaacaacc ggattggctg tctcacctcc gagaccttcc agggcctccc     480
caggcttctc cgactaaaca tatctggaaa catcttctcc agtctgcaac ctggggtctt     540
tgatgagctg ccagccctta aggttgtgga cttgggcacc gagttcctga cctgtgactg     600
ccacctgcgc tggctgctgc cctgggccca gaatcgctcc ctgcagctgt cggaacacac     660
gctctgtgct taccccagtg ccctgcatgc tcaggccctg ggcagcctcc aggaggccca     720
gctctgctgc gaggggcccc tggagctgca cacacaccac ctcatcccgt ccctacgcca     780
agtggtgttc caggggggatc ggctgccctt ccagtgctct gccagctacc tgggcaacga     840
cacccgcatc cgctggtacc acaaccgagc ccctgtggag ggtgatgagc aggcgggcat     900
cctcctggcc gagagcctca tccacgactg caccttcatc accagtgagc tgacgctgtc     960
tcacatcggc gtgtgggcct caggcgagtg ggagtgcacc gtgtccatgg cccaaggcaa    1020
cgccagcaag aaggtggaga tcgtggtgct ggagacctct gcctcctact gccccgccga    1080
gcgtgttgcc aacaaccgcg gggacttcag gtggccccga actctggctg gcatcacagc    1140
ctaccagtcc tgcctgcagt atcccttcac ctcagtgccc ctgggcgggg gtgccccggg    1200
cacccgagcc tcccgccggt gtgaccgtgc cggccgctgg gagccagggg actactccca    1260
ctgtctctac accaacgaca tcaccagggt gctgtacacc ttcgtgctga tgcccatcaa    1320
tgcctccaat gcgctgaccc tggctcacca gctgcgcgtg tacacagccg aggccgctag    1380
cttttcagac atgatggatg tagtctatgt ggctcagatg atccagaaat tttgggttta    1440
tgtcgaccag atcaaagagc tggtagaggt gatggtggac atggccagca acctgatgct    1500
ggtggacgag cacctgctgt ggctggccca gcgcgaggac aaggcctgca gccgcatcgt    1560
gggtgccctg gagcgcattg gggggccgc cctcagcccc catgcccagc acatctcagt    1620
gaatgcgagg aacgtggcat tggaggccta cctcatcaag ccgcacagct acgtgggcct    1680
gacctgcaca gccttccaga ggagggaggg aggggtgccg ggcacacggc caggaagccc    1740
tggccagaac cccccacctg agcccgagcc cccagctgac cagcagctcc gcttccgctg    1800
caccaccggg aggcccaatg tttctctgtc gtccttccac atcaagaaca gcgtggccct    1860
ggcctccatc cagctgcccc cgagtctatt ctcatccctt ccggctgccc tggctccccc    1920
ggtgccccca gactgcaccc tgcaactgct cgtcttccga aatggccgcc tcttccacag    1980
ccacagcaac acctcccgcc ctggagctgc tgggcctggc aagaggcgtg gcgtggccac    2040
ccccgtcatc ttcgcaggaa ccagtggctg tggcgtggga aacctgacag agccagtggc    2100
cgtttcgctg cggcactggg ctgagggagc cgaacctgtg gccgcttggt ggagccagga    2160
ggggcccggg gaggctgggg gctggacctc ggagggctgc cagctccgct ccagccagcc    2220
caatgtcagc gccctgcact gccagcactt gggcaatgtg gccgtgctca tggagctgag    2280
cgcctttccc agggaggtgg ggggcgccgg ggcagggctg caccccgtgg tataccccctg    2340
cacggccttg ctgctgctct gcctcttcgc caccatcatc acctacatcc tcaaccacag    2400
ctccatccgt gtgtcccgga aaggctggca catgctgctg aacttgtgct tccacatagc    2460
catgacctct gctgtctttg cgggggggcat cacactcacc aactaccaga tggtctgcca    2520
ggcggtgggc atcaccctgc actactcctc cctatccacg ctgctctgga tgggcgtgaa    2580
ggcgcgagtg ctccataagg agctcacctg gagggcaccc cctccgcaag aaggggaccc    2640
cgctctgcct actcccagtc ctatgctccg gttctatttg atcgctggag ggattccact    2700
cattatctgt ggcatcacag ctgcagtcaa catccacaac taccgggacc acagccccta    2760
ctgctggctg gtgtggcgtc caagccttgg cgccttctac atccctgtgg ctttgattct    2820
gctcatcacc tggatctatt tcctgtgcgc cgggctacgc ttacggggtc ctctggcaca    2880
gaaccccaag gcgggcaaca gcagggcctc cctggaggca ggggaggagc tgaggggttc    2940
caccaggctc aggggcagcg gccccctcct gagtgactca ggttcccttc ttgctactgg    3000
gagcgcgcga gtggggacgc ccgggccccc ggaggatggt gacagcctct attctccggg    3060
```

agtccagcta ggggcgctgg tgaccacgca cttcctgtac ttggccatgt gggcctgcgg 3120
ggctctggca gtgtcccagc gctggctgcc ccgggtggtg tgcagctgct tgtacggggt 3180
ggcagcctcc gccctgggcc tcttcgtctt cactcaccac tgtgccaggc ggagggacgt 3240
gagagcctcg tggcgcgcct gctgccccc tgcctctccc gcggcccccc atgccccgcc 3300
ccgggccctg cccgccgccg cagaggacgg ttccccggtg ttcggggagg ggcccccctc 3360
cctcaagtcc tccccaagcg gcagcagcgg ccatccgctg gctctgggcc cctgcaagct 3420
caccaacctg cagctggccc agagtcaggt gtgcgaggcg ggggcggcgg ccggcgggga 3480
aggagagccg gagccggcgg gcacccgggg aaacctcgcc caccgccacc ccaacaacgt 3540
gcaccacggg cgtcgggcgc acaagagccg ggccaaggga caccgcgcgg gggaggcctg 3600
cggcaagaac cggctcaagg ccctgcgcgg gggcgcggcg ggggcgctgg agctgctgtc 3660
cagcgagagc ggtagtctgc acaacagccc caccgacagc tacctgggca gcagccgcaa 3720
cagcccgggc gccggcctgc agctggaagg cgagcccatg ctcacgccgt ccgagggcag 3780
cgacaccagc gccgcgccgc tttctgaggc gggccgggca ggccagcgcc gcagcgccag 3840
ccgcgacagt ctcaagggcg gcggcgcgct ggagaaggag agccatcgcc gctcgtaccc 3900
gctcaacgcc gccagcctaa acggcgcccc caagggggc aagtacgacg acgtcaccct 3960
gatgggcgcg gaggtagcca gcggcggctg catgaagacc ggactctgga agagcgaaac 4020
taccgtctaa ggtggggcgg gcgacgcggt agacgggctg gccacgcggc tcgttccccc 4080
gctcctcggg gccctccaag gtgtctccgt agtcagcagg ttggaggcag aggagccgat 4140
ggctggagga agcccacagg cggatgttcc ccacttgcct agagggcatc cctctggggt 4200
agcgacagac aatcccagaa acacgcataa tacatttccg tccagcccgg ggcagtctga 4260
ctgtcggtgc cctcccagga acggggaagg cctccgtctg tgtgaaaggg cacagcacat 4320
cccaggtgca ccctccccaa gtactcccac cccgcctact gtccatgcgg cctcactggg 4380
ggccatcagc ctcaccagca aagcagagat gagagcgtgg gaactgtgtt ctttcctccc 4440
tgccctctac tgatttcagc ccagcccctg cctagatcct aggtcccttt tcctcccgag 4500
tttggctggc acgagagcta gcccagcaca tgaagcaggt gatgttaagt cacaaggtgc 4560
tgcttttcag atccactatg caagagggga gggtggggcc acgtgaaagg cagctctaga 4620
catcaaccag tcctgggggga ggggagtggg aaccgggcac aactaggaac aatgccacca 4680
ttcccacagg agtggtactt aaaccagaca gcagggttca gaggtggcac accgggacaa 4740
agctgaggcc ctgcacctca acagctgact gccaggtgcc tgtgggtgaa ctgaggggag 4800
tagagggaga gggcaggtgg aactggggca gaatctagtc atgccctaaa gctagtcctg 4860
taaacaatgg tgccccagaa agctgcaggt ggtgtttgga gaagcagtta cttttcagtt 4920
acaagaccca tctccctagt ctcagcctta caacaccacg ggactaagga agagcacttc 4980
cttgcctccg taaggccaga ggaagaacca tcccaatcat ttgatctcca gctccacagt 5040
agagagaaac ctacaaaatg tcaaaccagc ttcccgactc ccaggagctc aagccaagcc 5100
cagaggcagt ggctggggtc cctgcaggtc atgaggggcc tatgccttta ctccttttaa 5160
acaccagcac ccgtcttttc cccaacctaa aaccaaccac cagcatttca ctacaggacc 5220
aaatggaaac cgagggaacc ctgggtcttg ggaagaacaa caggaaacca aggtctgacc 5280
tagggttccc tcccagtctt cacatcactc tggcctcatc accaaggtga cagaggacac 5340
aggggagggg gaaaacccac acacactcct tggaatgggt cctgttattt atgcttgctg 5400
cacagacata ttagaagaaa aaaaaaagct ttgtattatt cttccacata tgctggctgc 5460
tgtttacaca ccctgccaat gccttagcac tggagagctt tttgcaatat gctggggaaa 5520
ggggagggag ggaatgaaag tgccaaagaa aacatgtttt taagaactcg ggttttatac 5580
aatagaatgt tttctagcag atgcctcttg ttttaatata ttaaaatttt gcaaagccct 5640
ttgagctaca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5680

<210> 181
<211> 2157
<212> DNA
<213> *Homo sapiens*

<400> 181
ggcggcggca tggcgaggtt cccgaaggcc gacctggccg ctgcaggagt tatgttactt 60
tgccacttct tcacggacca gtttcagttc gccgatggga aacccggaga ccaaatcctt 120
gattggcagt atggagttac tcaggccttc cctcacacag aggaggaggt ggaagttgat 180
tcacacgcgt acagccacag gtggaaaaga aacttggact ttctcaaggc ggtagacacg 240
aaccgagcaa gcgtcggcca agactctcct gagcccagaa gcttcacaga cctgctgctg 300
gatgatgggc aggacaataa cactcagatc gaggaggata cagaccacaa ttactatata 360
tctcgaatat atggtccatc tgattctgcc agccgggatt tatgggtgaa catagaccaa 420
atggaaaaag ataaagtgaa gattcatgga atattgtcca atactcatcg gcaagctgca 480

agagtgaatc tgtccttcga ttttccattt tatggccact tcctacgtga aatcactgtg 540
gcaaccgggg gtttcatata cactggagaa gtcgtacatc gaatgctaac agccacacag 600
tacatagcac ctttaatggc aaatttcgat cccagtgtat ccagaaattc aactgtcaga 660
tattttgata atggcacagc acttgtggtc cagtgggacc atgtacatct ccaggataat 720
tataacctgg gaagcttcac attccaggca accctgctca tggatggacg aatcatcttt 780
ggatacaaag aaattcctgt cttggtcaca cagataagtt caaccaatca tccagtgaaa 840
gtcggactgt ccgatgcatt tgtcgttgtc cacaggatcc aacaaattcc caatgttcga 900
agaagaacaa tttatgaata ccaccgagta gagctacaaa tgtcaaaaat taccaacatt 960
tcggctgtgg agatgacccc attacccaca tgcctccagt ttaacagatg tggcccctgt 1020
gtatcttctc agattggctt caactgcagt tggtgtagta aacttcaaag atgttccagt 1080
ggatttgatc gtcatcggca ggactgggtg gacagtggat gccctgaaga gtcaaaagag 1140
aagatgtgtg agaatacaga accagtggaa acttcttctc gaaccaccac aaccatagga 1200
gcgacaacca cccagttcag ggtcctaact accaccagaa gagcagtgac ttctcagttt 1260
cccaccagcc tccctacaga agatgatacc aagatagcac tacatctaaa agataatgga 1320
gcttctacag atgacagtgc agctgagaag aaaggggGaa ccctccacgc tggcctcatc 1380
gttggaatcc tcatcctggt cctcattgta gccacagcca ttcttgtgac agtctatatg 1440
tatcaccacc caacatcagc agccagcatc ttctttattg agagacgccc aagcagatgg 1500
cctgcgatga agtttagaag aggctctgga catcctgcct atgctgaagt tgaaccagtt 1560
ggagagaaag aaggctttat tgtatcagag cagtgctaaa atttctagga cagaacaaca 1620
ccagtactgg tttacaggtg ttaagactaa aattttgcct ataccttttaa gacaaacaaa 1680
caaacacaca cacaaacaag ctctaagctg ctgtagcctg aagaagacaa gatttctgga 1740
caagctcagc ccaggaaaca aagggtaaac aaaaaactaa aacttataca agataccatt 1800
tacactgaac atagaattcc ctagtggaat gtcatctata gttcactcgg aacatctccc 1860
gtggacttat ctgaagtatg acaagattat aatgcttttg gcttaggtgc agggttgcaa 1920
agggatcaga aaaaaaaaat cataataaag ctttagttca tgagggatcg acacctttgg 1980
ttcaaatgtt ctctgatgtc tcaaagataa ctgttttcca aagcctgaac cctttcactc 2040
aaaagagcaa tgatgaatgt ctcaagattg ctaagaaaaa cagcccatgc aagagtgaga 2100
acaaacacaa aataagagat tttctacatt ttcaaaaaaa aaaaaaaaaa aaaaaa 2157

<210> 182
<211> 2535
<212> DNA
<213> Mus musculus

<400> 182
gtcgcgatgc tgctgcgcct gctgctggcc tgggtggccg cggtgcccgc actgggccag 60
gtcccctgga cgccggagcc tcgagccgcg tgcggcccca gcagctgcta cgcgctcttt 120
ccccggcgcc gcacattcct ggaagcttgg cgggcgtgcc gcgaattggg gggcaacctg 180
gccacaccgc ggaccccaga ggaggcccag cgtgtggaca gcctggtggg ggtcgggccg 240
gccaacgggc tgctatggat tgggttgcag cggcaggcta ggcaatgcca gccgcagcgc 300
ccactgcggg gcttcatatg gaccacggga gaccaggaca ccgccttcac caactgggcc 360
cagccggcta cggaaggacc ctgcccagcc cagcgctgtg cagcccttga ggccagcgga 420
gagcatcgct ggctcgaagg ctcgtgcaca ctggctgtcg atggctacct ctgccagttt 480
ggtttgagg gtgcctgccc tgccttgccg cttgaggtgg gtcaggccgg tcccgctgtc 540
tacaccacac ccttcaacct ggtttccagc gagttcgaat ggctgccctt tggctccgtg 600
gcagctgtgc agtgccaagc tggcagggga gcttctctgc tgtgcgtgaa acagccttca 660
ggtggcgtgg gctggtccca gactggcccg ctgtgcccag ggactggctg tggtcctgac 720
aatgggggtt gcgaacatga gtgtgtggaa gaggtggacg gtgctgtgtc ctgccgctgc 780
agtgaaggct tccgtctagc agcagatggg cacagttgtg aagacccctg tgcccaggcc 840
ccctgtgagc agcagtgtga acctggaggg ccacaaggct atagctgcca ctgtcgcctt 900
ggcttccggc cagctgagga tgatccacac cgctgcgtgg acacggatga gtgccagatt 960
gctggtgtgt gccagcagat gtgtgtcaac tatgttggtg gctttgagtg ttactgcagc 1020
gagggtcacg agcttgaggc agatggtatc agctgtagcc ctgcaggagc catgggtgcc 1080
caggcttccc aggatctcag agatgagttg ctggatgatg gagaagaagg ggaggatgaa 1140
gaggagccct gggaggactt tgatggcacc tggacagagg aacaggggat cctatggctg 1200
gcacctacac atccacctga ctttggcctg ccctataggc ccaacttccc acaggatgga 1260
gagcctcaga gattgcacct ggagcctacc tggccacccc cacttagtgc cccccagggc 1320
ccctaccact cctcagtggt gtctgccaca cggcccatgg tgatctctgc cactcgaccc 1380
acactacctt ctgcccacaa gacctctgtt atttcagcta cacgcccacc cctgagccct 1440
gtccacccac ctgccatggc ccctgccaca cctccagctg tgttctctga gcaccagatc 1500
cccaaaatca aggccaatta tccagacctg ccttttggcc acaagcctgg gataacctcg 1560

gccactcacc cagcacggtc tcctccgtac cagccccccca ttatctcaac caactatccc 1620
caagtcttcc ctccccacca ggcccctatg tctccagata cccacactat cacttatttg 1680
cctccagtcc cccctcacct tgatcctggg gataccactt ctaaagccca tcaacaccct 1740
ttgctcccag atgctccagg tatcagaacc caggcccccc agctttctgt ctcagctctc 1800
cagccccctc ttcctaccaa ctccaggtct tctgtccatg aaactcctgt gcctgctgcc 1860
aaccagcccc cagccttccc ttcttctccc ctcccccctc agaggcccac taaccagacc 1920
tcatctatca gccctacaca ttcctattcc agagcccctc tagtcccaag ggaaggagtt 1980
cccagtccca aatcagtgcc acagctgccc tcggtgccct ccacagcagc tccaacagcc 2040
ctggcagagt caggtcttgc aggccaaagc caaagggatg accgctggct gctggtggca 2100
ctcctggtgc caacatgtgt cttcttggtg gtgctgcttg ccctgggcat tgtgtactgc 2160
actcgctgtg gctcccacgc acccaacaag cggatcacgg actgctatcg ctgggtcaca 2220
catgctggga acaagagctc aacagaaccc atgcccccca gaggcagcct tacaggggta 2280
cagacctgta gaaccagtgt gtgatgggt gcagatgccc ctttgtggga tagaagaaaa 2340
ggacttgctt tggacacatg gctgagacca caccaaggac ttatgggggc tgcccagctg 2400
acagaggagg ttctgttctt tgagcccagc atccatggca aaggacacac caggactcca 2460
ggacctcaag ggtgggtgc tgggatcttc tccaataaat ggggtgccaa cctcacccaa 2520
aaaaaaaaaa aaaaa 2535

<210> 183
<211> 5520
<212> DNA
<213> Mus musculus

<400> 183
gggcgcccgg gactcccgct gagcactcct cccgcacgcc cgggtccctc cggccggcga 60
gccgtccggc ccctgcgctg taggtccccg cggggcgatg ggttgatggg cgcgggggga 120
cgcaggatgc cggtgcctcc cgcgcgtttg ctgctgctgc cgctgctgcc ttgtcttctg 180
ctcctggctc ctggaactcg gggtgcgcct ggctgcccgg tccctatccg cggttgcaag 240
tgctctgggg agcggcccaa gggactaagt ggcggcgccc acaacccggc tcgaaggagg 300
gtggtgtgcg gcggtgggga tctccccgaa cctccagatc ccggccttct gccaaacggc 360
accatcacct tgctcttgag caacaacaag attactgggc tccgcaatgg atccttcttg 420
ggactgtccc tgttggagaa gttggacctg aggagcaatg tcatcagcac tgtgcagcct 480
ggagccttcc taggtctggg agagctaaaa cgcttagatc tctccaacaa tcggattggc 540
tgtctcacct ctgagacatt tcaagggctc cctagacttc tcagactaaa catatctgga 600
aacatctact ctagtctgca acctggggtc tttgatgagc tgccagccct taagattgtg 660
gactttggta ctgagtttct gacctgtgac tgccgcctgc gctggctgct gccctgggcc 720
cggaatcact ccctgcagct gtctgagcgc acactctgtg cctaccccag tgccctgcac 780
gcccatgccc tgagcagcct ccaggagtcc cagcttcgct gtgaaggggc cctggaactg 840
cacacccact acctcatccc atcccttcgc caagtggtgt tccagggtga ccgcctgccc 900
ttccagtgct cagccagcta cttgggcaac gatacccgga tccactggta ccacaatggg 960
gctcctatgg agagcgatga gcaggccggc atcgtccttg ctgaaaacct tatccatgat 1020
tgcaccttca tcaccagtga gctgaccctg tctcacattg gtgtgtgggc ctctggtgaa 1080
tgggagtgct ccgtgtccac agtccaaggc aacaccagca agaaggtgga gatagtagtg 1140
ctggagacct ctgcctccta ctgccctgca gagcgggtga ccaacaaccg tggggacttc 1200
aggtggcccc gaaccttggc tggcatcacg gcttaccagt cctgtttaca gtaccccttc 1260
acctctgtgc ccttgagtgg gggagccccg ggtacccgag cctcacgcag gtgtgaccga 1320
gctggccgct gggagccagg ggactactcg cactgtctgt acaccaatga catcactcgg 1380
gtgctctaca ccttgtgct gatgcccatc aacgcctcca atgcattgac gttggcccac 1440
cagctgcgag tgtataccgc agaggccgcc agcttctcag acatgatgga cgtggtctat 1500
gtggctcaga tgatccagaa gtttttgggt tacgttgacc agatcaagga gctggtggag 1560
gtgatggtgg acatggccag caacctgatg ctggtggatg agcaccttct gtggctggcc 1620
cagagagaag acaaagcctg cagtggcatt gtgggtgccc tggagcgaat cggaggagct 1680
gctcttagcc cccatgccca gcacatctct gtgaattcaa gaaatgtggc actggaggcc 1740
tacctcatca agcctcacag ctacgtgggt ctgacttgca cggctttcca gaggagggag 1800
gtaggagtgt cgggtgcaca gccaagcagc gtcggccagg atgccccagt ggagcccgaa 1860
cccctagctg atcagcagct taggttccgc tgcaccactg ggaggcccaa catttctctg 1920
tcatccttcc acatcaagaa tagcgtggcc ctggcctcca tccagctgcc ccccagcctg 1980
ttctcaaccc ttccggctgc cctggctccc ccagtccctc cagattgcac cctgcaactg 2040
ctggtcttca gaaatggccg tcttttccgc agccacggca acaacacttc ccgtcctgga 2100
gcagctgggc ctggcaagag gcgtggtgtg gccaccccag tcatatttgc aggaaccagt 2160
ggctgtggtg tgggaaactt gacggagccc gtggctgtgt cactgaggca ctgggctgaa 2220

ggagctgacc ccatggcagc ttggtggaac caggacgggc ctggaggctg gagttctgaa 2280
ggctgcaggc tccgctacag ccagcccaac gtcagctccc tgtactgcca gcacttgggc 2340
aatgtggccg tgcttatgga gctgaatgca ttcccgcggg aggcaggagg ctctggggct 2400
gggttgcatc ccgtcgtgta cccctgcacg gctttgctgc tactctgtct cttctccacc 2460
atcatcacgt acatcctcaa ccacagctcc atccacgtgt cccggaaggg ttggcacatg 2520
ctgctgaacc tttgtttcca tatggccatg acctctgctg tcttcgtggg gggcgtcacg 2580
ctcaccaact accaaatggt ttgtcaagcg gtgggcatca ctctgcacta ctcttccttg 2640
tcgtcactgc tctggatggg ggtcaaggct cgagtcctcc acaaggagct tagttggagg 2700
gcacccccctc tggaagaagg ggaagcagct ccgcctggtc ctcgccccat gctccggttc 2760
tacttgattg ctggagggat ccccctcata atctgcggca tcaccgctgc ggtcaacatc 2820
cacaactacc gggaccacag tccctattgt tggctggtgt ggcgtccaag ccttggtgcc 2880
ttctacatac cggtggcgtt gattctgcct atcacctgga tctacttctt gtgtgcaggc 2940
cttcacttac ggagccatgt ggcccagaat ccaaagcagg gtaacaggat ctctctggag 3000
ccaggggaag agctgagggg ttccaccagg ctcaggagta gtggcgtcct cctgaatgac 3060
tctggttctc ttttggctac agttagcgca ggagtaggga cacctgcgcc cccagaggat 3120
ggtgatggcg tatattctcc tggagtccag ctgggggcgc tgatgaccac gcatttcctg 3180
tacctggcta tgtgggcttg tggtgccttg gcggtgtctc agcgctggct gccccgagtg 3240
gtgtgtagct gtctgtacgg cgtggcagct tcagctcttg gtctgtttgt cttcactcac 3300
cactgtgcca gacgtagaga tgtccgggct tcctggcgcg cctgctgccc tcctgcttcg 3360
ccctcggcct cccatgtccc agcccgggcc ctgccgactg ctacagagga tggatcccca 3420
gtgttggggg agggaccagc ctctctcaag tcctccccaa gtggcagcag tggccgcgcg 3480
ccgccacccc cctgcaaact caccaatctg caggtggccc agagtcaggt gtgcgaggca 3540
agcgtggccg cccgcggaga tggagagcca gagcccaccg gctcccgtgg cagcctagct 3600
ccccggcacc ataacaacct gcatcatggg cgccgagtac acaagagtcg ggccaagggg 3660
caccgagccg gagagactgg tggtaagagc cggctcaagg cgttgcgcgc gggcacgtcc 3720
ccaggagctc ccgagctgtt gtccagtgag agcggcagtt tgcacaacag cccgtctgac 3780
agctacccgg gcagcagccg caacagtcca ggcgacggtc ttccactcga gggtgagccc 3840
atgcttacgc cgtcggaggg cagtgacaca agcgccgcgc caatcgctga gacggggcgc 3900
cccgggcagc gccgcagcgc cagccgtgac aacctcaagg gcagcggcag cgcgctggag 3960
agggagagca agcgccgctc ctatccgctc aacactacca gtcttaacgg tgcccccaaa 4020
gggggcaagt atgaggatgc cagtgtaact ggtgcagagg ccatagcggg aggctccatg 4080
aagactggcc tctggaaaag cgagaccacc gtctaggtcc agatttagga tgggcgggtc 4140
acgcgggctt gtttactccc aaatcctctt gggcggtcca agccgtctac tgatgtgtat 4200
gtaggtttaa ggcggccatg ctgatgctgc ccttgagtcc accatcatta gttacccagg 4260
ctagggaaag gggagggagg cagatgcttg cccctactgt ggactatccc tcagcagtag 4320
cgacagacaa tcccagacca gttttggtgg ccaagttctt ggtatcctgc caggtaggca 4380
taaaacatcc atcggtccct agggtaaccc ataaactgag ttgaagagcc cagcccaggt 4440
aggctcagga aatgagaggg agaccgggga actgggttct ccacaccagc ccggcaaggt 4500
atcctgtgac tgccaagatc ccaggcctct ctcccagttt tggcttggga aaccatccca 4560
gcaggtgagc cagggggcgt aacaggtgct gcctttcaga ttaactatgc aaggggggatg 4620
ggggtgggag gggtagggca gtgtggtggg cagctctaga gatgagcttg tccctcagga 4680
ggcaggcagg tgggaaaagg tgcattaggg agacagaatc cctaactatg ggagtggtac 4740
acagtttttc cagcagagtt cacagcaaac cctgaacccc cacacacctg ggaagtgata 4800
ctgccagcag gtgccttaag actcaagggg agggagctga tatgtggatc tcacaaccta 4860
tacagtggtc tgcaagtggc tccacttagc tgcttaatta taatacccac tgtctgttcc 4920
cagccctcca actccggggg actgagggga aatgcctcca tgaggctcct gtggcaaagc 4980
catgctaata atctgacttc taacctcagt tagaaaccca aaatgccaaa ccacctccta 5040
actcgctgaa acccaaccac actctgaggc agcgcctggg tccaggctgc tcaagagcct 5100
atgcttccag cccccatttt cctcaactca agatgccttt taatacagaa ctacatggaa 5160
gtagaggaac ccttgggcac tgggaagtag cagggatccc agctctgatc aagtgagagg 5220
acagagcagg gaagacgcca tactcgctga gatgggtccc attatttatg ctttgctgca 5280
cagacactat tagaggaaaa gctttgtatt actctcccac gtgagctgct gctgtttacc 5340
ctgccaatgc cttagcactg gagagctttt tgcaatatgc tggggaaagg ggagggaggg 5400
gatgaagtgc caaagaaaac acattttaaa agctctggtt ttatacaata gaatgttttc 5460
cagcagatgc ctctttgttt taatatatta aaatcttgca aaaaaaaaaa aaaaaaaaaa 5520

<210> 184
<211> 2833

<212> DNA
<213> Mus musculus

<400> 184
cggggctgct ccctctgcag ccgccgccgc cgccgcgcag acccggaggt cgtccgcgcc 60
caccatgcga gctcagctct ggttgctgca gttgctgcta ctccgcgggg ccgcgcgcgc 120
gctcagtccc gcaacacccg caggtcacaa tgaaggtcaa gactctgcat ggactgccaa 180
gaggaccagg caaggctgga gtcggagacc ccgagagagc cccgcgcagg tgttgaagcc 240
aggcaagacc cagctaagcc aggacttggg tgggggctcc ctggccatcg acacacttcc 300
ggacaacagg actcgggtgg tggaggacaa ccataactac tacgtgtccc gtgtctacgg 360
ccctggtgag aaacaaagcc aggatctgtg ggtggacctg gctgtggcca accggagtca 420
tgtgaagatc cacaggattc tctccagttc tcaccgacag gcttcaagag tggtcttgtc 480
ctttgatttc cctttctatg ggcatcctct gcggcagatc accatagcaa ccggaggctt 540
catcttcatg ggggacatgc tccaccggat gctcacagct acgcagtatg tggcacccct 600
gatggccaac ttcaaccccg gctactctga caactccacg gttgcttact ttgacaatgg 660
gaccgttttt gtggttcagt gggatcatgt ttacctccag gaccgggagg acaggggcag 720
cttcaccttc caggcggccc tacaccgaga tggccgcatt gtcttcggct acaaagagat 780
ccccatggct gtcctggata tcagctctgc ccagcaccct gtcaaggcag gcctgtccga 840
cgctttcatg attctcaatt catccccaga ggtgccagag tctcagagac ggaccatttt 900
cgaataccac cgtgtggaac tggactccag caagatcacc accacctcgg ccgtggagtt 960
caccccgttg ccaacctgcc tccagcatca gagttgcgac acctgcgtgt cctcgaatct 1020
aaccttcaac tgcagctggt gccatgtcct gcagaggtgt tccagtggct ttgaccgata 1080
ccgccaagaa tggctgacct acggctgtgc ccaggaggca gaaggcaaga catgcgagga 1140
cttccaggat gatagccact actcagcctc ccctgacagc tccttcagcc cctttaatgg 1200
cgactccact acctcttcct ccctcttcat tgacagcctc accacagaag atgacaccaa 1260
gttgaatccc tacgcagaag gagacggcct tccggaccac tcatctccga agtccaaggg 1320
tcctcccgtg cacctgggca ccatcgtggg tatcgtgctt gctgtactcc tggtagcggc 1380
catcatcctg gctgggattt acatcagtgg ccaccctaat tccaatgctg cactcttctt 1440
catcgagcgg agacctcacc actggccagc catgaagttc cataaccacc ccaaccactc 1500
tacctacacc gaggtagagc cctccgggca cgagaaggaa ggcttcgtgg aggccgagca 1560
gtgctgagag agcatcgggc cagagacctg gagatggcat gaaagacaag tcacagcaca 1620
gagaagtgat tttttttcct ggcttcctcg gagctggccc tgggccagga agacaagaca 1680
acagcttgtg gtgccaacac tacagtttgg tctgcacacc ccatttaaag gggctcagt 1740
aatacaactg cgaaggctcc ttggggaaca ctgacctcaa gagttccctg tttcaatggg 1800
aggaggcttc gtttggggtc tctcagtggt ctgcagctat ggcggagccc ctgcccactg 1860
gagacagcct cctgtgttcc tcctgctcac tgaagcccac actgggccat tgcattccgg 1920
ggtctataga ttcaagagct ggtcttgcta gctatggagt cagtgcccctt ggctccaaac 1980
tttgtggctt agaagcctga agaaggggat ccccttccctc cgagagcgct taaccctgag 2040
atgcgctaac agagagaaaa gtaaccttgg ggaacttgca tttttctggc cttggtcctt 2100
tgcttcattg tttttttttgc agaggccggg gccaacatcc gagcactgta gcctgcagct 2160
cattctgtac cctgccctgc cctgcccctc agcctccacc ctgcaagctg gtcttgcatg 2220
gctgccagta atgagtgggg cccttactgt gccatgtgtc tggtgcctgc attactcgtt 2280
aacctgttct gttatcaacg gcagtagttt ccttcaaaga gggggacaat ttacctggct 2340
cctgttttaa cttggctgac cagagtcgag ttcttgtaac cattaaaaac aactaggggg 2400
ccgggtgtgg tggtgctcac actcaggagg ctgagctctg agatcaaggc cagcctggtc 2460
tacagagaga gcctgtcttg aagaaacaag acaaatgggg ggctagaggt ttccctgaga 2520
cacccctgcc ttagcaaggg gctccagttg gatcccgttg aagcacggtg gccgcgaagg 2580
tagggcagag aaatctggta tgggagggag agaccttgac ctggaaagcg gcctccatct 2640
ctccagctct gcaaagagct ttgggaactg ggagttgacg ttcccacact cagcctggtt 2700
ttaagggact tctgtccccg tggtggacca ggacggcttc taaaggacaa tgaaaaccta 2760
gagctcacct tcatcccaaa gaagcgtcat cagcaaataa ataaggtata gccctcaaaa 2820
aaaaaaaaaa aaa 2833

<210> 185
<211> 2009
<212> DNA
<213> Mus musculus

<400> 185
gagagaggtc gcggcagcgg catggcaagg ttccggaggg ccgacctggc cgcagcagga 60
gttatgttac tttgtcactt tttaacagac cggttccact tcgcccacgg ggagcctgga 120

caccatacca atgattggat ttatgaagtt acaaacgctt ttccttggaa tgaagagggg 180
gtagaagtgg actctcaagc atacaaccac aggtggaaaa gaaatgtgga cccttttaag 240
gcagtagaca caaacagagc cagcatgggc caagcctctc cagagtccaa agggttcact 300
gacctgctac tggatgacgg acaggacaat aacacccaga tagaggagga cacggatcac 360
aattactaca tttctcggat atatggtcca gcggattctg ccagccggga tctgtgggtt 420
aacatagacc aaatggaaaa agacaaagtg aagattcacg ggatactttc caacactcat 480
cggcaagctg caagagtgaa tctgtccttc gattttccat tttatggtca ttttctaaat 540
gaagtcactg tggcaactgg gggtttcata tatactggag aagttgtaca tcgaatgctc 600
acagctacac agtatatagc tcctttaatg gcaaattttg atcccagtgt atccagaaat 660
tcaactgtca gatattttga taatggcaca gctcttgttg tccagtggga ccatgtccac 720
ctgcaggata attacaacct gggaagcttc acattccagg ccacactcct catggacggg 780
cgcatcatct ttggatacaa agaaatccct gtcttggtca cacagataag ttctaccaac 840
catccagtga aagtcgggtt gtctgatgca tttgtcgtgg tccacaggat ccagcaaata 900
cccaatgttc gaagaagaac aatttatgaa tatcaccgag tagaactaca aatgtccaaa 960
attaccaaca tctcagctgt ggagatgact ccacttccca catgtctcca gttcaatggt 1020
tgtggccctt gtgtgtcctc gcagattggt ttcaactgca gttggtgcag caaacttcaa 1080
agatgctcca gtggatttga tcgccatcgg caggactggg tggacagtgg atgcccggaa 1140
gaggtacagt caaaagagaa gatgtgtgag aagacagagc caggagagac gtctcaaact 1200
accacgacct cccacacgac caccatgcaa ttcagggtcc tgaccaccac caggagagct 1260
gtgacatcgc agatgcctac cagcctgcct acagaagatg acacgaagat agccctacat 1320
ctcaaagaca gtggagcctc cacagatgac agtgcagctg agaagaaagg aggaaccctc 1380
catgcaggcc tcattgttgg aattctcatc ttggtcctca ttatagcagc ggccattctg 1440
gtgacagtgt atatgtatca ccatccaaca tcagcagcca gcatcttctt cattgagaga 1500
cgcccaagca gatggccagc aatgaagttt cgaagaggct caggacaccc tgcctatgca 1560
gaagttgaac cagttggaga gaaagaaggt tttattgtat cagagcagtg ctaaaatttt 1620
aggacagagc agcaccagta ctggcttaca ggtgttaaga ctaaaacttt gcttatgcat 1680
ttaagacaaa cagacacaca acccacaacc acacacaaag gagccctaaa ctgctgtaga 1740
cagaagggcg acgagatttc tggacaagcc cagcccagga acattgaaag gaaaactcag 1800
acttgtacaa gacaccatgt acaatgatta aagaattccc tagtggaatg acatccatgg 1860
ttcacaagga acatctccgg tggacttgcc aggagtgtga cgagatgacg atgcttttgg 1920
tttaggtgca gggttgcaaa gaaatcaagg aaaaaaaata tgacaataaa taaagcttta 1980
gttcacaagg gaaaaaaaaa aaaaaaaaa 2009

<210> 186
<211> 5220
<212> DNA
<213> Mus musculus

<400> 186
cggaactgct tcgactgcaa agcttcaagc gcagcctggg agcggcctgg tggccctatc 60
ccggcagctc cacacagcag aacgccctgg gtccctgaaa ctcgaaaccc gggctgagaa 120
ccagcggaaa ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgtttgc 180
tgagagccgg gggacctgac cggagcccag gccgcgtatg gcgcgcccct gatgtcacac 240
ggacgccagc gaggccagcg ctccggctgc agcatggacc gcgcggggcg cctgggtgcg 300
ggcctgcggg gactctgcgt ggctgcactc gtgctcgtgt gcgccggaca cgggggccgc 360
cgcgaggatg ggggaccagc ttgctacgga ggattcgacc tctacttcat cctggacaag 420
tcaggaagtg tgctgcacca ctggaatgaa atctactact tcgtggagca gttggctcat 480
agattcatca gcccacagct aaggatgtcc ttcattgtct tctctactcg agggacaact 540
ttaatgaaac taactgagga cagggaacag atccgacaag gcctagaaga gctccagaaa 600
gttctgccag gaggagacac ttacatgcac gaaggattcg agagggccag tgagcagatt 660
tactatgaga acagtcaagg atacaggacg gcgagcgtca tcatcgcgtt gacggatggg 720
gagctgcacg aggacctctt cttctactca gagagggagg ctaaccgatc ccgagacctt 780
ggtgcgattg tttactgcgt tggcgtgaag gatttcaatg aaactcagtt ggctcggatt 840
gcagacagta aggaccacgt gtttcctgtg aacgacggct tccaggctct ccaaggcatt 900
atccactcaa ttttaaagaa atcctgcatc gaaattctgg cggctgaacc atccaccatc 960
tgcgcgggag agtcctttca agtggtcgta agaggaaatg gcttccgaca tgcccgcaat 1020
gtggacaggg tcctctgcag cttcaaaatc aatgactcag tcacgctcaa tgagaagccc 1080
tttgctgtgg aagacactta tttgctgtgc ccagcaccaa tcttgaaaga agttggcatg 1140
aaagctgcac tgcaggtcag catgaacgac ggcctgtcct tcatctccag ttctgtcatc 1200
atcaccacca cacactgttc agacggctcc atcctggcga ttgctctgct ggtcctcttc 1260
ctgctgctgg ccctggcgct gctctggtgg ttctggcccc tctgctgcac agtgatcatc 1320

aaggaggtcc ctccaccccc tgttgaggag agtgaggaag aagacgatga tggtttgcca 1380
aagaagaaat ggcccacagt agatgcctct tattatggtg gacgcggtgt gggaggcatt 1440
aaaagaatgg aggtccgctg gggagaaaag ggctccacag aagaaggggc gaagttagaa 1500
aaggcaaaga atgcacgagt caagatgcca gagcaagaat atgagttccc agaaccccga 1560
aacctcaaca acaacatgcg ccggccttcc tcgcctcgga agtggtactc gcccatcaag 1620
ggaaaactcg atgccttgtg ggttctgctg agaaaaggat atgaccgagt gtctgtgatg 1680
aggccacagc caggagacac gggacgctgt atcaacttca ccagagtgaa gaacagtcag 1740
ccagccaagt atcccctgaa caacacctac caccccagct ccccacctcc cgctcctatc 1800
tacacacccc caccccctgc tccccactgc cctcccccag cccccagtgc cccactcct 1860
cccattcctt ccccaccatc cactctcccc cctcctcctc aggccccacc ccctaacagg 1920
gcacctcccc cctcccgacc tcctccaagg ccttctgtct agaacccaaa gtccgagctc 1980
tggctgcct gagcaactcc agcaggaggc ttctctgctg aaagaaagat ctgcccagcc 2040
tatgtggtga gtggcggctg atgtttgcac gatttaaaag caagtcgtga tgggcagaac 2100
aaaatgggca ttttgaactg cctgaagaca gacaatgaga caataacagt cacattatag 2160
cctgtgaccc ctcacctcta gaggaaggtt cccgagatgg ccacattgcc acagtgctct 2220
cagccagatt atgtcccatg aagaccagga agaaagtgac ttccaagaat ggaatgcagc 2280
attggataag aaacacctgg ctgagattct gacctcactg atttgactct tgattcttgg 2340
actgggagcc aggccatctc cacccctggt accacccagc aactctgaaa atgtgcagtg 2400
tccctagtat gcatcgaata ggtatccaac tgggatctgc aggttgcctt ataaagagca 2460
tatgctctat tctctttccc gaacttcctg gtttcccagt gatgagggaa ggggaaaggt 2520
gttgccatgc ttagaagtta gaggacgtca gtgctcagca ctgatggaga agcgttgatg 2580
ggagtgtcca gctcttacat ctagaaatgg ctggcttcag caggcacagt tcctaaacca 2640
acaagccttg tcattgtcaa aggcaaccta ctaatgattc accttaaaca tcaaggttga 2700
ctgtggcata ggtcagagct gatcacacag aaccttcccc atgaaatcgc aaggttcctc 2760
atcttcaaat acccaggacc ccagagattt ctaaatccag ctaagagaca gtagtcctga 2820
cttggcaaga aaaccattcc cagttgtttt actctgaaac aggccgttgt atgtatggta 2880
tatctctcct tggcctttca acctgctcac aagtattacc agttatgaag caaggagaaa 2940
tacatccagt gtgtaataga aaagctctgc ccacaatccc catgtcactc ctctacatta 3000
ttctgaagct gcttggtcag tgagcccttt aacctcatgt agactctgga cactgtcacc 3060
caatcatgaa aacagaggtc attgtcaaag gcagtgtata gcctgtacaa aaatgatgct 3120
tccttcctca gtttccacag gccccaaaat tcctgtctta ggctcctaaa cctctaaact 3180
ttttcctgga acaaaagata taaaacgggc ataagttttt atgttttggg ctgtgatctc 3240
caaagatcct tcaagaactc aagttagcct cattcttcca gcttgtttag aacagaggca 3300
tccaggtgtc atgcactcca tagacaccaa tccttgttcc caaggcagac attattaatc 3360
aatctcagca ctagttctca atttaatcca attatatttt tccacagtac ttcacatctc 3420
ttatgacctg ttggtcatca gttagaattg agagagataa acactgtttg taatccctac 3480
cttagaaaga aaagcagagg agaatggggg aaccaccagc ataaaagtta ttatctgggg 3540
aaaatcgacc tgaaagaacg cccaagtcca agacctatgg tgctgacacc aaagtaacac 3600
tttcccaagt gtaccccaga ccccactctt ctccctgtgg ccaccactcc ctgcttttca 3660
ggagttgtga aaaagatctc cttcaccctt actgtgcccc catattagaa caaggcttgt 3720
ttagtgtagt ccttgttaaa caggtgccag aatgtctcag ccacctgaga tgacactgct 3780
gggccccaga aaaccattcc aaggagaatg ggctccccag gctcagagca tgcaactatg 3840
agcccatggc aactgttttg actgctggca gtacaaaacg ggccacccca cattacagct 3900
gcaggatttg tgcagccata agaaagtatg aaccaagatg ctggtgttgc tgttcaacaa 3960
gcatgggctt cggggaaggc agcagactcc gagagcaggc cttgtgcagt gtcccaaggg 4020
gctgtggtga agtgtctgag gaaaaatgaa tgctgataca tggtgattct gagaagaatt 4080
tgcaaggttt gaccttagaa tttatggaat gtcttccctg gtcattcaga attatggcta 4140
gaagtttcta gaaaccgtca aggttaatac ctttcagagt aggtgattac aggcaggaag 4200
agctttgatg tggtttacaa agcccatcag ttctgtgtca ttccctgtaa gcaacaggag 4260
atggtggttg tgattagcaa actgcatgtg ttatttgttt gactccttgt tattgtcctt 4320
acggaggatt ttttttatat aagccaaatt ttgttgtata tattcatatt ccacgtgaca 4380
gatggaagca cgtcctatca gtgtgaataa aaagaacagt tgtagtaaat tattaaagcc 4440
agtgatttca tggcaggtta ccctaccaag ctgtgcttgt tgatctccca tgaccatact 4500
gcttttacaa tgtacaaata gttcctaggt gacgagaccc tcctttacat aatgccgatg 4560
acagccttgc tgggaactgc ggtccttctg ctgtgacagc cagctcgaaa acaggtcctg 4620
cctggagctt gccacacact ttagggagac ataagagctg tctttcccca gcgtcaggga 4680
caaagctacc ataaagaagt ggaaaagtct tggctctcca gcctgggaca gaggtctctc 4740
tggaacccca aggaagagca gaaatgatcc ttgcctgcca ctgcacacaa tgtgatggtg 4800
gaaaatccat caaggaataa ttgtgagata atgaccgaca gttcaggcgc aaagggaatt 4860
catgctgtgt aaagtgggtg gaattcgttt gcaagctatg caaagcctga tcttactcac 4920
caggaggatg gaaagggttt ttttagttat ctgagctcag ctgagttatc acgcttggag 4980

aaccgattta aaggaattag aatatgattt ctgaatacac ataacattaa actcttctct 5040
ttttctatgg taatttagtt atggacgttc agcgtctctg agttattgtt ataaaagact 5100
tgtcatcacc gcactgtgct gtaggagact gggctgaacc tgtacaatgg tataccctgg 5160
aagttgcttt tttaaaaaaa aataataata aacacctaaa atcaaaaaaa aaaaaaaaaa 5220

<210> 187
<211> 564
<212> PRT
<213> Homo sapiens

<400> 187
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
1 5 10 15
Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
20 25 30
Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
35 40 45
Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
50 55 60
Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65 70 75 80
Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
85 90 95
Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
100 105 110
Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
115 120 125
Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
130 135 140
Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145 150 155 160
Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
165 170 175
Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
180 185 190
Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
195 200 205
Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
210 215 220
Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225 230 235 240
Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
245 250 255
Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
260 265 270
Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
275 280 285
Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
290 295 300
Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305 310 315 320
Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
325 330 335
Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
340 345 350
Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Glu Asp Asp Asp
355 360 365
Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly

370 375 380
Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385 390 395 400
Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
405 410 415
Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
420 425 430
Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
435 440 445
Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
450 455 460
Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465 470 475 480
Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
485 490 495
Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
500 505 510
Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
515 520 525
Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
530 535 540
Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
545 550 555 560
Arg Pro Ser Val

<210> 188
<211> 1331
<212> PRT
<213> Homo sapiens

<400> 188
Met Arg Gly Ala Pro Ala Arg Leu Leu Leu Pro Leu Leu Pro Trp Leu
1 5 10 15
Leu Leu Leu Leu Ala Pro Glu Ala Arg Gly Ala Pro Gly Cys Pro Leu
20 25 30
Ser Ile Arg Ser Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser
35 40 45
Gly Gly Val Pro Gly Pro Ala Arg Arg Arg Val Val Cys Ser Gly Gly
50 55 60
Asp Leu Pro Glu Pro Pro Glu Pro Gly Leu Leu Pro Asn Gly Thr Val
65 70 75 80
Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser
85 90 95
Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Asn Asn Ile
100 105 110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys
115 120 125
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr
130 135 140
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile
145 150 155 160
Phe Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys
165 170 175
Val Val Asp Leu Gly Thr Glu Phe Leu Thr Cys Asp Cys His Leu Arg
180 185 190
Trp Leu Leu Pro Trp Ala Gln Asn Arg Ser Leu Gln Leu Ser Glu His
195 200 205
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala Gln Ala Leu Gly Ser
210 215 220
Leu Gln Glu Ala Gln Leu Cys Cys Glu Gly Ala Leu Glu Leu His Thr

225 230 235 240
His His Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg
245 250 255
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile
260 265 270
Arg Trp Tyr His Asn Arg Ala Pro Val Glu Gly Asp Glu Gln Ala Gly
275 280 285
Ile Leu Leu Ala Glu Ser Leu Ile His Asp Cys Thr Phe Ile Thr Ser
290 295 300
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu
305 310 315 320
Cys Thr Val Ser Met Ala Gln Gly Asn Ala Ser Lys Lys Val Glu Ile
325 330 335
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Ala
340 345 350
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr
355 360 365
Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Gly
370 375 380
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly
385 390 395 400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
405 410 415
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
420 425 430
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
435 440 445
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
450 455 460
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
465 470 475 480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
485 490 495
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Arg Ile Val Gly Ala Leu
500 505 510
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
515 520 525
Val Asn Ala Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
530 535 540
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Gly Gly
545 550 555 560
Val Pro Gly Thr Arg Pro Gly Ser Pro Gly Gln Asn Pro Pro Pro Glu
565 570 575
Pro Glu Pro Pro Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
580 585 590
Arg Pro Asn Val Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
595 600 605
Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Ser Leu Pro Ala
610 615 620
Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
625 630 635 640
Phe Arg Asn Gly Arg Leu Phe His Ser His Ser Asn Thr Ser Arg Pro
645 650 655
Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val Ile
660 665 670
Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro Val
675 680 685
Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Glu Pro Val Ala Ala
690 695 700
Trp Trp Ser Gln Glu Gly Pro Gly Glu Ala Gly Gly Trp Thr Ser Glu
705 710 715 720

Gly Cys Gln Leu Arg Ser Ser Gln Pro Asn Val Ser Ala Leu His Cys
725 730 735
Gln His Leu Gly Asn Val Ala Val Leu Met Glu Leu Ser Ala Phe Pro
740 745 750
Arg Glu Val Gly Gly Ala Gly Ala Gly Leu His Pro Val Val Tyr Pro
755 760 765
Cys Thr Ala Leu Leu Leu Leu Cys Leu Phe Ala Thr Ile Ile Thr Tyr
770 775 780
Ile Leu Asn His Ser Ser Ile Arg Val Ser Arg Lys Gly Trp His Met
785 790 795 800
Leu Leu Asn Leu Cys Phe His Ile Ala Met Thr Ser Ala Val Phe Ala
805 810 815
Gly Gly Ile Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly
820 825 830
Ile Thr Leu His Tyr Ser Ser Leu Ser Thr Leu Leu Trp Met Gly Val
835 840 845
Lys Ala Arg Val Leu His Lys Glu Leu Thr Trp Arg Ala Pro Pro Pro
850 855 860
Gln Glu Gly Asp Pro Ala Leu Pro Thr Pro Ser Pro Met Leu Arg Phe
865 870 875 880
Tyr Leu Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala
885 890 895
Ala Val Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu
900 905 910
Val Trp Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile
915 920 925
Leu Leu Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu Arg Leu Arg
930 935 940
Gly Pro Leu Ala Gln Asn Pro Lys Ala Gly Asn Ser Arg Ala Ser Leu
945 950 955 960
Glu Ala Gly Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Gly Ser Gly
965 970 975
Pro Leu Leu Ser Asp Ser Gly Ser Leu Leu Ala Thr Gly Ser Ala Arg
980 985 990
Val Gly Thr Pro Gly Pro Pro Glu Asp Gly Asp Ser Leu Tyr Ser Pro
995 1000 1005
Gly Val Gln Leu Gly Ala Leu Val Thr Thr His Phe Leu Tyr Leu Ala
1010 1015 1020
Met Trp Ala Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg
1025 1030 1035 1040
Val Val Cys Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu
1045 1050 1055
Phe Val Phe Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser
1060 1065 1070
Trp Arg Ala Cys Cys Pro Pro Ala Ser Pro Ala Ala Pro His Ala Pro
1075 1080 1085
Pro Arg Ala Leu Pro Ala Ala Ala Glu Asp Gly Ser Pro Val Phe Gly
1090 1095 1100
Glu Gly Pro Pro Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly His
1105 1110 1115 1120
Pro Leu Ala Leu Gly Pro Cys Lys Leu Thr Asn Leu Gln Leu Ala Gln
1125 1130 1135
Ser Gln Val Cys Glu Ala Gly Ala Ala Ala Gly Gly Glu Gly Glu Pro
1140 1145 1150
Glu Pro Ala Gly Thr Arg Gly Asn Leu Ala His Arg His Pro Asn Asn
1155 1160 1165
Val His His Gly Arg Arg Ala His Lys Ser Arg Ala Lys Gly His Arg
1170 1175 1180
Ala Gly Glu Ala Cys Gly Lys Asn Arg Leu Lys Ala Leu Arg Gly Gly
1185 1190 1195 1200
Ala Ala Gly Ala Leu Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His

```
                1205                1210                1215
Asn Ser Pro Thr Asp Ser Tyr Leu Gly Ser Ser Arg Asn Ser Pro Gly
            1220                1225                1230
Ala Gly Leu Gln Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly
        1235                1240                1245
Ser Asp Thr Ser Ala Ala Pro Leu Ser Glu Ala Gly Arg Ala Gly Gln
    1250                1255                1260
Arg Arg Ser Ala Ser Arg Asp Ser Leu Lys Gly Gly Gly Ala Leu Glu
1265                1270                1275                1280
Lys Glu Ser His Arg Arg Ser Tyr Pro Leu Asn Ala Ala Ser Leu Asn
                1285                1290                1295
Gly Ala Pro Lys Gly Gly Lys Tyr Asp Asp Val Thr Leu Met Gly Ala
            1300                1305                1310
Glu Val Ala Ser Gly Gly Cys Met Lys Thr Gly Leu Trp Lys Ser Glu
        1315                1320                1325
Thr Thr Val
    1330

    <210> 189
    <211> 529
    <212> PRT
    <213> Homo sapiens

    <400> 189
Met Ala Arg Phe Pro Lys Ala Asp Leu Ala Ala Ala Gly Val Met Leu
 1               5                  10                  15
Leu Cys His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro
            20                  25                  30
Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro
        35                  40                  45
His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg
    50                  55                  60
Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala
65                  70                  75                  80
Ser Val Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu
                85                  90                  95
Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
            100                 105                 110
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser
        115                 120                 125
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
    130                 135                 140
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn
145                 150                 155                 160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr
                165                 170                 175
Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met
            180                 185                 190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
        195                 200                 205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
    210                 215                 220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
225                 230                 235                 240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
                245                 250                 255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
            260                 265                 270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
        275                 280                 285
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr
```

```
    290                 295                 300
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val
305                 310                 315                 320
Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro
                325                 330                 335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu
            340                 345                 350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp
        355                 360                 365
Ser Gly Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu
    370                 375                 380
Pro Val Glu Thr Ser Ser Arg Thr Thr Thr Thr Ile Gly Ala Thr Thr
385                 390                 395                 400
Thr Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln
                405                 410                 415
Phe Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His
            420                 425                 430
Leu Lys Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys
        435                 440                 445
Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu Val
    450                 455                 460
Leu Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His
465                 470                 475                 480
Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg
                485                 490                 495
Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala
            500                 505                 510
Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln
        515                 520                 525
Cys
```

```
<210> 190
<211> 765
<212> PRT
<213> Mus musculus

<400> 190
Met Leu Leu Arg Leu Leu Leu Ala Trp Val Ala Ala Val Pro Ala Leu
1               5                   10                  15
Gly Gln Val Pro Trp Thr Pro Glu Pro Arg Ala Ala Cys Gly Pro Ser
            20                  25                  30
Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp
        35                  40                  45
Arg Ala Cys Arg Glu Leu Gly Gly Asn Leu Ala Thr Pro Arg Thr Pro
    50                  55                  60
Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Val Gly Pro Ala Asn
65                  70                  75                  80
Gly Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Pro
                85                  90                  95
Gln Arg Pro Leu Arg Gly Phe Ile Trp Thr Thr Gly Asp Gln Asp Thr
            100                 105                 110
Ala Phe Thr Asn Trp Ala Gln Pro Ala Thr Glu Gly Pro Cys Pro Ala
        115                 120                 125
Gln Arg Cys Ala Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
    130                 135                 140
Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe
145                 150                 155                 160
Glu Gly Ala Cys Pro Ala Leu Pro Leu Glu Val Gly Gln Ala Gly Pro
                165                 170                 175
Ala Val Tyr Thr Thr Pro Phe Asn Leu Val Ser Ser Glu Phe Glu Trp
```

180 185 190
Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly
195 200 205
Ala Ser Leu Leu Cys Val Lys Gln Pro Ser Gly Gly Val Gly Trp Ser
210 215 220
Gln Thr Gly Pro Leu Cys Pro Gly Thr Gly Cys Gly Pro Asp Asn Gly
225 230 235 240
Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly Ala Val Ser Cys
245 250 255
Arg Cys Ser Glu Gly Phe Arg Leu Ala Ala Asp Gly His Ser Cys Glu
260 265 270
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly
275 280 285
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu
290 295 300
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly
305 310 315 320
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr
325 330 335
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro
340 345 350
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Arg Asp Glu Leu
355 360 365
Leu Asp Asp Gly Glu Glu Gly Glu Asp Glu Glu Glu Pro Trp Glu Asp
370 375 380
Phe Asp Gly Thr Trp Thr Glu Glu Gln Gly Ile Leu Trp Leu Ala Pro
385 390 395 400
Thr His Pro Pro Asp Phe Gly Leu Pro Tyr Arg Pro Asn Phe Pro Gln
405 410 415
Asp Gly Glu Pro Gln Arg Leu His Leu Glu Pro Thr Trp Pro Pro Pro
420 425 430
Leu Ser Ala Pro Arg Gly Pro Tyr His Ser Ser Val Val Ser Ala Thr
435 440 445
Arg Pro Met Val Ile Ser Ala Thr Arg Pro Thr Leu Pro Ser Ala His
450 455 460
Lys Thr Ser Val Ile Ser Ala Thr Arg Pro Pro Leu Ser Pro Val His
465 470 475 480
Pro Pro Ala Met Ala Pro Ala Thr Pro Pro Ala Val Phe Ser Glu His
485 490 495
Gln Ile Pro Lys Ile Lys Ala Asn Tyr Pro Asp Leu Pro Phe Gly His
500 505 510
Lys Pro Gly Ile Thr Ser Ala Thr His Pro Ala Arg Ser Pro Pro Tyr
515 520 525
Gln Pro Pro Ile Ile Ser Thr Asn Tyr Pro Gln Val Phe Pro Pro His
530 535 540
Gln Ala Pro Met Ser Pro Asp Thr His Thr Ile Thr Tyr Leu Pro Pro
545 550 555 560
Val Pro Pro His Leu Asp Pro Gly Asp Thr Thr Ser Lys Ala His Gln
565 570 575
His Pro Leu Leu Pro Asp Ala Pro Gly Ile Arg Thr Gln Ala Pro Gln
580 585 590
Leu Ser Val Ser Ala Leu Gln Pro Pro Leu Pro Thr Asn Ser Arg Ser
595 600 605
Ser Val His Glu Thr Pro Val Pro Ala Ala Asn Gln Pro Pro Ala Phe
610 615 620
Pro Ser Ser Pro Leu Pro Pro Gln Arg Pro Thr Asn Gln Thr Ser Ser
625 630 635 640
Ile Ser Pro Thr His Ser Tyr Ser Arg Ala Pro Leu Val Pro Arg Glu
645 650 655
Gly Val Pro Ser Pro Lys Ser Val Pro Gln Leu Pro Ser Val Pro Ser
660 665 670

Thr Ala Ala Pro Thr Ala Leu Ala Glu Ser Gly Leu Ala Gly Gln Ser
675 680 685
Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
690 695 700
Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
705 710 715 720
Cys Gly Ser His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
725 730 735
Val Thr His Ala Gly Asn Lys Ser Ser Thr Glu Pro Met Pro Pro Arg
740 745 750
Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
755 760 765

<210> 191
<211> 1329
<212> PRT
<213> Mus musculus

<400> 191
Met Pro Val Pro Pro Ala Arg Leu Leu Leu Leu Pro Leu Leu Pro Cys
1 5 10 15
Leu Leu Leu Leu Ala Pro Gly Thr Arg Gly Ala Pro Gly Cys Pro Val
20 25 30
Pro Ile Arg Gly Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser
35 40 45
Gly Gly Ala His Asn Pro Ala Arg Arg Arg Val Val Cys Gly Gly Gly
50 55 60
Asp Leu Pro Glu Pro Pro Asp Pro Gly Leu Leu Pro Asn Gly Thr Ile
65 70 75 80
Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser
85 90 95
Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Ser Asn Val
100 105 110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys
115 120 125
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr
130 135 140
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile
145 150 155 160
Tyr Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys
165 170 175
Ile Val Asp Phe Gly Thr Glu Phe Leu Thr Cys Asp Cys Arg Leu Arg
180 185 190
Trp Leu Leu Pro Trp Ala Arg Asn His Ser Leu Gln Leu Ser Glu Arg
195 200 205
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala His Ala Leu Ser Ser
210 215 220
Leu Gln Glu Ser Gln Leu Arg Cys Glu Gly Ala Leu Glu Leu His Thr
225 230 235 240
His Tyr Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg
245 250 255
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile
260 265 270
His Trp Tyr His Asn Gly Ala Pro Met Glu Ser Asp Glu Gln Ala Gly
275 280 285
Ile Val Leu Ala Glu Asn Leu Ile His Asp Cys Thr Phe Ile Thr Ser
290 295 300
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu
305 310 315 320
Cys Ser Val Ser Thr Val Gln Gly Asn Thr Ser Lys Lys Val Glu Ile
325 330 335

```
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Thr
            340                 345                 350
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr
        355                 360                 365
Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Ser
    370                 375                 380
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly
385                 390                 395                     400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
                405                 410                     415
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
            420                 425                 430
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
        435                 440                 445
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
    450                 455                 460
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
465                 470                 475                     480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
                485                 490                     495
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Gly Ile Val Gly Ala Leu
            500                 505                 510
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
        515                 520                 525
Val Asn Ser Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
    530                 535                 540
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Val Gly
545                 550                 555                     560
Val Ser Gly Ala Gln Pro Ser Ser Val Gly Gln Asp Ala Pro Val Glu
                565                 570                     575
Pro Glu Pro Leu Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
            580                 585                 590
Arg Pro Asn Ile Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
        595                 600                 605
Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Thr Leu Pro Ala
    610                 615                 620
Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
625                 630                 635                     640
Phe Arg Asn Gly Arg Leu Phe Arg Ser His Gly Asn Asn Thr Ser Arg
                645                 650                     655
Pro Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val
            660                 665                 670
Ile Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro
        675                 680                 685
Val Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Asp Pro Met Ala
    690                 695                 700
Ala Trp Trp Asn Gln Asp Gly Pro Gly Gly Trp Ser Ser Glu Gly Cys
705                 710                 715                     720
Arg Leu Arg Tyr Ser Gln Pro Asn Val Ser Ser Leu Tyr Cys Gln His
                725                 730                     735
Leu Gly Asn Val Ala Val Leu Met Glu Leu Asn Ala Phe Pro Arg Glu
            740                 745                 750
Ala Gly Gly Ser Gly Ala Gly Leu His Pro Val Val Tyr Pro Cys Thr
        755                 760                 765
Ala Leu Leu Leu Leu Cys Leu Phe Ser Thr Ile Ile Thr Tyr Ile Leu
    770                 775                 780
Asn His Ser Ser Ile His Val Ser Arg Lys Gly Trp His Met Leu Leu
785                 790                 795                     800
Asn Leu Cys Phe His Met Ala Met Thr Ser Ala Val Phe Val Gly Gly
                805                 810                     815
Val Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly Ile Thr
```

```
            820                 825                 830
Leu His Tyr Ser Ser Leu Ser Ser Leu Leu Trp Met Gly Val Lys Ala
        835                 840                 845
Arg Val Leu His Lys Glu Leu Ser Trp Arg Ala Pro Pro Leu Glu Glu
    850                 855                 860
Gly Glu Ala Ala Pro Pro Gly Pro Arg Pro Met Leu Arg Phe Tyr Leu
865                 870                 875                 880
Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala Ala Val
                885                 890                 895
Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu Val Trp
            900                 905                 910
Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile Leu Pro
        915                 920                 925
Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu His Leu Arg Ser His
    930                 935                 940
Val Ala Gln Asn Pro Lys Gln Gly Asn Arg Ile Ser Leu Glu Pro Gly
945                 950                 955                 960
Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Ser Ser Gly Val Leu Leu
                965                 970                 975
Asn Asp Ser Gly Ser Leu Leu Ala Thr Val Ser Ala Gly Val Gly Thr
            980                 985                 990
Pro Ala Pro Pro Glu Asp Gly Asp Gly Val Tyr Ser Pro Gly Val Gln
        995                 1000                1005
Leu Gly Ala Leu Met Thr Thr His Phe Leu Tyr Leu Ala Met Trp Ala
    1010                1015                1020
Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg Val Val Cys
1025                1030                1035                1040
Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu Phe Val Phe
                1045                1050                1055
Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser Trp Arg Ala
            1060                1065                1070
Cys Cys Pro Pro Ala Ser Pro Ser Ala Ser His Val Pro Ala Arg Ala
        1075                1080                1085
Leu Pro Thr Ala Thr Glu Asp Gly Ser Pro Val Leu Gly Glu Gly Pro
    1090                1095                1100
Ala Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly Arg Ala Pro Pro
1105                1110                1115                1120
Pro Pro Cys Lys Leu Thr Asn Leu Gln Val Ala Gln Ser Gln Val Cys
                1125                1130                1135
Glu Ala Ser Val Ala Ala Arg Gly Asp Gly Glu Pro Glu Pro Thr Gly
            1140                1145                1150
Ser Arg Gly Ser Leu Ala Pro Arg His His Asn Asn Leu His His Gly
        1155                1160                1165
Arg Arg Val His Lys Ser Arg Ala Lys Gly His Arg Ala Gly Glu Thr
    1170                1175                1180
Gly Gly Lys Ser Arg Leu Lys Ala Leu Arg Ala Gly Thr Ser Pro Gly
1185                1190                1195                1200
Ala Pro Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His Asn Ser Pro
                1205                1210                1215
Ser Asp Ser Tyr Pro Gly Ser Ser Arg Asn Ser Pro Gly Asp Gly Leu
            1220                1225                1230
Pro Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly Ser Asp Thr
        1235                1240                1245
Ser Ala Ala Pro Ile Ala Glu Thr Gly Arg Pro Gly Gln Arg Arg Ser
    1250                1255                1260
Ala Ser Arg Asp Asn Leu Lys Gly Ser Gly Ser Ala Leu Glu Arg Glu
1265                1270                1275                1280
Ser Lys Arg Arg Ser Tyr Pro Leu Asn Thr Thr Ser Leu Asn Gly Ala
                1285                1290                1295
Pro Lys Gly Gly Lys Tyr Glu Asp Ala Ser Val Thr Gly Ala Glu Ala
            1300                1305                1310
```

Ile Ala Gly Gly Ser Met Lys Thr Gly Leu Trp Lys Ser Glu Thr Thr
1315 1320 1325
Val

<210> 192
<211> 500
<212> PRT
<213> Mus musculus

<400> 192
Met Arg Ala Gln Leu Trp Leu Leu Gln Leu Leu Leu Leu Arg Gly Ala
1 5 10 15
Ala Arg Ala Leu Ser Pro Ala Thr Pro Ala Gly His Asn Glu Gly Gln
20 25 30
Asp Ser Ala Trp Thr Ala Lys Arg Thr Arg Gln Gly Trp Ser Arg Arg
35 40 45
Pro Arg Glu Ser Pro Ala Gln Val Leu Lys Pro Gly Lys Thr Gln Leu
50 55 60
Ser Gln Asp Leu Gly Gly Gly Ser Leu Ala Ile Asp Thr Leu Pro Asp
65 70 75 80
Asn Arg Thr Arg Val Val Glu Asp Asn His Asn Tyr Tyr Val Ser Arg
85 90 95
Val Tyr Gly Pro Gly Glu Lys Gln Ser Gln Asp Leu Trp Val Asp Leu
100 105 110
Ala Val Ala Asn Arg Ser His Val Lys Ile His Arg Ile Leu Ser Ser
115 120 125
Ser His Arg Gln Ala Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe
130 135 140
Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile
145 150 155 160
Phe Met Gly Asp Met Leu His Arg Met Leu Thr Ala Thr Gln Tyr Val
165 170 175
Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr
180 185 190
Val Ala Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His
195 200 205
Val Tyr Leu Gln Asp Arg Glu Asp Arg Gly Ser Phe Thr Phe Gln Ala
210 215 220
Ala Leu His Arg Asp Gly Arg Ile Val Phe Gly Tyr Lys Glu Ile Pro
225 230 235 240
Met Ala Val Leu Asp Ile Ser Ser Ala Gln His Pro Val Lys Ala Gly
245 250 255
Leu Ser Asp Ala Phe Met Ile Leu Asn Ser Ser Pro Glu Val Pro Glu
260 265 270
Ser Gln Arg Arg Thr Ile Phe Glu Tyr His Arg Val Glu Leu Asp Ser
275 280 285
Ser Lys Ile Thr Thr Thr Ser Ala Val Glu Phe Thr Pro Leu Pro Thr
290 295 300
Cys Leu Gln His Gln Ser Cys Asp Thr Cys Val Ser Ser Asn Leu Thr
305 310 315 320
Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe
325 330 335
Asp Arg Tyr Arg Gln Glu Trp Leu Thr Tyr Gly Cys Ala Gln Glu Ala
340 345 350
Glu Gly Lys Thr Cys Glu Asp Phe Gln Asp Asp Ser His Tyr Ser Ala
355 360 365
Ser Pro Asp Ser Ser Phe Ser Pro Phe Asn Gly Asp Ser Thr Thr Ser
370 375 380
Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu
385 390 395 400

Asn Pro Tyr Ala Glu Gly Asp Gly Leu Pro Asp His Ser Ser Pro Lys
405 410 415
Ser Lys Gly Pro Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu
420 425 430
Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Ser
435 440 445
Gly His Pro Asn Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro
450 455 460
His His Trp Pro Ala Met Lys Phe His Asn His Pro Asn His Ser Thr
465 470 475 480
Tyr Thr Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Val Glu
485 490 495
Ala Glu Gln Cys
500

<210> 193
<211> 530
<212> PRT
<213> Mus musculus

<400> 193
Met Ala Arg Phe Arg Arg Ala Asp Leu Ala Ala Ala Gly Val Met Leu
1 5 10 15
Leu Cys His Phe Leu Thr Asp Arg Phe His Phe Ala His Gly Glu Pro
20 25 30
Gly His His Thr Asn Asp Trp Ile Tyr Glu Val Thr Asn Ala Phe Pro
35 40 45
Trp Asn Glu Glu Gly Val Glu Val Asp Ser Gln Ala Tyr Asn His Arg
50 55 60
Trp Lys Arg Asn Val Asp Pro Phe Lys Ala Val Asp Thr Asn Arg Ala
65 70 75 80
Ser Met Gly Gln Ala Ser Pro Glu Ser Lys Gly Phe Thr Asp Leu Leu
85 90 95
Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
100 105 110
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ala Asp Ser Ala Ser
115 120 125
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
130 135 140
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn
145 150 155 160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Asn Glu Val Thr
165 170 175
Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met
180 185 190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
195 200 205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
210 215 220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
225 230 235 240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
245 250 255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
260 265 270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
275 280 285
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr
290 295 300
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val
305 310 315 320

Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Gly Cys Gly Pro
325 330 335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu
340 345 350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp
355 360 365
Ser Gly Cys Pro Glu Glu Val Gln Ser Lys Glu Lys Met Cys Glu Lys
370 375 380
Thr Glu Pro Gly Glu Thr Ser Gln Thr Thr Thr Thr Ser His Thr Thr
385 390 395 400
Thr Met Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser
405 410 415
Gln Met Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu
420 425 430
His Leu Lys Asp Ser Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys
435 440 445
Lys Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu
450 455 460
Val Leu Ile Ile Ala Ala Ala Ile Leu Val Thr Val Tyr Met Tyr His
465 470 475 480
His Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser
485 490 495
Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr
500 505 510
Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu
515 520 525
Gln Cys
530

<210> 194
<211> 562
<212> PRT
<213> Mus musculus

<400> 194
Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys Val
1 5 10 15
Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg Glu Asp
20 25 30
Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
35 40 45
Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
50 55 60
Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
65 70 75 80
Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
85 90 95
Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
100 105 110
Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
115 120 125
Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
130 135 140
Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
145 150 155 160
Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
165 170 175
Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
180 185 190
Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
195 200 205

Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
210 215 220
Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
225 230 235 240
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
245 250 255
Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
260 265 270
Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
275 280 285
Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
290 295 300
Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile
305 310 315 320
Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Leu Ala Leu Ala Leu
325 330 335
Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
340 345 350
Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Glu Asp Asp Asp Gly Leu
355 360 365
Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
370 375 380
Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
385 390 395 400
Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val
405 410 415
Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
420 425 430
Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
435 440 445
Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
450 455 460
Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
465 470 475 480
Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
485 490 495
Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr Pro
500 505 510
Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
515 520 525
Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro Gln Ala
530 535 540
Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro Arg Pro
545 550 555 560
Ser Val

<210> 195
<211> 2565
<212> DNA
<213> Homo sapiens

<400> 195
tcgcgatgct gctgcgcctg ttgctggcct gggcggccgc agggcccaca ctgggccagg 60
acccctgggc tgctgagccc cgtgccgcct gcggccccag cagctgctac gctctcttcc 120
cacggcgccg caccttcctg gaggcctggc gggcctgccg cgagctgggg ggcgacctgg 180
ccactcctcg gacccccgag gaggcccagc gtgtggacag cctggtgggt gcgggcccag 240
ccagccggct gctgtggatc gggctgcagc ggcaggcccg gcaatgccag ctgcagcgcc 300
cactgcgcgg cttcacgtgg accacagggg accaggacac ggctttcacc aactgggccc 360
agccagcctc tggaggcccc tgcccggccc agcgctgtgt ggccctggag gcaagtggcg 420
agcaccgctg gctggagggc tcgtgcacgc tggctgtcga cggctacctg tgccagtttg 480

gcttcgaggg cgcctgcccg gcgctgcaag atgaggcggg ccaggccggc ccagccgtgt 540
ataccacgcc cttccacctg gtctccacag agtttgagtg gctgcccttc ggctctgtgg 600
ccgctgtgca gtgccaggct ggcaggggag cctctctgct ctgcgtgaag cagcctgagg 660
gaggtgtggg ctggtcacgg gctgggcccc tgtgcctggg gactggctgc agccctgaca 720
acgggggctg cgaacacgaa tgtgtggagg aggtggatgg tcacgtgtcc tgccgctgca 780
ctgagggctt ccggctggca gcagacgggc gcagttgcga ggacccctgt gcccaggctc 840
cgtgcgagca gcagtgtgag cccggtgggc cacaaggcta cagctgccac tgtcgcctgg 900
gtttccggcc agcggaggat gatccgcacc gctgtgtgga cacagatgag tgccagattg 960
ccggtgtgtg ccagcagatg tgtgtcaact acgttggtgg cttcgagtgt tattgtagcg 1020
agggacatga gctggaggct gatggcatca gctgcagccc tgcaggggcc atgggtgccc 1080
aggcttccca ggacctcgga gatgagttgc tggatgacgg ggaggatgag gaagatgaag 1140
acgaggcctg gaaggccttc aacggtggct ggacggagat gcctgggatc ctgtggatgg 1200
agcctacgca gccgcctgac tttgccctgg cctatagacc gagcttccca gaggacagag 1260
agccacagat accctacccg gagcccacct ggccaccccc gctcagtgcc cccagggtcc 1320
cctaccactc ctcagtgctc tccgtcaccc ggcctgtggt ggtctctgcc acgcatccca 1380
cactgccttc tgcccaccag cctcctgtga tccctgccac acacccagct ttgtcccgtg 1440
accaccagat ccccgtgatc gcagccaact atccagatct gccttctgcc taccaacccg 1500
gtattctctc tgtctctcat tcagcacagc ctcctgccca ccagccccct atgatctcaa 1560
ccaaatatcc ggagctcttc cctgcccacc agtcccccat gtttccagac acccgggtcg 1620
ctggcaccca gaccaccact catttgcctg gaatcccacc taaccatgcc cctctggtca 1680
ccaccctcgg tgcccagcta ccccctcaag ccccagatgc ccttgtcctc agaacccagg 1740
ccacccagct tcccattatc ccaactgccc agccctctct gaccaccacc tccaggtccc 1800
ctgtgtctcc tgcccatcaa atctctgtgc ctgctgccac ccagcccgca gccctcccca 1860
ccctcctgcc ctctcagagc cccactaacc agacctcacc catcagccct acacatcccc 1920
attccaaagc cccccaaatc ccaagggaag atggccccag tcccaagttg gccctgtggc 1980
tgccctcacc agctcccaca gcagccccaa cagccctggg ggaggctggt cttgccgagc 2040
acagccagag ggatgaccgg tggctgctgg tggcactcct ggtgccaacg tgtgtctttt 2100
tggtggtcct gcttgcactg ggcatcgtgt actgcacccg ctgtggcccc catgcaccca 2160
acaagcgcat cactgactgc tatcgctggg tcatccatgc tgggagcaag agcccaacag 2220
aacccatgcc ccccaggggc agcctcacag gggtgcagac ctgcagaacc agcgtgtgat 2280
ggggtgcaga ccccccctcat ggagtatggg gcgctggaca catggccggg gctgcaccag 2340
ggacccatgg gggctgccca gctggacaga tggcttcctg ctccccaggc ccagccaggg 2400
tcctctctca accactagac ttggctctca ggaactctgc ttcctggccc agcgctcgtg 2460
accaaggata caccaaagcc cttaagacct caggggggcgg gtgctggggt cttctccaat 2520
aaatggggtg tcaaccttaa aaaaaaaaaa aaaaaaaaaa aaaaa 2565

<210> 196
<211> 757
<212> PRT
<213> Homo sapiens

<400> 196
Met Leu Leu Arg Leu Leu Leu Ala Trp Ala Ala Ala Gly Pro Thr Leu
1 5 10 15
Gly Gln Asp Pro Trp Ala Ala Glu Pro Arg Ala Ala Cys Gly Pro Ser
20 25 30
Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp
35 40 45
Arg Ala Cys Arg Glu Leu Gly Gly Asp Leu Ala Thr Pro Arg Thr Pro
50 55 60
Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Ala Gly Pro Ala Ser
65 70 75 80
Arg Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Leu
85 90 95
Gln Arg Pro Leu Arg Gly Phe Thr Trp Thr Thr Gly Asp Gln Asp Thr
100 105 110
Ala Phe Thr Asn Trp Ala Gln Pro Ala Ser Gly Gly Pro Cys Pro Ala
115 120 125
Gln Arg Cys Val Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
130 135 140
Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe

145 150 155 160
Glu Gly Ala Cys Pro Ala Leu Gln Asp Glu Ala Gly Gln Ala Gly Pro
165 170 175
Ala Val Tyr Thr Thr Pro Phe His Leu Val Ser Thr Glu Phe Glu Trp
180 185 190
Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly
195 200 205
Ala Ser Leu Leu Cys Val Lys Gln Pro Glu Gly Gly Val Gly Trp Ser
210 215 220
Arg Ala Gly Pro Leu Cys Leu Gly Thr Gly Cys Ser Pro Asp Asn Gly
225 230 235 240
Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly His Val Ser Cys
245 250 255
Arg Cys Thr Glu Gly Phe Arg Leu Ala Ala Asp Gly Arg Ser Cys Glu
260 265 270
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly
275 280 285
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu
290 295 300
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly
305 310 315 320
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr
325 330 335
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro
340 345 350
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Gly Asp Glu Leu
355 360 365
Leu Asp Asp Gly Glu Asp Glu Glu Asp Glu Asp Glu Ala Trp Lys Ala
370 375 380
Phe Asn Gly Gly Trp Thr Glu Met Pro Gly Ile Leu Trp Met Glu Pro
385 390 395 400
Thr Gln Pro Pro Asp Phe Ala Leu Ala Tyr Arg Pro Ser Phe Pro Glu
405 410 415
Asp Arg Glu Pro Gln Ile Pro Tyr Pro Glu Pro Thr Trp Pro Pro Pro
420 425 430
Leu Ser Ala Pro Arg Val Pro Tyr His Ser Ser Val Leu Ser Val Thr
435 440 445
Arg Pro Val Val Val Ser Ala Thr His Pro Thr Leu Pro Ser Ala His
450 455 460
Gln Pro Pro Val Ile Pro Ala Thr His Pro Ala Leu Ser Arg Asp His
465 470 475 480
Gln Ile Pro Val Ile Ala Ala Asn Tyr Pro Asp Leu Pro Ser Ala Tyr
485 490 495
Gln Pro Gly Ile Leu Ser Val Ser His Ser Ala Gln Pro Pro Ala His
500 505 510
Gln Pro Pro Met Ile Ser Thr Lys Tyr Pro Glu Leu Phe Pro Ala His
515 520 525
Gln Ser Pro Met Phe Pro Asp Thr Arg Val Ala Gly Thr Gln Thr Thr
530 535 540
Thr His Leu Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr
545 550 555 560
Leu Gly Ala Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg
565 570 575
Thr Gln Ala Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu
580 585 590
Thr Thr Thr Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val
595 600 605
Pro Ala Ala Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln
610 615 620
Ser Pro Thr Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser
625 630 635 640

```
Lys Ala Pro Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala
                645                 650                 655
Leu Trp Leu Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly
            660                 665                 670
Glu Ala Gly Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu
        675                 680                 685
Val Ala Leu Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala
    690                 695                 700
Leu Gly Ile Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys
705                 710                 715                 720
Arg Ile Thr Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser
                725                 730                 735
Pro Thr Glu Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr
            740                 745                 750
Cys Arg Thr Ser Val
        755
```

<210> 197
<211> 2973
<212> DNA
<213> Homo sapiens

<400> 197

```
gccccttgcg cctccttgcc cggccgcgcc cagcccggcg tcccgagcag cgcaggggag      60
gatccccgcg cagtgacccg ggagccacca cagactctgg gaggctcggc ggctggagca     120
gcaggcagct ccccgcagct cccggcgctt ccaggcagct ctctgagccg tgccagaggc     180
ccggcccgcc attcccagcc ccgagccatg atgaagactt tgtccagcgg gaactgcacg     240
ctcagtgtgc ccgccaaaaa ctcataccgc atggtggtgc tgggtgcctc tcgggtgggc     300
aagagctcca tcgtgtctcg cttcctcaat ggccgctttg aggaccagta cacacccacc     360
atcgaggact tccaccgtaa ggtatacaac atccgcggcg acatgtacca gctcgacatc     420
ctggatacct ctggcaacca cccattcccc gccatgcgca ggctgtccat cctcacaggg     480
gatgtcttca tcctggtgtt cagcctggat aaccgggagt ccttcgatga ggtcaagcgc     540
cttcagaagc agatcctgga ggtcaagtcc tgcctgaaga acaagaccaa ggaggcggcg     600
gagctgccca tggtcatctg tggcaacaag aacgaccacg gcgagctgtg ccgccaggtg     660
cccaccaccg aggccgagct gctggtgtcg ggcgacgaga actgcgccta cttcgaggtg     720
tcggccaaga agaacaccaa cgtggacgag atgttctacg tgctcttcag catggccaag     780
ctgccacacg agatgagccc cgccctgcat cgcaagatct ccgtgcagta cggtgacgcc     840
ttccacccca ggcccttctg catgcgccgc gtcaaggaga tggacgccta tggcatggtc     900
tcgcccttcg cccgccgccc cagcgtcaac agtgacctca agtacatcaa ggccaaggtc     960
cttcgggaag gccaggcccg tgagagggac aagtgcacca tccagtgagc gagggatgct    1020
ggggcggggc ttggccagtg ccttcaggga ggtggcccca gatgcccact gtgcgcatct    1080
ccccaccgag gccccggcag cagtcttgtt cacagacctt aggcaccaga ctggaggccc    1140
ccgggcgctg gcctccgcac attcgtctgc cttctcacag ctttcctgag tccgcttgtc    1200
cacagctcct tggtggtttc atctcctctg tgggaggaca catctctgca gcctcaagag    1260
ttaggcagag actcaagtta caccttcctc tcctggggtt ggaagaaatg ttgatgccag    1320
aggggtgagg attgctgcgt catatggagc ctcctgggac aagcctcagg atgaaaagga    1380
cacagaaggc cagatgagaa aggtctcctc tctcctggca taacacccag cttggtttgg    1440
gtggcagctg ggagaacttc tctcccagcc ctgcaactct tacgctctgg ttcagctgcc    1500
tctgcacccc ctcccacccc cagcacacac acaagttggc cccagctgc gcctgacatt    1560
gagccagtgg actctgtgtc tgaagggggc gtggccacac ctcctagacc acgcccacca    1620
cttagaccac gcccacctcc tgaccgcgtt cctcagcctc ctctcctagg tccctccgcc    1680
cgacagttgt gctttgttgt ggttgcagct gttttcgtgt catgtatagt agtagaaatg    1740
gaaatcattg tactgtaaaa gcctagtgac tccctccttg gccaggccct cacccagttc    1800
agatccacgg cctccacccg ggacgccttc ctcctctgct cccaaacagg gtttccgtgg    1860
cctgtttgca gctagacatt gacctccgcc attgagctcc acggtttaca gacaattgca    1920
caagcgtggg gtgggcaggc caggactgct ttttttaat gctcccattt cacagaggat    1980
accaccgaga ctcggagggg acacgatgag caccaggccc cacctttgtc ccctagcaaa    2040
ttcagggtac agctccacct agaaccaggc tgccctctac tgtgctcgtt cctcaagcat    2100
ttattaagca cctactgggt gctgggttca ctgtgtccta ggaaaccaag aggtccccca    2160
gtcctggcct ctgcccgccc ctgctgcccc accaccttct gcacacacag cggtggggag    2220
gcggggagga gcagctggga cccagaactg agcctgggag ggatccgaca gaaaagctca    2280
```

gggcgggtct tctccttgtg cccgggattg ggctatgctg ggtaccacca tgtactcagg 2340
catggtgggt tttgaaccca taaaccaaag gcccttgtca tcagctctta acaagtatat 2400
tttgtatttt aatctctcta aacatattga agttttaggg ccctaaggaa ccttagtgat 2460
cttctattgg gtctttctga ggttcagaga gggtaagtaa cttcctccag gtcacacagc 2520
aagtctgtgg gtggcagaag caagctagcg ctgggcattc agtacatacc acgatgtgct 2580
ccctctcttg atgcttggcc cctggggcct tcagggcttt gggacatctt gtcctcaacc 2640
ctctccctag atcagtctgt gagggtccct gtagatattg tgtacaccat gcccatgtat 2700
atacaagtac acacagatgt acacacagat gtacacatgc tccagcccca gctctgcata 2760
cctgcacctg caccccagcc ttggccctg cctgcgtctg tgctcaaagc agcagctcca 2820
accctgcctc tgtccccttc cccacccact gcctgagcct tctgagcaga ccaggtacct 2880
tggctgcacc ggtgtgtggc ccgctctcac ccaggcacag ccccgccacc atggatctcc 2940
gtgtacacta tcaataaaag tgggtttgtt aca 2973

<210> 198
<211> 266
<212> PRT
<213> Homo sapiens

<400> 198
Met Met Lys Thr Leu Ser Ser Gly Asn Cys Thr Leu Ser Val Pro Ala
1 5 10 15
Lys Asn Ser Tyr Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys
20 25 30
Ser Ser Ile Val Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr
35 40 45
Thr Pro Thr Ile Glu Asp Phe His Arg Lys Val Tyr Asn Ile Arg Gly
50 55 60
Asp Met Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe
65 70 75 80
Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu
85 90 95
Val Phe Ser Leu Asp Asn Arg Glu Ser Phe Asp Glu Val Lys Arg Leu
100 105 110
Gln Lys Gln Ile Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys
115 120 125
Glu Ala Ala Glu Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His
130 135 140
Gly Glu Leu Cys Arg Gln Val Pro Thr Thr Glu Ala Glu Leu Leu Val
145 150 155 160
Ser Gly Asp Glu Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn
165 170 175
Thr Asn Val Asp Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu
180 185 190
Pro His Glu Met Ser Pro Ala Leu His Arg Lys Ile Ser Val Gln Tyr
195 200 205
Gly Asp Ala Phe His Pro Arg Pro Phe Cys Met Arg Arg Val Lys Glu
210 215 220
Met Asp Ala Tyr Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val
225 230 235 240
Asn Ser Asp Leu Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln
245 250 255
Ala Arg Glu Arg Asp Lys Cys Thr Ile Gln
260 265

<210> 199
<211> 2159
<212> DNA
<213> Homo sapiens

<400> 199
ggcggcggca tggcgaggtt cccgaaggcc gacctggccg ctgcaggagt tatgttactt 60

tgccacttct tcacggacca gtttcagttc gccgatggga aacccggaga ccaaatcctt 120
gattggcagt atggagttac tcaggccttc cctcacacag aggaggaggt ggaagttgat 180
tcacacgcgt acagccacag gtggaaaaga aacttggact ttctcaaggc ggtagacacg 240
aaccgagcaa gcgtcggcca agactctcct gagcccagaa gcttcacaga cctgctgctg 300
gatgatgggc aggacaataa cactcagatc gaggaggata cagaccacaa ttactatata 360
tctcgaatat atggtccatc tgattctgcc agccgggatt tatgggtgaa catagaccaa 420
atggaaaaag ataaagtgaa gattcatgga atattgtcca atactcatcg gcaagctgca 480
agagtgaatc tgtccttcga ttttccattt tatggccact tcctacgtga aatcactgtg 540
gcaaccgggg gtttcatata cactggagaa gtcgtacatc gaatgctaac agccacacag 600
tacatagcac ctttaatggc aaatttcgat cccagtgtat ccagaaattc aactgtcaga 660
tattttgata atggcacagc acttgtggtc cagtgggacc atgtacatct ccaggataat 720
tataacctgg gaagcttcac attccaggca accctgctca tggatggacg aatcatcttt 780
ggatacaaag aaattcctgt cttggtcaca cagataagtt caaccaatca tccagtgaaa 840
gtcggactgt ccgatgcatt tgtcgttgtc cacaggatcc aacaaattcc caatgttcga 900
agaagaacaa tttatgaata ccaccgagta gagctacaaa tgtcaaaaat taccaacatt 960
tcggctgtgg agatgacccc attacccaca tgcctccagt ttaacagatg tggcccctgt 1020
gtatcttctc agattggctt caactgcagt tggtgtagta aacttcaaag atgttccagt 1080
ggatttgatc gtcatcggca ggactgggtg gacagtggat gccctgaaga gtcaaaagag 1140
aagatgtgtg agaatacaga accagtggaa acttcttctc gaaccaccac aaccatagga 1200
gcgacaacca cccagttcag ggtcctaact accaccagaa gagcagtgac ttctcagttt 1260
cccaccagcc tccctacaga agatgatacc aagatagcac tacatctaaa agataatgga 1320
gcttctacag atgacagtgc agctgagaag aaaggggga ccctccacgc tggcctcatc 1380
gttggaatcc tcatcctggt cctcattgta gccacagcca ttcttgtgac agtctatatg 1440
tatcaccacc caacatcagc agccagcatc ttctttattg agagacgccc aagcagatgg 1500
cctgcgatga agtttagaag aggctctgga catcctgcct atgctgaagt tgaaccagtt 1560
ggagagaaag aaggctttat tgtatcagag cagtgctaaa atttctagga cagaacaaca 1620
ccagtactgg tttacaggtg ttaagactaa aattttgcct ataccttaaa gacaaacaaa 1680
caaacacaca cacaaacaag ctctaagctg ctgtagcctg aagaagacaa gatttctgga 1740
caagctcagc ccaggaaaca aagggtaaac aaaaaactaa aacttataca agataccatt 1800
tacactgaac atagaattcc ctagtggaat gtcatctata gttcactcgg aacatctccc 1860
gtggacttat ctgaagtatg acaagattat aatgcttttg gcttaggtgc agggttgcaa 1920
agggatcaga aaaaaaaaat cataataaag ctttagttca tgagggatcg acacctttgg 1980
ttcaaatgtt ctctgatgtc tcaaagataa ctgttttcca aagcctgaac cctttcactc 2040
aaaagagcaa tgatgaatgt ctcaagattg ctaagaaaaa cagcccatgc aagagtgaga 2100
acaaacacaa aataagagat tttctacatt ttcaaaaaaa aaaaaaaaaa aaaaaaaa 2159

<210> 200
<211> 529
<212> PRT
<213> Homo sapiens

<400> 200
Met Ala Arg Phe Pro Lys Ala Asp Leu Ala Ala Ala Gly Val Met Leu
1 5 10 15
Leu Cys His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro
20 25 30
Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro
35 40 45
His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg
50 55 60
Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala
65 70 75 80
Ser Val Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu
85 90 95
Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
100 105 110
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser
115 120 125
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
130 135 140
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn

145 150 155 160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr
165 170 175
Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met
180 185 190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
195 200 205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
210 215 220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
225 230 235 240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
245 250 255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
260 265 270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
275 280 285
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr
290 295 300
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val
305 310 315 320
Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro
325 330 335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu
340 345 350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp
355 360 365
Ser Gly Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu
370 375 380
Pro Val Glu Thr Ser Ser Arg Thr Thr Thr Thr Ile Gly Ala Thr Thr
385 390 395 400
Thr Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser Gln
405 410 415
Phe Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His
420 425 430
Leu Lys Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys
435 440 445
Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu Val
450 455 460
Leu Ile Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His
465 470 475 480
Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg
485 490 495
Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala
500 505 510
Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln
515 520 525
Cys

<210> 201
<211> 2608
<212> DNA
<213> Homo sapiens

<400> 201
gaggtagggg ctgagagagg cttgaggtgg aagtgggggt cggcactct gacctggtcg 60
aggaggggct agggtttgaa ccggggacag agtctaggtg agctggggct gggagctatt 120
agcgtagagg atccgggttc ggttgctctg gcgagggctc cagcatcaca ggcggcggct 180
gcgggcgcag agcggaaatg cagcggcttg ggccacccct gctgtgcctg ctgctggcgg 240
cggcggtccc cacggccccc gcgcccgctc cgacggcgac ctcggctcca gtcaagcccg 300

```
gcccggctct cagctacccg caggaggagg ccaccctcaa tgagatgttc cgcgaggttg      360
aggaactgat ggaggacacg cagcacaaat tgcgcagcgc ggtggaagag atggaggcag      420
aagaagctgc tgctaaagca tcatcagaag tgaacctggc aaacttacct cccagctatc      480
acaatgagac caacacagac acgaaggttg gaaataatac catccatgtg caccgagaaa      540
ttcacaagat aaccaacaac cagactggac aaatggtctt ttcagagaca gttatcacat      600
ctgtgggaga cgaagaaggc agaaggagcc acgagtgcat catcgacgag gactgtgggc      660
ccagcatgta ctgccagttt gccagcttcc agtacacctg ccagccatgc cggggccaga      720
ggatgctctg cacccgggac agtgagtgct gtggagacca gctgtgtgtc tggggtcact      780
gcaccaaaat ggccaccagg ggcagcaatg ggaccatctg tgacaaccag agggactgcc      840
agccggggct gtgctgtgcc ttccagagag gcctgctgtt ccctgtgtgc acacccctgc      900
ccgtggaggg cgagctttgc catgaccccg ccagccggct tctggacctc atcacctggg      960
agctagagcc tgatggagcc ttggaccgat gcccttgtgc cagtggcctc ctctgccagc     1020
cccacagcca cagcctggtg tatgtgtgca agccgacctt cgtggggagc cgtgaccaag     1080
atggggagat cctgctgccc agagaggtcc ccgatgagta tgaagttggc agcttcatgg     1140
aggaggtgcg ccaggagctg gaggacctgg agaggagcct gactgaagag atggcgctgg     1200
gggagcctgc ggctgccgcc gctgcactgc tgggaggggga agagatttag atctggacca     1260
ggctgtgggt agatgtgcaa tagaaatagc taatttattt ccccaggtgt gtgctttagg     1320
cgtgggctga ccaggcttct tcctacatct tcttcccagt aagtttcccc tctggcttga     1380
cagcatgagg tgttgtgcat ttgttcagct cccccaggct gttctccagg cttcacagtc     1440
tggtgcttgg gagagtcagg cagggttaaa ctgcaggagc agtttgccac ccctgtccag     1500
attattggct gctttgcctc taccagttgg cagacagccg tttgttctac atggctttga     1560
taattgtttg aggggaggag atggaaacaa tgtggagtct ccctctgatt ggttttgggg     1620
aaatgtggag aagagtgccc tgctttgcaa acatcaacct ggcaaaaatg caacaaatga     1680
atttccacg cagttctttc catgggcata ggtaagctgt gccttcagct gttgcagatg      1740
aaatgttctg ttcaccctgc attacatgtg tttattcatc cagcagtgtt gctcagctcc     1800
tacctctgtg ccagggcagc attttcatat ccaagatcaa ttccctctct cagcacagcc     1860
tggggagggg gtcattgttc tcctcgtcca tcagggatct cagaggctca gagactgcaa     1920
gctgcttgcc caagtcacac agctagtgaa gaccagagca gtttcatctg gttgtgactc     1980
taagctcagt gctctctcca ctaccccaca ccagccttgg tgccaccaaa agtgctcccc     2040
aaaaggaagg agaatgggat ttttcttttg aggcatgcac atctggaatt aaggtcaaac     2100
taattctcac atccctctaa aagtaaacta ctgttaggaa cagcagtgtt ctcacagtgt     2160
ggggcagccg tccttctaat gaagacaatg atattgacac tgtccctctt tggcagttgc     2220
attagtaact ttgaaaggta tatgactgag cgtagcatac aggttaacct gcagaaacag     2280
tacttaggta attgtagggc gaggattata aatgaaattt gcaaaatcac ttagcagcaa     2340
ctgaagacaa ttatcaacca cgtggagaaa atcaaaccga gcagggctgt gtgaaacatg     2400
gttgtaatat gcgactgcga acactgaact ctacgccact ccacaaatga tgttttcagg     2460
tgtcatggac tgttgccacc atgtattcat ccagagttct taaagtttaa agttgcacat     2520
gattgtataa gcatgctttc tttgagtttt aaattatgta taaacataag ttgcatttag     2580
aaatcaagca taaatcactt caactgct                                        2608
```

<210> 202
<211> 350
<212> PRT
<213> Homo sapiens

<400> 202

```
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
1               5                   10                  15
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
            20                  25                  30
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
        35                  40                  45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
    50                  55                  60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65                  70                  75                  80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
                85                  90                  95
Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
            100                 105                 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
```

```
            115                 120                 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
        130                 135                 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145                 150                 155                 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
                165                 170                 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
            180                 185                 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
        195                 200                 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
    210                 215                 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225                 230                 235                 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
                245                 250                 255
Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
            260                 265                 270
Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
        275                 280                 285
Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
    290                 295                 300
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305                 310                 315                 320
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
                325                 330                 335
Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
            340                 345                 350
```

<210> 203
<211> 7540
<212> DNA
<213> Homo sapiens

<400> 203

```
gtgagttacg ccactatggc ggacggggca ccccggcccc agctttaccg cagcgtctcg      60
ttcaagctgc tggagcgctg gagcggcggc cccgggctga gggaggagga cacggacacc     120
cccggcttga ggcgacgcgc ctcgtgccgg ccgaccacgg ctgcccgggg ccagccctct     180
cggcgcgtgt ccaagctggc gtctgggccc ctggccgccc ccgcgcagcc gcgcccgctc     240
cgcagcctct cgccgtcggt tcgccagctc tcccggcgct tcgacgcgcc gcgtctggac     300
gacggctccg ctgggacccg agacggaggc gtcttacccg cggccgcgga agaagcggcc     360
gagggcccag cgcgaggagc ctggcccagc gtcaccgaga tgcgcaagct cttcggcggt     420
cctggctcca ggaggcccag cgccgactct gaatccccag gaacgcccag ccccgacggt     480
gccgcgtggg agcctccggc tcgggagtcg cggcagccac cgacgccacc ccctcggaca     540
tgcttccccc tggcgggtct gcgttcggcg cggcccctga ccgggccgga gaccgaaggg     600
aggctgcgcc ggccgcagca gcaacaggag cgggcgcagc gtccagcgga tggtttacat     660
tcttggcata tcttctccca accgcaggcc ggggcccggg cctcctgctc ctcctcctcc     720
atcgccgcct cctatcctgt cagccgcagt cgtgctgcca gctccagcga ggaggaagag     780
gagggcccgc cgcagctgcc tggagcccag agtccggcct accacggcgg ccactcctcg     840
ggcagtgacg acgaccgaga cggtgagggc ggccaccgct ggggagggag gcccgggctc     900
aggcctggaa gctccctatt ggatcaggac tgcaggcctg acagtgatgg gttaaatcta     960
agcagcatga actcagcagg ggtttctggg agccctgagc cccaacatc  tccaagagcc    1020
cctagagaag aaggactccg ggagtggggt agtggctctc cgccctgcgt cccaggtccc    1080
caggagggac ttcggcctat gtctgactct gtgggaggag ctttccgtgt ggccaaggtg    1140
agctttccct cgtacctggc cagcccccgca ggctcccgcg gtagcagccg ttattccagc    1200
acggagaccc tcaaggacga cgacctatgg tctagtaggg gttctggggg ctggggcgtg    1260
taccgctccc ctagctttgg agctggggaa gggctcctgc ggtcccaggc tcgaacccgt    1320
gccaaaggac ctggaggcac ctctagggca ttgagggatg gaggatttga gcctgaaaag    1380
agtcgacagc ggaagtccct gtcaaatcca gatatcgcct cagagaccct gacgcttctc    1440
agtttcctgc gctcagacct ttcagagctg agggtccgaa aacctggtgg gagctccggg    1500
```

gaccgtggaa gcaaccccct agatggcaga gactcaccat ccgcaggtgg ccctgtgggg 1560
caacttgaac ccatacccat cccagcccca gcatcacctg gcacgcgccc cacactcaag 1620
gacttgacag ccactctgcg gagagcaaag tcattcacct gctctgagaa gcccatggcc 1680
cgccgcctgc cccgcaccag tgctctgaag tccagctcct ccgagctcct gctcacaggc 1740
cctggtgccg aggaggatcc gctgcccctc atcgtccagg accaatatgt gcaggaggcc 1800
cgccaggttt ttgagaagat ccagcgcatg ggtgcccaac aagatgatgg aagcgatgcc 1860
ccccctggaa gccctgactg ggcaggggat gtgacccgag ggcagcggtc ccaggaggag 1920
ctctcaggcc ctgagtccag tctgacagat gaaggcattg ggcagaccc tgagcctcct 1980
gttgcagcat tttgcggcct gggtaccaca gggatgtggc gacctctttc ctcatcctcg 2040
gcccagacga accaccatgg ccctgggact gaggacagtc tgggcgggtg ggccctggtg 2100
tcgcctgaga cccctcccac accaggtgcc ctccgccgac gacgcaaagt cccaccttca 2160
ggttctggtg ggagcgaatt gagcaatggg gaggcagggg aggcctacag gtccctgagt 2220
gacccaattc ctcagcgcca ccgggctgcc acctctgaag agcctactgg gttctctgtg 2280
gacagcaacc tcctgggctc actgagcccc aagacagggc tccctgccac ctcagccatg 2340
gatgagggct tgaccagtgg tcacagtgac tggtctgtgg gcagtgaaga gagcaaggga 2400
tatcaggagg ttattcagag catagttcag ggccctggca ccctggggcg tgtggtggac 2460
gacaggattg ctggcaaagc cccaagaag aaatccctga gtgaccccag ccgccgtggg 2520
gagctggctg ggcctggatt cgagggccct ggaggggagc ccatccgaga agttgagccc 2580
atgctgcctc catccagcag cgagcccatc cttgtagagc agcgggcaga gccagaagaa 2640
cctggtgcca ccaggagccg ggcacagtct gaaagggccc tacctgaggc tctgcctccc 2700
cctgccactg cccaccgaaa ctttcacctt gaccccaagc tggctgacat tctgtccccg 2760
aggctaatcc gccgaggctc caagaagcgc ccagctcgga gtagtcacca ggagcttcgg 2820
agagacgagg gcagtcagga ccagactggc agcctgtctc gggcccggcc ctcctccaga 2880
cacgttcgcc atgccagtgt gcccgccaca tttatgccta ttgtggtgcc tgagccacca 2940
acttctgttg gtccccctgt ggctgtgcca gaacccatag gcttccctac ccgagcccat 3000
cccacgttgc aggcaccatc gctcgaggac gtcaccaagc agtacatgct gaacctgcac 3060
tccggtgagg tccctgcccc agtgccagtg gacatgccct gcttgcctct ggctgcaccg 3120
ccctctgctg aggccaagcc ccctgaggca gctcggcctg cagatgagcc taccccctgcc 3180
agcaagtgct gcagcaagcc acaggtggac atgcggaagc acgtggccat gaccctgctg 3240
gacacagagc agtcgtatgt ggagtcgctg cgcaccctga tgcagggcta catgcagccg 3300
ctgaagcagc cagagaactc cgtgctctgt gacccttcac tggtggacga gatcttcgac 3360
cagatccccg agctcctgga gcaccacgag caattcctgg agcaggttcg gcactgcatg 3420
cagacctggc atgcccagca gaaggtggga gccctgctcg tccagtcgtt ctccaaggat 3480
gtcctagtaa acatctattc tgcctatatc gataacttcc tcaatgcaaa ggatgctgtg 3540
cgtgtggcca aggaggcgag gcctgccttt ctcaagttcc tagagcaaag catgcgtgag 3600
aacaaggaga agcaggcgct gtctgacctc atgatcaagc ctgtgcagcg gatcccacgc 3660
tacgagcttc tggtgaagga cctcctgaag catacacctg aggaccaccc ggaccatcca 3720
ctcctgctgg aggcgcagcg gaacatcaag caggtggctg agcgcatcaa caagggtgtg 3780
cggagtgccg aggaggcgga gcgccatgcc cgtgtgctgc aggagataga ggctcacatc 3840
gagggcatgg aggatctcca ggcccctctg cggcggttcc tgagacagga gatggtcatt 3900
gaagtgaagg cgatcggtgg caagaaggac cggtctctct tcctgttcac ggacctcatc 3960
gtctgcacca ctctgaagcg aaagtcaggc tccctgcggc gcagctccat gagcctgtac 4020
acggcagcca gtgtcattga cacagccagc aagtacaaga tgctgtggaa gctgccgctg 4080
gaagacgcag acatcatcaa aggggcatcc caagccacca atcgggagaa catccagaag 4140
gccatcagcc gccttgatga ggacctcacc accctgggcc aaatgagcaa gctctctgag 4200
agccttggtt tcccccacca gagcctggac gatgcactgc gggacctctc agctgccatg 4260
caccgggacc tgtcggagaa gcaggcgctg tgctacgcgc tttccttccc gccaaccaag 4320
ctggagctgt gcgccactcg gcccgagggc accgactcct acatttttga gttccctcac 4380
cctgacgccc gccttggttt tgaacaggcc ttcgatgagg ccaagaggaa gctggcatcc 4440
agcaaaagct gtctagaccc tgagttcctg aaggccatcc ccatcatgaa aacccgcagt 4500
ggcatgcagt tctcctgtgc ggctcccacc ctgaacagct gcccggagcc ctcgcctgag 4560
gtatgggtct gcaacagcga cggctacgtg ggccaggtgt gcctgctgag cctgcgcgcc 4620
gagccggacg tggaggcctg catcgccgtc tgttccgccc gcatcctctg catcggggcg 4680
gtgcccgggc tgcagcctcg ctgccaccgg gagcctcctc cgtcgctgag gagtcctcca 4740
gagacggcac cggagcccgc cgggccggag ctggacgtcg aggccgctgc agacgaggaa 4800
gccgcgacgc tcgcggagcc ggggccgcag ccctgccttc acatctccat tgcaggctcg 4860
ggcttggaga tgacgccggg cctcggcgag ggtgaccccc gcccagagct ggtgcccttt 4920
gacagtgact ctgacgatga gtcttcgccc agcccctcgg ggacgctgca gagccaggcc 4980
agccggtcca ccatctcctc cagctttggc aatgaggaga ccccgagttc caaggaggcc 5040
acggcagaga ccaccagctc agaggaggag caggagccag gcttcctgcc actgtctggc 5100
tcctttgggc ctggtggtcc ctgcggcacc agcccaatgg atgggagagc ccttcgccgc 5160

tccagccacg gctccttcac ccggggcagc cttgaggacc tgctgagtgt cgaccctgag 5220
gcctaccaga gctccgtgtg gctgggcact gaggatggct gtgtccacgt gtaccagtcc 5280
tccgacagca tccgtgaccg caggaacagc atgaagctcc agcatgcggc ctctgtgacc 5340
tgcatcttgt atctgaataa ccaggtgttt gtgtctctgg ccaatggaga gcttgtggtc 5400
taccaaaggg aagcaggcca tttctgggac cccagaact tcaaatcagt gaccttgggc 5460
acccagggga gccccatcac caagatggta tctgtgggtg ggcggctgtg gtgtggctgc 5520
cagaaccgag tccttgtcct gagccctgac acgctgcagc tggagcacat gttttacgtg 5580
ggtcaggatt caagccgctg cgtggcttgc atggtggact ccagcctggg tgtgtgggtg 5640
acattgaaag gtagtgccca cgtgtgtctc taccatccag acacctttga gcagctggca 5700
gaagtagacg tcactcctcc cgtgcacagg atgctggcag gctcggatgc catcatccgg 5760
cagcacaagg ctgcctgtct gcgaatcaca gcgctgctgg tgtgtgagga gctgctgtgg 5820
gtgggcacca gtgctggtgt cgtcctcacc atgcccactt cgcccggtac tgtcagctgc 5880
ccacgggcac cactcagtcc cacaggcctc ggccagggac acaccggcca cgtccgcttc 5940
ttggctgcag tccagctgcc agatggcttc aacctgctct gcccaacccc accacctccc 6000
ccagacacag gccccgagaa gctgccatca ctggagcacc gggactcccc ttggcaccga 6060
ggccccgccc ctgccaggcc taaaatgctg gttatcagtg gaggtgatgg ctatgaggac 6120
ttccgactca gcagtggggg cggcagcagc agtgagactg tgggtcgaga cgacagcaca 6180
aaccacctcc tcctgtggag ggtgtgaccc tgtctgccgt ggcccaggac tcgcccgccc 6240
acctgccttc agcctgcttg cctctcccta gcccacacgc agactttgac caggagtatc 6300
cagccagggg cacacatgtg cctgcgtggg ctctgccttg tcttcgcgga agcattcctg 6360
atggaacacc cactggccag ccaggccatg gcttctcccg accctctggc tgccccggtg 6420
cttccagtca tgatcgggtg ggggacatgt gggctgacca ggacctctga ccctgggagc 6480
ttctaccaaa gacacagctg ggtctggacc ccacggggct ggggagggcc atgtgcaata 6540
tttggagggt tttctggagg gcagcaggaa ggctggggaa ttccccatgt acagtattta 6600
tgtttctttt tagatgtgta ccttcccaag cacttattta tgcagtgacc tggtcacctg 6660
gggtgggggt gatttgagga aatgacatga ggaaaagaaa cctattcctg ccctggggac 6720
caccctggga ctctaaccaa gccttcctgg agggacccat gcgcccctga gccccattcc 6780
attcatacag acacacacgt acgcacactg catgtccaag gccctaaaca ttgcccgttg 6840
acataaactt tccagggccc cagcctgatg ggctgccct cagtcctcta gatcaagatg 6900
ctgactatta gggggcagtg attgccatct ggggacctgt caggctttgt catttcccag 6960
tttgttggtg gtgcctttag tggttcccta atttgggaac actgatgggg ccttggacag 7020
ggctttctct caggtaggag aaatgggccc atgatctcct cacagtcgcc cccagtcctt 7080
ggccctgctt ccctgtgtct catgcactgg cacatatggt caccttggag ggcagaccta 7140
ggagcccctc tgaccactga atccgtctcc acacccctc tgccaaggga agccccttca 7200
ggaaggaccc cccaaagctg aggggctgaa tgtagccttt tcaacagaga aggctcccac 7260
ttgagagcag cctctacctg accccctgga ccacagagag ccactctgac cctcagcccc 7320
ctcgcttctt cagctaaaac tccaaaggtt tggtttcaga tggggtttgt tttgttctgt 7380
ttggttttgg ttttgtttgg ggtgggtggg tcattgcggt cttagattat gtttctcttg 7440
ctaccaaaca gtcatgtatt aactctcttt ggatgatgaa gtttaaagag tcaataaata 7500
gaaacaccag atgactgcaa aaaaaaaaa aaaaaaaaa 7540

<210> 204
<211> 2063
<212> PRT
<213> Homo sapiens

<400> 204
Met Ala Asp Gly Ala Pro Arg Pro Gln Leu Tyr Arg Ser Val Ser Phe
1 5 10 15
Lys Leu Leu Glu Arg Trp Ser Gly Gly Pro Gly Leu Arg Glu Glu Asp
20 25 30
Thr Asp Thr Pro Gly Leu Arg Arg Arg Ala Ser Cys Arg Pro Thr Thr
35 40 45
Ala Ala Arg Gly Gln Pro Ser Arg Arg Val Ser Lys Leu Ala Ser Gly
50 55 60
Pro Leu Ala Ala Pro Ala Gln Pro Arg Pro Leu Arg Ser Leu Ser Pro
65 70 75 80
Ser Val Arg Gln Leu Ser Arg Arg Phe Asp Ala Pro Arg Leu Asp Asp
85 90 95

Gly Ser Ala Gly Thr Arg Asp Gly Gly Val Leu Pro Ala Ala Ala Glu
100 105 110
Glu Ala Ala Glu Gly Pro Ala Arg Gly Ala Trp Pro Ser Val Thr Glu
115 120 125
Met Arg Lys Leu Phe Gly Gly Pro Gly Ser Arg Arg Pro Ser Ala Asp
130 135 140
Ser Glu Ser Pro Gly Thr Pro Ser Pro Asp Gly Ala Ala Trp Glu Pro
145 150 155 160
Pro Ala Arg Glu Ser Arg Gln Pro Pro Thr Pro Pro Pro Arg Thr Cys
165 170 175
Phe Pro Leu Ala Gly Leu Arg Ser Ala Arg Pro Leu Thr Gly Pro Glu
180 185 190
Thr Glu Gly Arg Leu Arg Arg Pro Gln Gln Gln Gln Glu Arg Ala Gln
195 200 205
Arg Pro Ala Asp Gly Leu His Ser Trp His Ile Phe Ser Gln Pro Gln
210 215 220
Ala Gly Ala Arg Ala Ser Cys Ser Ser Ser Ser Ile Ala Ala Ser Tyr
225 230 235 240
Pro Val Ser Arg Ser Arg Ala Ala Ser Ser Ser Glu Glu Glu Glu Glu
245 250 255
Gly Pro Pro Gln Leu Pro Gly Ala Gln Ser Pro Ala Tyr His Gly Gly
260 265 270
His Ser Ser Gly Ser Asp Asp Asp Arg Asp Gly Glu Gly Gly His Arg
275 280 285
Trp Gly Gly Arg Pro Gly Leu Arg Pro Gly Ser Ser Leu Leu Asp Gln
290 295 300
Asp Cys Arg Pro Asp Ser Asp Gly Leu Asn Leu Ser Ser Met Asn Ser
305 310 315 320
Ala Gly Val Ser Gly Ser Pro Glu Pro Pro Thr Ser Pro Arg Ala Pro
325 330 335
Arg Glu Glu Gly Leu Arg Glu Trp Gly Ser Gly Ser Pro Pro Cys Val
340 345 350
Pro Gly Pro Gln Glu Gly Leu Arg Pro Met Ser Asp Ser Val Gly Gly
355 360 365
Ala Phe Arg Val Ala Lys Val Ser Phe Pro Ser Tyr Leu Ala Ser Pro
370 375 380
Ala Gly Ser Arg Gly Ser Ser Arg Tyr Ser Ser Thr Glu Thr Leu Lys
385 390 395 400
Asp Asp Asp Leu Trp Ser Ser Arg Gly Ser Gly Gly Trp Gly Val Tyr
405 410 415
Arg Ser Pro Ser Phe Gly Ala Gly Glu Gly Leu Leu Arg Ser Gln Ala
420 425 430
Arg Thr Arg Ala Lys Gly Pro Gly Gly Thr Ser Arg Ala Leu Arg Asp
435 440 445
Gly Gly Phe Glu Pro Glu Lys Ser Arg Gln Arg Lys Ser Leu Ser Asn
450 455 460
Pro Asp Ile Ala Ser Glu Thr Leu Thr Leu Leu Ser Phe Leu Arg Ser
465 470 475 480
Asp Leu Ser Glu Leu Arg Val Arg Lys Pro Gly Gly Ser Ser Gly Asp
485 490 495
Arg Gly Ser Asn Pro Leu Asp Gly Arg Asp Ser Pro Ser Ala Gly Gly
500 505 510
Pro Val Gly Gln Leu Glu Pro Ile Pro Ile Pro Ala Pro Ala Ser Pro
515 520 525
Gly Thr Arg Pro Thr Leu Lys Asp Leu Thr Ala Thr Leu Arg Arg Ala
530 535 540
Lys Ser Phe Thr Cys Ser Glu Lys Pro Met Ala Arg Arg Leu Pro Arg
545 550 555 560
Thr Ser Ala Leu Lys Ser Ser Ser Ser Glu Leu Leu Leu Thr Gly Pro
565 570 575
Gly Ala Glu Glu Asp Pro Leu Pro Leu Ile Val Gln Asp Gln Tyr Val

580 585 590
Gln Glu Ala Arg Gln Val Phe Glu Lys Ile Gln Arg Met Gly Ala Gln
595 600 605
Gln Asp Asp Gly Ser Asp Ala Pro Pro Gly Ser Pro Asp Trp Ala Gly
610 615 620
Asp Val Thr Arg Gly Gln Arg Ser Gln Glu Glu Leu Ser Gly Pro Glu
625 630 635 640
Ser Ser Leu Thr Asp Glu Gly Ile Gly Ala Asp Pro Glu Pro Pro Val
645 650 655
Ala Ala Phe Cys Gly Leu Gly Thr Thr Gly Met Trp Arg Pro Leu Ser
660 665 670
Ser Ser Ser Ala Gln Thr Asn His His Gly Pro Gly Thr Glu Asp Ser
675 680 685
Leu Gly Gly Trp Ala Leu Val Ser Pro Glu Thr Pro Pro Thr Pro Gly
690 695 700
Ala Leu Arg Arg Arg Arg Lys Val Pro Pro Ser Gly Ser Gly Gly Ser
705 710 715 720
Glu Leu Ser Asn Gly Glu Ala Gly Glu Ala Tyr Arg Ser Leu Ser Asp
725 730 735
Pro Ile Pro Gln Arg His Arg Ala Ala Thr Ser Glu Glu Pro Thr Gly
740 745 750
Phe Ser Val Asp Ser Asn Leu Leu Gly Ser Leu Ser Pro Lys Thr Gly
755 760 765
Leu Pro Ala Thr Ser Ala Met Asp Glu Gly Leu Thr Ser Gly His Ser
770 775 780
Asp Trp Ser Val Gly Ser Glu Glu Ser Lys Gly Tyr Gln Glu Val Ile
785 790 795 800
Gln Ser Ile Val Gln Gly Pro Gly Thr Leu Gly Arg Val Val Asp Asp
805 810 815
Arg Ile Ala Gly Lys Ala Pro Lys Lys Lys Ser Leu Ser Asp Pro Ser
820 825 830
Arg Arg Gly Glu Leu Ala Gly Pro Gly Phe Glu Gly Pro Gly Gly Glu
835 840 845
Pro Ile Arg Glu Val Glu Pro Met Leu Pro Pro Ser Ser Ser Glu Pro
850 855 860
Ile Leu Val Glu Gln Arg Ala Glu Pro Glu Glu Pro Gly Ala Thr Arg
865 870 875 880
Ser Arg Ala Gln Ser Glu Arg Ala Leu Pro Glu Ala Leu Pro Pro Pro
885 890 895
Ala Thr Ala His Arg Asn Phe His Leu Asp Pro Lys Leu Ala Asp Ile
900 905 910
Leu Ser Pro Arg Leu Ile Arg Arg Gly Ser Lys Lys Arg Pro Ala Arg
915 920 925
Ser Ser His Gln Glu Leu Arg Arg Asp Glu Gly Ser Gln Asp Gln Thr
930 935 940
Gly Ser Leu Ser Arg Ala Arg Pro Ser Ser Arg His Val Arg His Ala
945 950 955 960
Ser Val Pro Ala Thr Phe Met Pro Ile Val Val Pro Glu Pro Pro Thr
965 970 975
Ser Val Gly Pro Pro Val Ala Val Pro Glu Pro Ile Gly Phe Pro Thr
980 985 990
Arg Ala His Pro Thr Leu Gln Ala Pro Ser Leu Glu Asp Val Thr Lys
995 1000 1005
Gln Tyr Met Leu Asn Leu His Ser Gly Glu Val Pro Ala Pro Val Pro
1010 1015 1020
Val Asp Met Pro Cys Leu Pro Leu Ala Ala Pro Pro Ser Ala Glu Ala
1025 1030 1035 1040
Lys Pro Pro Glu Ala Ala Arg Pro Ala Asp Glu Pro Thr Pro Ala Ser
1045 1050 1055
Lys Cys Cys Ser Lys Pro Gln Val Asp Met Arg Lys His Val Ala Met
1060 1065 1070

Thr Leu Leu Asp Thr Glu Gln Ser Tyr Val Glu Ser Leu Arg Thr Leu
1075 1080 1085
Met Gln Gly Tyr Met Gln Pro Leu Lys Gln Pro Glu Asn Ser Val Leu
1090 1095 1100
Cys Asp Pro Ser Leu Val Asp Glu Ile Phe Asp Gln Ile Pro Glu Leu
1105 1110 1115 1120
Leu Glu His His Glu Gln Phe Leu Glu Gln Val Arg His Cys Met Gln
1125 1130 1135
Thr Trp His Ala Gln Gln Lys Val Gly Ala Leu Leu Val Gln Ser Phe
1140 1145 1150
Ser Lys Asp Val Leu Val Asn Ile Tyr Ser Ala Tyr Ile Asp Asn Phe
1155 1160 1165
Leu Asn Ala Lys Asp Ala Val Arg Val Ala Lys Glu Ala Arg Pro Ala
1170 1175 1180
Phe Leu Lys Phe Leu Glu Gln Ser Met Arg Glu Asn Lys Glu Lys Gln
1185 1190 1195 1200
Ala Leu Ser Asp Leu Met Ile Lys Pro Val Gln Arg Ile Pro Arg Tyr
1205 1210 1215
Glu Leu Leu Val Lys Asp Leu Leu Lys His Thr Pro Glu Asp His Pro
1220 1225 1230
Asp His Pro Leu Leu Leu Glu Ala Gln Arg Asn Ile Lys Gln Val Ala
1235 1240 1245
Glu Arg Ile Asn Lys Gly Val Arg Ser Ala Glu Glu Ala Glu Arg His
1250 1255 1260
Ala Arg Val Leu Gln Glu Ile Glu Ala His Ile Glu Gly Met Glu Asp
1265 1270 1275 1280
Leu Gln Ala Pro Leu Arg Arg Phe Leu Arg Gln Glu Met Val Ile Glu
1285 1290 1295
Val Lys Ala Ile Gly Gly Lys Lys Asp Arg Ser Leu Phe Leu Phe Thr
1300 1305 1310
Asp Leu Ile Val Cys Thr Thr Leu Lys Arg Lys Ser Gly Ser Leu Arg
1315 1320 1325
Arg Ser Ser Met Ser Leu Tyr Thr Ala Ala Ser Val Ile Asp Thr Ala
1330 1335 1340
Ser Lys Tyr Lys Met Leu Trp Lys Leu Pro Leu Glu Asp Ala Asp Ile
1345 1350 1355 1360
Ile Lys Gly Ala Ser Gln Ala Thr Asn Arg Glu Asn Ile Gln Lys Ala
1365 1370 1375
Ile Ser Arg Leu Asp Glu Asp Leu Thr Thr Leu Gly Gln Met Ser Lys
1380 1385 1390
Leu Ser Glu Ser Leu Gly Phe Pro His Gln Ser Leu Asp Asp Ala Leu
1395 1400 1405
Arg Asp Leu Ser Ala Ala Met His Arg Asp Leu Ser Glu Lys Gln Ala
1410 1415 1420
Leu Cys Tyr Ala Leu Ser Phe Pro Pro Thr Lys Leu Glu Leu Cys Ala
1425 1430 1435 1440
Thr Arg Pro Glu Gly Thr Asp Ser Tyr Ile Phe Glu Phe Pro His Pro
1445 1450 1455
Asp Ala Arg Leu Gly Phe Glu Gln Ala Phe Asp Glu Ala Lys Arg Lys
1460 1465 1470
Leu Ala Ser Ser Lys Ser Cys Leu Asp Pro Glu Phe Leu Lys Ala Ile
1475 1480 1485
Pro Ile Met Lys Thr Arg Ser Gly Met Gln Phe Ser Cys Ala Ala Pro
1490 1495 1500
Thr Leu Asn Ser Cys Pro Glu Pro Ser Pro Glu Val Trp Val Cys Asn
1505 1510 1515 1520
Ser Asp Gly Tyr Val Gly Gln Val Cys Leu Leu Ser Leu Arg Ala Glu
1525 1530 1535
Pro Asp Val Glu Ala Cys Ile Ala Val Cys Ser Ala Arg Ile Leu Cys
1540 1545 1550
Ile Gly Ala Val Pro Gly Leu Gln Pro Arg Cys His Arg Glu Pro Pro

1555 1560 1565
Pro Ser Leu Arg Ser Pro Pro Glu Thr Ala Pro Glu Pro Ala Gly Pro
1570 1575 1580
Glu Leu Asp Val Glu Ala Ala Ala Asp Glu Glu Ala Ala Thr Leu Ala
1585 1590 1595 1600
Glu Pro Gly Pro Gln Pro Cys Leu His Ile Ser Ile Ala Gly Ser Gly
1605 1610 1615
Leu Glu Met Thr Pro Gly Leu Gly Glu Gly Asp Pro Arg Pro Glu Leu
1620 1625 1630
Val Pro Phe Asp Ser Asp Ser Asp Asp Glu Ser Ser Pro Ser Pro Ser
1635 1640 1645
Gly Thr Leu Gln Ser Gln Ala Ser Arg Ser Thr Ile Ser Ser Ser Phe
1650 1655 1660
Gly Asn Glu Glu Thr Pro Ser Ser Lys Glu Ala Thr Ala Glu Thr Thr
1665 1670 1675 1680
Ser Ser Glu Glu Glu Gln Glu Pro Gly Phe Leu Pro Leu Ser Gly Ser
1685 1690 1695
Phe Gly Pro Gly Gly Pro Cys Gly Thr Ser Pro Met Asp Gly Arg Ala
1700 1705 1710
Leu Arg Arg Ser Ser His Gly Ser Phe Thr Arg Gly Ser Leu Glu Asp
1715 1720 1725
Leu Leu Ser Val Asp Pro Glu Ala Tyr Gln Ser Ser Val Trp Leu Gly
1730 1735 1740
Thr Glu Asp Gly Cys Val His Val Tyr Gln Ser Ser Asp Ser Ile Arg
1745 1750 1755 1760
Asp Arg Arg Asn Ser Met Lys Leu Gln His Ala Ala Ser Val Thr Cys
1765 1770 1775
Ile Leu Tyr Leu Asn Asn Gln Val Phe Val Ser Leu Ala Asn Gly Glu
1780 1785 1790
Leu Val Val Tyr Gln Arg Glu Ala Gly His Phe Trp Asp Pro Gln Asn
1795 1800 1805
Phe Lys Ser Val Thr Leu Gly Thr Gln Gly Ser Pro Ile Thr Lys Met
1810 1815 1820
Val Ser Val Gly Gly Arg Leu Trp Cys Gly Cys Gln Asn Arg Val Leu
1825 1830 1835 1840
Val Leu Ser Pro Asp Thr Leu Gln Leu Glu His Met Phe Tyr Val Gly
1845 1850 1855
Gln Asp Ser Ser Arg Cys Val Ala Cys Met Val Asp Ser Ser Leu Gly
1860 1865 1870
Val Trp Val Thr Leu Lys Gly Ser Ala His Val Cys Leu Tyr His Pro
1875 1880 1885
Asp Thr Phe Glu Gln Leu Ala Glu Val Asp Val Thr Pro Pro Val His
1890 1895 1900
Arg Met Leu Ala Gly Ser Asp Ala Ile Ile Arg Gln His Lys Ala Ala
1905 1910 1915 1920
Cys Leu Arg Ile Thr Ala Leu Leu Val Cys Glu Glu Leu Leu Trp Val
1925 1930 1935
Gly Thr Ser Ala Gly Val Val Leu Thr Met Pro Thr Ser Pro Gly Thr
1940 1945 1950
Val Ser Cys Pro Arg Ala Pro Leu Ser Pro Thr Gly Leu Gly Gln Gly
1955 1960 1965
His Thr Gly His Val Arg Phe Leu Ala Ala Val Gln Leu Pro Asp Gly
1970 1975 1980
Phe Asn Leu Leu Cys Pro Thr Pro Pro Pro Pro Pro Asp Thr Gly Pro
1985 1990 1995 2000
Glu Lys Leu Pro Ser Leu Glu His Arg Asp Ser Pro Trp His Arg Gly
2005 2010 2015
Pro Ala Pro Ala Arg Pro Lys Met Leu Val Ile Ser Gly Gly Asp Gly
2020 2025 2030
Tyr Glu Asp Phe Arg Leu Ser Ser Gly Gly Gly Ser Ser Ser Glu Thr
2035 2040 2045

Val Gly Arg Asp Asp Ser Thr Asn His Leu Leu Leu Trp Arg Val
2050 2055 2060

<210> 205
<211> 2247
<212> DNA
<213> Homo sapiens

<400> 205
ccggggcgga tggctccggc cgcctggctc cgcagcgcgg ccgcgcgcgc cctcctgccc 60
ccgatgctgc tgctgctgct ccagccgccg ccgctgctgg cccgggctct gccgccggac 120
gtccaccacc tccatgccga gaggaggggg ccacagccct ggcatgcagc cctgcccagt 180
agcccggcac ctgcccctgc cacgcaggaa gcccccggc ctgccagcag cctcaggcct 240
ccccgctgtg gcgtgcccga cccatctgat gggctgagtg cccgcaaccg acagaagagg 300
ttcgtgcttt ctggcgggcg ctgggagaag acggacctca cctacaggat ccttcggttc 360
ccatggcagt tggtgcagga gcaggtgcgg cagacgatgg cagaggccct aaaggtatgg 420
agcgatgtga cgccactcac ctttactgag gtgcacgagg gccgtgctga catcatgatc 480
gacttcgcca ggtactggca tggggacgac ctgccgtttg atgggcctgg gggcatcctg 540
gcccatgcct tcttccccaa gactcaccga gaaggggatg tccacttcga ctatgatgag 600
acctggacta tcggggatga ccagggcaca gacctgctgc aggtggcagc ccatgaattt 660
ggccacgtgc tggggctgca gcacacaaca gcagccaagg ccctgatgtc cgccttctac 720
acctttcgct acccactgag tctcagccca gatgactgca ggggcgttca acacctatat 780
ggccagccct ggcccactgt cacctccagg accccagccc tgggccccca ggctgggata 840
gacaccaatg agattgcacc gctggagcca gacgccccgc cagatgcctg tgaggcctcc 900
tttgacgcgg tctccaccat ccgaggcgag ctcttttttct tcaaagcggg ctttgtgtgg 960
cgcctccgtg gggccagct gcagcccggc tacccagcat tggcctctcg ccactggcag 1020
ggactgccca gccctgtgga cgctgccttc gaggatgccc agggccacat ttggttcttc 1080
caaggtgctc agtactgggt gtacgacggt gaaaagccag tcctgggccc cgcacccctc 1140
accgagctgg gcctggtgag gttcccggtc catgctgcct tggtctgggg tcccgagaag 1200
aacaagatct acttcttccg aggcagggac tactggcgtt tccaccccag caccggcgt 1260
gtagacagtc ccgtgccccg cagggccact gactggagag ggtgccctc tgagatcgac 1320
gctgccttcc aggatgctga tggctatgcc tacttcctgc gcggccgcct ctactggaag 1380
tttgaccctg tgaaggtgaa ggctctggaa ggcttccccc gtctcgtggg tcctgacttc 1440
tttggctgtg ccgagcctgc caacactttc ctctgaccat ggcttggatg ccctcagggg 1500
tgctgacccc tgccaggcca cgaatatcag gctagagacc catggccatc tttgtggctg 1560
tgggcaccag gcatgggact gagcccatgt ctcctgcagg gggatggggt ggggtacaac 1620
caccatgaca actgccggga gggccacgca ggtcgtggtc acctgccagc gactgtctca 1680
gactgggcag ggaggctttg gcatgactta agaggaaggg cagtcttggg acccgctatg 1740
caggtcctgg caaacctggc tgccctgtct catccctgtc cctcagggta gcaccatggc 1800
aggactgggg gaactggagt gtccttgctg tatccctgtt gtgaggttcc ttccaggggc 1860
tggcactgaa gcaagggtgc tggggcccca tggccttcag ccctggctga gcaactgggc 1920
tgtagggcag ggccacttcc tgaggtcagg tcttggtagg tgcctgcatc tgtctgcctt 1980
ctggctgaca atcctggaaa tctgttctcc agaatccagg ccaaaaagtt cacagtcaaa 2040
tggggagggg tattcttcat gcaggagacc ccaggccctg gaggctgcaa catacctcaa 2100
tcctgtccca ggccggatcc tcctgaagcc cttttcgcag cactgctatc ctccaaagcc 2160
attgtaaatg tgtgtacagt gtgtataaac cttcttcttc tttttttttt ttaaactgag 2220
gattgtcatt aaacacagtt gttttct 2247

<210> 206
<211> 488
<212> PRT
<213> Homo sapiens

<400> 206
Met Ala Pro Ala Ala Trp Leu Arg Ser Ala Ala Ala Arg Ala Leu Leu
1 5 10 15
Pro Pro Met Leu Leu Leu Leu Leu Gln Pro Pro Pro Leu Leu Ala Arg
20 25 30
Ala Leu Pro Pro Asp Val His His Leu His Ala Glu Arg Arg Gly Pro
35 40 45
Gln Pro Trp His Ala Ala Leu Pro Ser Ser Pro Ala Pro Ala Pro Ala

```
    50                  55                  60
Thr Gln Glu Ala Pro Arg Pro Ala Ser Ser Leu Arg Pro Pro Arg Cys
65                  70                  75                  80
Gly Val Pro Asp Pro Ser Asp Gly Leu Ser Ala Arg Asn Arg Gln Lys
                85                  90                  95
Arg Phe Val Leu Ser Gly Gly Arg Trp Glu Lys Thr Asp Leu Thr Tyr
            100                 105                 110
Arg Ile Leu Arg Phe Pro Trp Gln Leu Val Gln Glu Gln Val Arg Gln
        115                 120                 125
Thr Met Ala Glu Ala Leu Lys Val Trp Ser Asp Val Thr Pro Leu Thr
    130                 135                 140
Phe Thr Glu Val His Glu Gly Arg Ala Asp Ile Met Ile Asp Phe Ala
145                 150                 155                 160
Arg Tyr Trp His Gly Asp Asp Leu Pro Phe Asp Gly Pro Gly Gly Ile
                165                 170                 175
Leu Ala His Ala Phe Phe Pro Lys Thr His Arg Glu Gly Asp Val His
            180                 185                 190
Phe Asp Tyr Asp Glu Thr Trp Thr Ile Gly Asp Asp Gln Gly Thr Asp
        195                 200                 205
Leu Leu Gln Val Ala Ala His Glu Phe Gly His Val Leu Gly Leu Gln
    210                 215                 220
His Thr Thr Ala Ala Lys Ala Leu Met Ser Ala Phe Tyr Thr Phe Arg
225                 230                 235                 240
Tyr Pro Leu Ser Leu Ser Pro Asp Asp Cys Arg Gly Val Gln His Leu
                245                 250                 255
Tyr Gly Gln Pro Trp Pro Thr Val Thr Ser Arg Thr Pro Ala Leu Gly
            260                 265                 270
Pro Gln Ala Gly Ile Asp Thr Asn Glu Ile Ala Pro Leu Glu Pro Asp
        275                 280                 285
Ala Pro Pro Asp Ala Cys Glu Ala Ser Phe Asp Ala Val Ser Thr Ile
    290                 295                 300
Arg Gly Glu Leu Phe Phe Phe Lys Ala Gly Phe Val Trp Arg Leu Arg
305                 310                 315                 320
Gly Gly Gln Leu Gln Pro Gly Tyr Pro Ala Leu Ala Ser Arg His Trp
                325                 330                 335
Gln Gly Leu Pro Ser Pro Val Asp Ala Ala Phe Glu Asp Ala Gln Gly
            340                 345                 350
His Ile Trp Phe Phe Gln Gly Ala Gln Tyr Trp Val Tyr Asp Gly Glu
        355                 360                 365
Lys Pro Val Leu Gly Pro Ala Pro Leu Thr Glu Leu Gly Leu Val Arg
    370                 375                 380
Phe Pro Val His Ala Ala Leu Val Trp Gly Pro Glu Lys Asn Lys Ile
385                 390                 395                 400
Tyr Phe Phe Arg Gly Arg Asp Tyr Trp Arg Phe His Pro Ser Thr Arg
                405                 410                 415
Arg Val Asp Ser Pro Val Pro Arg Arg Ala Thr Asp Trp Arg Gly Val
            420                 425                 430
Pro Ser Glu Ile Asp Ala Ala Phe Gln Asp Ala Asp Gly Tyr Ala Tyr
        435                 440                 445
Phe Leu Arg Gly Arg Leu Tyr Trp Lys Phe Asp Pro Val Lys Val Lys
    450                 455                 460
Ala Leu Glu Gly Phe Pro Arg Leu Val Gly Pro Asp Phe Phe Gly Cys
465                 470                 475                 480
Ala Glu Pro Ala Asn Thr Phe Leu
                485
```

<210> 207
<211> 3074
<212> DNA
<213> Homo sapiens

<400> 207
ggcacgaggc tcaggcggtg gctggaggct gcgcatctgg ggctttaaac atacaaaggg 60
attgccagga cctgcggcgg cggcggcggc ggcgggggct ggggcgcggg ggccggacca 120
tgagccgctg agccgggcaa accccaggcc accgagccag cggaccctcg gagcgcagcc 180
ctgcgccgcg gagcaggctc caaccaggcg gcgacgcggc cacacgcacc gagccagcga 240
cccccgggcg acgcgcgggg ccagggagcg ctacgatgga ggcgctaatg gcccggggcg 300
cgctcacggg tcccctgagg gcgctctgtc tcctgggctg cctgctgagc cacgccgccg 360
ccgcgccgtc gcccatcatc aagttccccg gcgatgtcgc ccccaaaacg gacaaagagt 420
tggcagtgca atacctgaac accttctatg gctgccccaa ggagagctgc aacctgtttg 480
tgctgaagga cacactaaag aagatgcaga agttctttgg actgccccag acaggtgatc 540
ttgaccagaa taccatcgag accatgcgga agccacgctg cggcaaccca gatgtggcca 600
actacaactt cttccctcgc aagcccaagt gggacaagaa ccagatcaca tacaggatca 660
ttggctacac acctgatctg gacccagaga cagtggatga tgcctttgct cgtgccttcc 720
aagtctggag cgatgtgacc ccactgcggt tttctcgaat ccatgatgga gaggcagaca 780
tcatgatcaa ctttggccgc tgggagcatg gcgatggata cccctttgac ggtaaggacg 840
gactcctggc tcatgccttc gccccaggca ctggtgttgg gggagactcc cattttgatg 900
acgatgagct atggaccttg ggagaaggcc aagtggtccg tgtgaagtat ggcaacgccg 960
atggggagta ctgcaagttc cccttcttgt tcaatggcaa ggagtacaac agctgcactg 1020
ataccggccg cagcgatggc ttcctctggt gctccaccac ctacaacttt gagaaggatg 1080
gcaagtacgg cttctgtccc catgaagccc tgttcaccat gggcggcaac gctgaaggac 1140
agccctgcaa gtttccattc cgcttccagg gcacatccta tgacagctgc accactgagg 1200
gccgcacgga tggctaccgc tggtgcggca ccactgagga ctacgaccgc gacaagaagt 1260
atggcttctg ccctgagacc gccatgtcca ctgttggtgg gaactcagaa ggtgcccccт 1320
gtgtcttccc cttcactttc ctgggcaaca aatatgagag ctgcaccagc gccggccgca 1380
gtgacggaaa gatgtggtgt gcgaccacag ccaactacga tgacgaccgc aagtggggct 1440
tctgccctga ccaagggtac agcctgttcc tcgtggcagc ccacgagttt ggccacgcca 1500
tggggctgga gcactcccaa gaccctgggg ccctgatggc acccatttac acctacacca 1560
agaacttccg tctgtcccag gatgacatca agggcattca ggagctctat ggggcctctc 1620
ctgacattga ccttggcacc ggccccaccc ccacactggg ccctgtcact cctgagatct 1680
gcaaacagga cattgtattt gatggcatcg ctcagatccg tggtgagatc ttcttcttca 1740
aggaccggtt catttggcgg actgtgacgc cacgtgacaa gcccatgggg cccctgctgg 1800
tggccacatt ctggcctgag ctcccggaaa agattgatgc ggtatacgag gccccacagg 1860
aggagaaggc tgtgttcttt gcagggaatg aatactggat ctactcagcc agcaccctgg 1920
agcgagggta ccccaagcca ctgaccagcc tgggactgcc ccctgatgtc cagcgagtgg 1980
atgccgcctt taactggagc aaaaacaaga agacatacat ctttgctgga gacaaattct 2040
ggagatacaa tgaggtgaag aagaaaatgg atcctggctt tcccaagctc atcgcagatg 2100
cctggaatgc catccccgat aacctggatg ccgtcgtgga cctgcagggc ggcggtcaca 2160
gctacttctt caagggtgcc tattacctga agctggagaa ccaaagtctg aagagcgtga 2220
agtttggaag catcaaatcc gactggctag gctgctgagc tggccctggc tcccacaggc 2280
ccttcctctc cactgccttc gatacaccgg gcctggagaa ctagagaagg acccggaggg 2340
gcctggcagc cgtgccttca gctctacagc taatcagcat tctcactcct acctggtaat 2400
ttaagattcc agagagtggc tcctcccggt gcccaagaat agatgctgac tgtactcctc 2460
ccaggcgccc cttcccccтc caatcccacc aaccctcaga gccaccccta aagagatcct 2520
ttgatatttt caacgcagcc ctgctttggg ctgccctggt gctgccacac ttcaggctct 2580
tctcctttca caaccttctg tggctcacag aacccttgga gccaatggag actgtctcaa 2640
gagggcactg gtggcccgac agcctggcac agggcagtgg gacagggcat ggccaggtgg 2700
ccactccaga cccctggctt ttcactgctg gctgccttag aacctttctt acattagcag 2760
tttgctttgt atgcactttg tttttttctt tgggtcttgt ttttttttc cacttagaaa 2820
ttgcatttcc tgacagaagg actcaggttg tctgaagtca ctgcacagtg catctcagcc 2880
cacatagtga tggttcccct gttcactcta cttagcatgt ccctaccgag tctcttctcc 2940
actggatgga ggaaaaccaa gccgtggctt cccgctcagc cctccctgcc cctcccttca 3000
accattcccc atgggaaatg tcaacaagta tgaataaaga cacctactga gtgaaaaaaa 3060
aaaaaaaaaa aaaa 3074

<210> 208
<211> 660
<212> PRT
<213> Homo sapiens

<400> 208
Met Glu Ala Leu Met Ala Arg Gly Ala Leu Thr Gly Pro Leu Arg Ala

1 5 10 15
Leu Cys Leu Leu Gly Cys Leu Leu Ser His Ala Ala Ala Ala Pro Ser
20 25 30
Pro Ile Ile Lys Phe Pro Gly Asp Val Ala Pro Lys Thr Asp Lys Glu
35 40 45
Leu Ala Val Gln Tyr Leu Asn Thr Phe Tyr Gly Cys Pro Lys Glu Ser
50 55 60
Cys Asn Leu Phe Val Leu Lys Asp Thr Leu Lys Lys Met Gln Lys Phe
65 70 75 80
Phe Gly Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr Ile Glu Thr
85 90 95
Met Arg Lys Pro Arg Cys Gly Asn Pro Asp Val Ala Asn Tyr Asn Phe
100 105 110
Phe Pro Arg Lys Pro Lys Trp Asp Lys Asn Gln Ile Thr Tyr Arg Ile
115 120 125
Ile Gly Tyr Thr Pro Asp Leu Asp Pro Glu Thr Val Asp Asp Ala Phe
130 135 140
Ala Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro Leu Arg Phe Ser
145 150 155 160
Arg Ile His Asp Gly Glu Ala Asp Ile Met Ile Asn Phe Gly Arg Trp
165 170 175
Glu His Gly Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala
180 185 190
His Ala Phe Ala Pro Gly Thr Gly Val Gly Gly Asp Ser His Phe Asp
195 200 205
Asp Asp Glu Leu Trp Thr Leu Gly Glu Gly Gln Val Val Arg Val Lys
210 215 220
Tyr Gly Asn Ala Asp Gly Glu Tyr Cys Lys Phe Pro Phe Leu Phe Asn
225 230 235 240
Gly Lys Glu Tyr Asn Ser Cys Thr Asp Thr Gly Arg Ser Asp Gly Phe
245 250 255
Leu Trp Cys Ser Thr Thr Tyr Asn Phe Glu Lys Asp Gly Lys Tyr Gly
260 265 270
Phe Cys Pro His Glu Ala Leu Phe Thr Met Gly Gly Asn Ala Glu Gly
275 280 285
Gln Pro Cys Lys Phe Pro Phe Arg Phe Gln Gly Thr Ser Tyr Asp Ser
290 295 300
Cys Thr Thr Glu Gly Arg Thr Asp Gly Tyr Arg Trp Cys Gly Thr Thr
305 310 315 320
Glu Asp Tyr Asp Arg Asp Lys Lys Tyr Gly Phe Cys Pro Glu Thr Ala
325 330 335
Met Ser Thr Val Gly Gly Asn Ser Glu Gly Ala Pro Cys Val Phe Pro
340 345 350
Phe Thr Phe Leu Gly Asn Lys Tyr Glu Ser Cys Thr Ser Ala Gly Arg
355 360 365
Ser Asp Gly Lys Met Trp Cys Ala Thr Thr Ala Asn Tyr Asp Asp Asp
370 375 380
Arg Lys Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val
385 390 395 400
Ala Ala His Glu Phe Gly His Ala Met Gly Leu Glu His Ser Gln Asp
405 410 415
Pro Gly Ala Leu Met Ala Pro Ile Tyr Thr Tyr Thr Lys Asn Phe Arg
420 425 430
Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Glu Leu Tyr Gly Ala Ser
435 440 445
Pro Asp Ile Asp Leu Gly Thr Gly Pro Thr Pro Thr Leu Gly Pro Val
450 455 460
Thr Pro Glu Ile Cys Lys Gln Asp Ile Val Phe Asp Gly Ile Ala Gln
465 470 475 480
Ile Arg Gly Glu Ile Phe Phe Phe Lys Asp Arg Phe Ile Trp Arg Thr
485 490 495

```
Val Thr Pro Arg Asp Lys Pro Met Gly Pro Leu Leu Val Ala Thr Phe
            500                 505                 510
Trp Pro Glu Leu Pro Glu Lys Ile Asp Ala Val Tyr Glu Ala Pro Gln
        515                 520                 525
Glu Glu Lys Ala Val Phe Phe Ala Gly Asn Glu Tyr Trp Ile Tyr Ser
    530                 535                 540
Ala Ser Thr Leu Glu Arg Gly Tyr Pro Lys Pro Leu Thr Ser Leu Gly
545                 550                 555                 560
Leu Pro Pro Asp Val Gln Arg Val Asp Ala Ala Phe Asn Trp Ser Lys
            565                 570                 575
Asn Lys Lys Thr Tyr Ile Phe Ala Gly Asp Lys Phe Trp Arg Tyr Asn
            580                 585                 590
Glu Val Lys Lys Lys Met Asp Pro Gly Phe Pro Lys Leu Ile Ala Asp
        595                 600                 605
Ala Trp Asn Ala Ile Pro Asp Asn Leu Asp Ala Val Val Asp Leu Gln
    610                 615                 620
Gly Gly Gly His Ser Tyr Phe Phe Lys Gly Ala Tyr Tyr Leu Lys Leu
625                 630                 635                 640
Glu Asn Gln Ser Leu Lys Ser Val Lys Phe Gly Ser Ile Lys Ser Asp
            645                 650                 655
Trp Leu Gly Cys
            660
```

<210> 209
<211> 4160
<212> DNA
<213> Homo sapiens

<400> 209

```
ggggcggggc cggggcgggg cctgacttcc cgactgggag ccttagccgc ggggctgaga      60
ccaggcagcc tgcgttcgcc atgaagcgac ccaaggagcc gagcggctcc gacggggagt     120
ccgacggacc catcgacgtg ggccaagagg gccagctgag ccagatggcc aggccgctgt     180
ccaccccccag ctcttcgcag atgcaagcca ggaagaaacg cagagggatc atagagaaac   240
ggcgtcgaga ccgcatcaac agtagccttt ctgaattgcg acgcttggtc cccactgcct     300
ttgagaaaca gggctcttcc aagctggaga aagccgaggt cttgcagatg acggtggatc     360
acttgaaaat gctccatgcc actggtggga caggattctt tgatgcccga gccctggcag     420
ttgacttccg gagcattggt tttcgggagt gcctcactga ggtcatcagg tacctggggg     480
tccttgaagg gcccagcagc cgtgcagacc ccgtccggat tcgccttctc tcccacctca     540
acagctacgc agccgagatg gagccttcgc ccacgcccac tggccctttg gccttccctg     600
cctggccctg gtctttcttc catagctgtc cagggctgcc agccctgagc aaccagctcg     660
ccatcctggg aagagtgccc agccctgtcc tccccggtgt ctcctctcct gcttacccca     720
tcccagccct ccgaaccgct ccccttcgca gagccacagg catcatcctg ccagcccgga     780
ggaatgtgct gcccagtcga ggggcatctt ccacccggag ggcccgcccc ctagagaggc     840
cagcgacccc tgtgcctgtc gcccccagca gcagggctgc caggagcagc cacatcgctc     900
ccctcctgca gtcttcctcc ccaacacccc ctggtcctac agggtcggct gcttacgtgg     960
ctgttcccac ccccaactca tcctccccag ggccagctgg gaggccagcg ggagccatgc    1020
tctaccactc ctgggtctct gaaatcactg aaatcggggc tttctgagct gccccttcac    1080
caccccgccc caaggaataa ggaaggttct tttaccagga gcccaaaaaa gggcactgcc    1140
ttttctgctt tgcttcgtgg actggctcat atgtgaaggc acgttctcca gccatcagag    1200
gcccccctcct cctccaaccc atctctcctt ctcactgtta tcccagctta tccacccagc   1260
tctcctggag ctgttctggt ctcagaggct tggttccatt tctcacctga acagatgagt    1320
cctgggagag accctcagag atccgcccag accccctctcc tgccctctgc acaccagcag   1380
caggcatgaa ccttgggtct gggaaaaagc tttaacctgc agggcaccag gacccaaggc    1440
aggctgttcc ttggggcggt cagaccccag tcaggagcaa tgactgactg gctgcagcct    1500
tcccacgcca agaggctgga acatagtgtc tgcctcgctt cctggagata gtaactgagc    1560
aggggctaca aagaggtctc ctgggaaccc tgtctgcccc ttcccacctg tccttgggcc    1620
acaccatcac actgaaccac aggacagacc ctttctccac cacagccaag gcctggagac    1680
tgggggccca gcagagcctg ctcccaccct cctcccagca gcagacaccc accctctcac    1740
tgactaacag gtccctgcac acagctggcc tggtaaaccc agctgggagg tttctaggca    1800
gcagcaaaac tctgtgacag ggtgtcctca caccaggcct tggacagctc tcccagacag    1860
gagccagggt tgagcaatgg agagcccagc ccccacgtct tacagtcgcc atcctccagg    1920
```

cgtgtggtcc ctccccattg ggtgcacagt gcagaggggc cgtggcccca tgtgatggtg 1980
cgcagagagg aacctcttgg gattcagcac cagacgtctg tgctgcctgg tttgcatccg 2040
gctcacagag cccagactgc tggaacagcc aaggactgtc aggctggaca aaaataactg 2100
caaggagggg caagagaaag gatgattcga ggcaccttgg cccttcaagg tcatgcagtg 2160
ggtcgagcgc ctgagatcct gttcaccagg actccacaga gctggctctg ctcagaagcc 2220
atttcattcc ccggctccac cctaggccac tttttctaac agaggaaaca aatggtccag 2280
cagtcgttcc cagcagaaca gcggagcctg gactgacacc cagtgggacc agtgttgcca 2340
caccagttga taaaatgcag aaacccttct gtactcgttg gtaaatatct actcccccaa 2400
gtgactccag gtgcccccca ccgcctggca cttcccccag gactcctacg atctggttac 2460
tgcctggccg atccaaggct gtggagtccc agagccagca gttcactggt gctcattcca 2520
cactggttag atacttcagt tgtcacccct gggaagattc tcccacctcc tccctttgat 2580
ggaaccaccc tccccagagg ctgcattgag gagactccac agactgaaaa gtgagtttgc 2640
agaaaccttg gggaaaaggg ccctttcaaa gaagtggata agagggagga gatcattgag 2700
tgacccagaa agctcttttg aaaagacaga ctcctcaagg agagataaag aggaaagcac 2760
ctctttcatt ttttagtgtg agctaattcc atcagactgc tgtcctcctg gacccatctg 2820
agatgtgcag tagcaaggag aggggggatc atttagaga gtgggtcatt ggcagggagt 2880
gctccggagg gaggcagagg ggagactgtg gtagaaggaa gacagaactc acacatgctc 2940
ccaggattgg ggacagggac agaggaggta acagaaggca aaggccagtt tccccgttat 3000
catgaagggg cccactcagg acaggaacaa ggacaactcc tcctcctcct cctcctctcc 3060
tgctgctcct gggataccag gtcagtgatg tagtcttgca gtttggcaac ttcctagcct 3120
gagaatccct agtggggctg tgggaaacac atttccacgt tgcaagcatg caactccaaa 3180
gaatctgtga tgccactgaa atgagatggg aatgatccag ctctttcagc atcttggttg 3240
aacttgcttt cattgtccct gggatattgt ggaaggaaag gtgactgtgt gatctgattc 3300
tgtggtcaag gacttgcatc ttgtgtttct atccccaagc cttcctggtg tctccaactc 3360
ctaccccatt gcatgggttg ttgcggacat ccaataaaga ttttttttagt gcttctggaa 3420
acttccagta gattctactt ctaaactatc tctggagtcc atccacttct gtctgcaccc 3480
acagccatcc tggccaggcc acatcacctc cccagatca ctgccctggc ctcagaaagg 3540
tcttccctct tgctttgtca atcagttctc agtagcagca gagagaaatt gaaagctgca 3600
ggtcatatcg tatcatcttt agtttgaaaa cctcactctc ttaccctatt gttctaaagg 3660
tcttcttttg gtcccaacct cacttccagc ctcatttctt gccagtccca gacttgctcc 3720
ctgagcttct gccacctgcc cttccttcat ttcctcgaca ttccagcctt gttcccacct 3780
ccagcacttt gcatatgctg ttccctttgc caagaatgct cttcccctac cctgtgcatg 3840
gctgagttct gcagaccctc aggccttggc ttcaacgttg cctcgtccaa gaggccttcc 3900
tcgactactt tacttgtgga gttcctctat cacaaggcct ctgttctttc ccttcatgga 3960
gaatttgcca ctgcatatcc atttgtgtaa tttacttgtt ggttgactgt gcctcccact 4020
cgagtgtaag ctcatgaggc caggtgccat gcctggttca gtctccactc tgtacccagc 4080
attgagcaca gggcctggtc catagttggc gttcaataaa tacttgttga agaagtgaaa 4140
aaaaaaaaaa aaaaaaaaaa 4160

<210> 210
<211> 328
<212> PRT
<213> Homo sapiens

<400> 210

Met Lys Arg Pro Lys Glu Pro Ser Gly Ser Asp Gly Glu Ser Asp Gly
1   5   10   15
Pro Ile Asp Val Gly Gln Glu Gly Gln Leu Ser Gln Met Ala Arg Pro
            20   25   30
Leu Ser Thr Pro Ser Ser Ser Gln Met Gln Ala Arg Lys Lys Arg Arg
        35   40   45
Gly Ile Ile Glu Lys Arg Arg Arg Asp Arg Ile Asn Ser Ser Leu Ser
    50   55   60
Glu Leu Arg Arg Leu Val Pro Thr Ala Phe Glu Lys Gln Gly Ser Ser
65   70   75   80
Lys Leu Glu Lys Ala Glu Val Leu Gln Met Thr Val Asp His Leu Lys
                85   90   95
Met Leu His Ala Thr Gly Gly Thr Gly Phe Phe Asp Ala Arg Ala Leu
            100   105   110
Ala Val Asp Phe Arg Ser Ile Gly Phe Arg Glu Cys Leu Thr Glu Val
        115   120   125

Ile Arg Tyr Leu Gly Val Leu Glu Gly Pro Ser Ser Arg Ala Asp Pro
130 135 140
Val Arg Ile Arg Leu Leu Ser His Leu Asn Ser Tyr Ala Ala Glu Met
145 150 155 160
Glu Pro Ser Pro Thr Pro Thr Gly Pro Leu Ala Phe Pro Ala Trp Pro
165 170 175
Trp Ser Phe Phe His Ser Cys Pro Gly Leu Pro Ala Leu Ser Asn Gln
180 185 190
Leu Ala Ile Leu Gly Arg Val Pro Ser Pro Val Leu Pro Gly Val Ser
195 200 205
Ser Pro Ala Tyr Pro Ile Pro Ala Leu Arg Thr Ala Pro Leu Arg Arg
210 215 220
Ala Thr Gly Ile Ile Leu Pro Ala Arg Arg Asn Val Leu Pro Ser Arg
225 230 235 240
Gly Ala Ser Ser Thr Arg Arg Ala Arg Pro Leu Glu Arg Pro Ala Thr
245 250 255
Pro Val Pro Val Ala Pro Ser Ser Arg Ala Ala Arg Ser Ser His Ile
260 265 270
Ala Pro Leu Leu Gln Ser Ser Ser Pro Thr Pro Pro Gly Pro Thr Gly
275 280 285
Ser Ala Ala Tyr Val Ala Val Pro Thr Pro Asn Ser Ser Ser Pro Gly
290 295 300
Pro Ala Gly Arg Pro Ala Gly Ala Met Leu Tyr His Ser Trp Val Ser
305 310 315 320
Glu Ile Thr Glu Ile Gly Ala Phe
325

<210> 211
<211> 5680
<212> DNA
<213> Homo sapiens

<400> 211
gggcgatggg ttgatgggcg ccgggggacg caggatgcgg ggggcgcccg cgcgcctgct 60
gctgccgctg ctgccgtggc tcctgctgct cctggcgccc gaggctcggg gcgcgcccgg 120
ctgcccgcta tccatccgca gctgcaagtg ctcgggggag cggcccaagg ggctgagcgg 180
cggcgtccct ggcccggctc ggcggagggt ggtgtgcagc ggcggggacc tcccggagcc 240
tcccgagccc ggccttctgc ctaacggcac cgttaccctg ctcttgagca ataacaagat 300
cacggggctc cgcaatggct ccttcctggg actgtcactg ctggagaagc tggacctgag 360
gaacaacatc atcagcacag tgcagccggg cgccttcctg ggcctggggg agctgaagcg 420
tttagatctc tccaacaacc ggattggctg tctcacctcc gagaccttcc agggcctccc 480
caggcttctc cgactaaaca tatctggaaa catcttctcc agtctgcaac ctggggtctt 540
tgatgagctg ccagccctta aggttgtgga cttgggcacc gagttcctga cctgtgactg 600
ccacctgcgc tggctgctgc cctgggccca gaatcgctcc ctgcagctgt cggaacacac 660
gctctgtgct taccccagtg ccctgcatgc tcaggccctg ggcagcctcc aggaggccca 720
gctctgctgc gaggggggccc tggagctgca cacacaccac ctcatcccgt ccctacgcca 780
agtggtgttc caggggggatc ggctgccctt ccagtgctct gccagctacc tgggcaacga 840
cacccgcatc cgctggtacc acaaccgagc ccctgtggag ggtgatgagc aggcgggcat 900
cctcctggcc gagagcctca tccacgactg caccttcatc accagtgagc tgacgctgtc 960
tcacatcggc gtgtgggcct caggcgagtg ggagtgcacc gtgtccatgg cccaaggcaa 1020
cgccagcaag aaggtggaga tcgtggtgct ggagacctct gcctcctact gccccgccga 1080
gcgtgttgcc aacaaccgcg gggacttcag gtggccccga actctggctg gcatcacagc 1140
ctaccagtcc tgcctgcagt atcccttcac ctcagtgccc ctgggcgggg gtgccccggg 1200
cacccgagcc tcccgccggt gtgaccgtgc cggccgctgg gagccagggg actactccca 1260
ctgtctctac accaacgaca tcaccagggt gctgtacacc ttcgtgctga tgcccatcaa 1320
tgcctccaat gcgctgaccc tggctcacca gctgcgcgtg tacacagccg aggccgctag 1380
cttttcagac atgatggatg tagtctatgt ggctcagatg atccagaaat ttttgggtta 1440
tgtcgaccag atcaaagagc tggtagaggt gatggtggac atggccagca acctgatgct 1500
ggtggacgag cacctgctgt ggctggccca gcgcgaggac aaggcctgca gccgcatcgt 1560
gggtgccctg gagcgcattg ggggggccgc cctcagcccc catgcccagc acatctcagt 1620
gaatgcgagg aacgtggcat tggaggccta cctcatcaag ccgcacagct acgtgggcct 1680

gacctgcaca gccttccaga ggagggaggg aggggtgccg ggcacacggc caggaagccc 1740
tggccagaac cccccacctg agcccgagcc cccagctgac cagcagctcc gcttccgctg 1800
caccaccggg aggcccaatg tttctctgtc gtccttccac atcaagaaca gcgtggccct 1860
ggcctccatc cagctgcccc cgagtctatt ctcatccctt ccggctgccc tggctccccc 1920
ggtgccccca gactgcaccc tgcaactgct cgtcttccga aatggccgcc tcttccacag 1980
ccacagcaac acctcccgcc ctggagctgc tgggcctggc aagaggcgtg gcgtggccac 2040
ccccgtcatc ttcgcaggaa ccagtggctg tggcgtggga aacctgacag agccagtggc 2100
cgtttcgctg cggcactggg ctgagggagc cgaacctgtg gccgcttggt ggagccagga 2160
ggggcccggg gaggctgggg gctggacctc ggagggctgc cagctccgct ccagccagcc 2220
caatgtcagc gccctgcact gccagcactt gggcaatgtg gccgtgctca tggagctgag 2280
cgcctttccc agggaggtgg ggggcgccgg ggcagggctg caccccgtgg tataccccctg 2340
cacggccttg ctgctgctct gcctcttcgc caccatcatc acctacatcc tcaaccacag 2400
ctccatccgt gtgtcccgga aaggctggca catgctgctg aacttgtgct tccacatagc 2460
catgacctct gctgtctttg cgggggggcat cacactcacc aactaccaga tggtctgcca 2520
ggcggtgggc atcaccctgc actactcctc cctatccacg ctgctctgga tgggcgtgaa 2580
ggcgcgagtg ctccataagg agctcacctg gagggcaccc cctccgcaag aaggggaccc 2640
cgctctgcct actcccagtc ctatgctccg gttctatttg atcgctggag ggattccact 2700
cattatctgt ggcatcacag ctgcagtcaa catccacaac taccgggacc acagccccta 2760
ctgctggctg gtgtggcgtc caagccttgg cgccttctac atccctgtgg ctttgattct 2820
gctcatcacc tggatctatt tcctgtgcgc cgggctacgc ttacggggtc ctctggcaca 2880
gaaccccaag gcgggcaaca gcagggcctc cctggaggca ggggaggagc tgaggggttc 2940
caccaggctc aggggcagcg gcccccctcct gagtgactca ggttcccttc ttgctactgg 3000
gagcgcgcga gtggggacgc ccgggccccc ggaggatggt gacagcctct attctccggg 3060
agtccagcta ggggcgctgg tgaccacgca cttcctgtac ttggccatgt gggcctgcgg 3120
ggctctggca gtgtcccagc gctggctgcc ccgggtggtg tgcagctgct tgtacggggt 3180
ggcagcctcc gccctgggcc tcttcgtctt cactcaccac tgtgccaggc ggagggacgt 3240
gagagcctcg tggcgcgcct gctgcccccc tgcctctccc gcggcccccc atgccccgcc 3300
ccgggccctg cccgccgccg cagaggacgg ttccccggtg ttcggggagg ggcccccctc 3360
cctcaagtcc tccccaagcg gcagcagcgg ccatccgctg gctctgggcc cctgcaagct 3420
caccaacctg cagctggccc agagtcaggt gtgcgaggcg gggcggcgg ccggcgggga 3480
aggagagccg gagccggcgg gcacccgggg aaacctcgcc caccgccacc ccaacaacgt 3540
gcaccacggg cgtcgggcgc acaagagccg ggccaaggga caccgcgcgg gggaggcctg 3600
cggcaagaac cggctcaagg ccctgcgcgg gggcgcggcg ggggcgctgg agctgctgtc 3660
cagcgagagc ggtagtctgc acaacagccc caccgacagc tacctgggca gcagccgcaa 3720
cagcccgggc gccggcctgc agctggaagg cgagcccatg ctcacgccgt ccgagggcag 3780
cgacaccagc gccgcgccgc tttctgaggc gggccgggca ggccagcgcc gcagcgccag 3840
ccgcgacagt ctcaagggcg gcggcgcgct ggagaaggag agccatcgcc gctcgtaccc 3900
gctcaacgcc gccagcctaa acggcgcccc caaggggggc aagtacgacg acgtcaccct 3960
gatgggcgcg gaggtagcca gcggcggctg catgaagacc ggactctgga agagcgaaac 4020
taccgtctaa ggtggggcgg gcgacgcggt agacgggctg gccacgcggc tcgttccccc 4080
gctcctcggg gccctccaag gtgtctccgt agtcagcagg ttggaggcag aggagccgat 4140
ggctggagga agcccacagg cggatgttcc ccacttgcct agagggcatc cctctggggt 4200
agcgacagac aatcccagaa acacgcataa tacatttccg tccagcccgg ggcagtctga 4260
ctgtcggtgc cctcccagga acggggaagg cctccgtctg tgtgaaaggg cacagcacat 4320
cccaggtgca ccctccccaa gtactcccac cccgcctact gtccatgcgg cctcactggg 4380
ggccatcagc ctcaccagca aagcagagat gagagcgtgg gaactgtgtt ctttcctccc 4440
tgccctctac tgatttcagc ccagcccctg cctagatcct aggtcccttt tcctcccgag 4500
tttggctggc acgagagcta gcccagcaca tgaagcaggt gatgttaagt cacaaggtgc 4560
tgcttttcag atccactatg caagagggga gggtggggcc acgtgaaagg cagctctaga 4620
catcaaccag tcctggggga ggggagtggg aaccgggcac aactaggaac aatgccacca 4680
ttcccacagg agtggtactt aaaccagaca gcagggttca gaggtggcac accgggacaa 4740
agctgaggcc ctgcacctca acagctgact gccaggtgcc tgtgggtgaa ctgaggggag 4800
tagagggaga gggcaggtgg aactggggca gaatctagtc atgccctaaa gctagtcctg 4860
taaacaatgg tgccccagaa agctgcaggt ggtgtttgga gaagcagtta cttttcagtt 4920
acaagaccca tctccctagt ctcagcctta caacaccacg ggactaagga agagcacttc 4980
cttgcctccg taaggccaga ggaagaacca tcccaatcat ttgatctcca gctccacagt 5040
agagagaaac ctacaaaatg tcaaaccagc ttcccgactc ccaggagctc aagccaagcc 5100
cagaggcagt ggctggggtc cctgcaggtc atgaggggcc tatgccttta ctcctttttaa 5160
acaccagcac ccgtcttttc cccaacctaa aaccaaccac cagcatttca ctacaggacc 5220
aaatggaaac cgagggaacc ctgggtcttg ggaagaacaa caggaaacca aggtctgacc 5280
tagggttccc tcccagtctt cacatcactc tggcctcatc accaaggtga cagaggacac 5340

aggggagggg gaaaacccac acacactcct tggaatgggt cctgttattt atgcttgctg 5400
cacagacata ttagaagaaa aaaaaaagct ttgtattatt cttccacata tgctggctgc 5460
tgtttacaca ccctgccaat gccttagcac tggagagctt tttgcaatat gctggggaaa 5520
ggggagggag ggaatgaaag tgccaaagaa aacatgtttt taagaactcg ggttttatac 5580
aatagaatgt tttctagcag atgcctcttg ttttaatata ttaaaatttt gcaaagccct 5640
ttgagctaca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5680

<210> 212
<211> 1331
<212> PRT
<213> Homo sapiens

<400> 212
Met Arg Gly Ala Pro Ala Arg Leu Leu Leu Pro Leu Leu Pro Trp Leu
1 5 10 15
Leu Leu Leu Leu Ala Pro Glu Ala Arg Gly Ala Pro Gly Cys Pro Leu
20 25 30
Ser Ile Arg Ser Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser
35 40 45
Gly Gly Val Pro Gly Pro Ala Arg Arg Arg Val Val Cys Ser Gly Gly
50 55 60
Asp Leu Pro Glu Pro Pro Glu Pro Gly Leu Leu Pro Asn Gly Thr Val
65 70 75 80
Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser
85 90 95
Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Asn Asn Ile
100 105 110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys
115 120 125
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr
130 135 140
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile
145 150 155 160
Phe Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys
165 170 175
Val Val Asp Leu Gly Thr Glu Phe Leu Thr Cys Asp Cys His Leu Arg
180 185 190
Trp Leu Leu Pro Trp Ala Gln Asn Arg Ser Leu Gln Leu Ser Glu His
195 200 205
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala Gln Ala Leu Gly Ser
210 215 220
Leu Gln Glu Ala Gln Leu Cys Cys Glu Gly Ala Leu Glu Leu His Thr
225 230 235 240
His His Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg
245 250 255
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile
260 265 270
Arg Trp Tyr His Asn Arg Ala Pro Val Glu Gly Asp Glu Gln Ala Gly
275 280 285
Ile Leu Leu Ala Glu Ser Leu Ile His Asp Cys Thr Phe Ile Thr Ser
290 295 300
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu
305 310 315 320
Cys Thr Val Ser Met Ala Gln Gly Asn Ala Ser Lys Lys Val Glu Ile
325 330 335
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Ala
340 345 350
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr
355 360 365

Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Gly
370 375 380
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly
385 390 395 400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
405 410 415
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
420 425 430
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
435 440 445
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
450 455 460
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
465 470 475 480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
485 490 495
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Arg Ile Val Gly Ala Leu
500 505 510
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
515 520 525
Val Asn Ala Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
530 535 540
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Gly Gly
545 550 555 560
Val Pro Gly Thr Arg Pro Gly Ser Pro Gly Gln Asn Pro Pro Pro Glu
565 570 575
Pro Glu Pro Pro Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
580 585 590
Arg Pro Asn Val Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
595 600 605
Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Ser Leu Pro Ala
610 615 620
Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
625 630 635 640
Phe Arg Asn Gly Arg Leu Phe His Ser His Ser Asn Thr Ser Arg Pro
645 650 655
Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val Ile
660 665 670
Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro Val
675 680 685
Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Glu Pro Val Ala Ala
690 695 700
Trp Trp Ser Gln Glu Gly Pro Gly Glu Ala Gly Gly Trp Thr Ser Glu
705 710 715 720
Gly Cys Gln Leu Arg Ser Ser Gln Pro Asn Val Ser Ala Leu His Cys
725 730 735
Gln His Leu Gly Asn Val Ala Val Leu Met Glu Leu Ser Ala Phe Pro
740 745 750
Arg Glu Val Gly Gly Ala Gly Ala Gly Leu His Pro Val Val Tyr Pro
755 760 765
Cys Thr Ala Leu Leu Leu Leu Cys Leu Phe Ala Thr Ile Ile Thr Tyr
770 775 780
Ile Leu Asn His Ser Ser Ile Arg Val Ser Arg Lys Gly Trp His Met
785 790 795 800
Leu Leu Asn Leu Cys Phe His Ile Ala Met Thr Ser Ala Val Phe Ala
805 810 815
Gly Gly Ile Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly
820 825 830
Ile Thr Leu His Tyr Ser Ser Leu Ser Thr Leu Leu Trp Met Gly Val
835 840 845
Lys Ala Arg Val Leu His Lys Glu Leu Thr Trp Arg Ala Pro Pro Pro

850 855 860
Gln Glu Gly Asp Pro Ala Leu Pro Thr Pro Ser Pro Met Leu Arg Phe
865 870 875 880
Tyr Leu Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala
885 890 895
Ala Val Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu
900 905 910
Val Trp Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile
915 920 925
Leu Leu Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu Arg Leu Arg
930 935 940
Gly Pro Leu Ala Gln Asn Pro Lys Ala Gly Asn Ser Arg Ala Ser Leu
945 950 955 960
Glu Ala Gly Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Gly Ser Gly
965 970 975
Pro Leu Leu Ser Asp Ser Gly Ser Leu Leu Ala Thr Gly Ser Ala Arg
980 985 990
Val Gly Thr Pro Gly Pro Pro Glu Asp Gly Asp Ser Leu Tyr Ser Pro
995 1000 1005
Gly Val Gln Leu Gly Ala Leu Val Thr Thr His Phe Leu Tyr Leu Ala
1010 1015 1020
Met Trp Ala Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg
1025 1030 1035 1040
Val Val Cys Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu
1045 1050 1055
Phe Val Phe Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser
1060 1065 1070
Trp Arg Ala Cys Cys Pro Pro Ala Ser Pro Ala Ala Pro His Ala Pro
1075 1080 1085
Pro Arg Ala Leu Pro Ala Ala Ala Glu Asp Gly Ser Pro Val Phe Gly
1090 1095 1100
Glu Gly Pro Pro Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly His
1105 1110 1115 1120
Pro Leu Ala Leu Gly Pro Cys Lys Leu Thr Asn Leu Gln Leu Ala Gln
1125 1130 1135
Ser Gln Val Cys Glu Ala Gly Ala Ala Ala Gly Gly Glu Gly Glu Pro
1140 1145 1150
Glu Pro Ala Gly Thr Arg Gly Asn Leu Ala His Arg His Pro Asn Asn
1155 1160 1165
Val His His Gly Arg Arg Ala His Lys Ser Arg Ala Lys Gly His Arg
1170 1175 1180
Ala Gly Glu Ala Cys Gly Lys Asn Arg Leu Lys Ala Leu Arg Gly Gly
1185 1190 1195 1200
Ala Ala Gly Ala Leu Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His
1205 1210 1215
Asn Ser Pro Thr Asp Ser Tyr Leu Gly Ser Ser Arg Asn Ser Pro Gly
1220 1225 1230
Ala Gly Leu Gln Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly
1235 1240 1245
Ser Asp Thr Ser Ala Ala Pro Leu Ser Glu Ala Gly Arg Ala Gly Gln
1250 1255 1260
Arg Arg Ser Ala Ser Arg Asp Ser Leu Lys Gly Gly Gly Ala Leu Glu
1265 1270 1275 1280
Lys Glu Ser His Arg Arg Ser Tyr Pro Leu Asn Ala Ala Ser Leu Asn
1285 1290 1295
Gly Ala Pro Lys Gly Gly Lys Tyr Asp Asp Val Thr Leu Met Gly Ala
1300 1305 1310
Glu Val Ala Ser Gly Gly Cys Met Lys Thr Gly Leu Trp Lys Ser Glu
1315 1320 1325
Thr Thr Val
1330

<210> 213
<211> 5086
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(5086)
<223> n = A,T,C or G

<400> 213
agcaccacgg cagcaggagg tttcggncta agttggaggt actggnccac gactgcatgc 60
ccgcgcccgc caggtgatac ctccgccggt gacccagggg ctctgcgaca caaggagtct 120
gcatgtctaa gtgctagaca tgctcagctt tgtggatacg cggactttgt tgctgcttgc 180
agtaacctta tgcctagcaa catgccaatc tttacaagag gaaactgtaa gaaagggccc 240
agccggagat agaggaccac gtggagaaag gggtccacca ggccccccag gcagagatgg 300
tgaagatggt cccacaggcc ctcctggtcc acctggtcct cctggccccc ctggtctcgg 360
tgggaacttt gctgctcagt atgatggaaa aggagttgga cttggccctg gaccaatggg 420
cttaatggga cctagaggcc cacctggtgc agctggagcc ccaggccctc aaggtttcca 480
aggacctgct ggtgagcctg gtgaacctgg tcaaactggt cctgcaggtg ctcgtggtcc 540
agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaacccg gacgacctgg 600
tgagagagga gttgttggac cacagggtgc tcgtggtttc cctggaactc ctggacttcc 660
tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaagggac agcccggtgc 720
tcctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg 780
agcccgtggg cttcctggtg agagaggacg tgttggtgcc cctggcccag ctggtgcccg 840
tggcagtgat ggaagtgtgg gtcccgtggg tcctgctggt cccattgggt ctgctggccc 900
tccaggcttc ccaggtgccc ctggccccaa gggtgaaatt ggagctgttg gtaacgctgg 960
tcctgctggt cccgccggtc cccgtggtga agtgggtctt ccaggcctct ccggccccgt 1020
tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccaagggtg ctgctggcct 1080
tcccggcgtt gctggggctc ccggcctccc tggaccccgc ggtattcctg gccctgttgg 1140
tgctgccggt gctactggtg ccagaggact tgttggtgag cctggtccag ctggctccaa 1200
aggagagagc ggtaacaagg gtgagcccgg ctctgctggg ccccaaggtc ctcctggtcc 1260
cagtggtgaa gaaggaaaga gaggccctaa tggggaagct ggatctgccg gccctccagg 1320
acctcctggg ctgagaggta gtcctggttc tcgtggtctt cctggagctg atggcagagc 1380
tggcgtcatg ggccctcctg gtagtcgtgg tgcaagtggc cctgctggag tccgaggacc 1440
taatggagat gctggtcgcc ctggggagcc tggtctcatg ggacccagag gtcttcctgg 1500
ttcccctgga aatatcggcc ccgctggaaa agaaggtcct gtcggcctcc ctggcatcga 1560
cggcaggcct ggcccaattg gcccagctgg agcaagagga gagcctggca acattggatt 1620
ccctggaccc aaaggcccca ctggtgatcc tggcaaaaac ggtgataaag gtcatgctgg 1680
tcttgctggt gctcggggtg ctccaggtcc tgatggaaac aatggtgctc agggacctcc 1740
tggaccacag ggtgttcaag gtggaaaagg tgaacagggt cccgctggtc ctccaggctt 1800
ccagggtctg cctggcccct caggtcccgc tggtgaagtt ggcaaaccag gagaaagggg 1860
tctccatggt gagtttggtc tccctggtcc tgctggtcca agaggggaac gcggtccccc 1920
aggtgagagt ggtgctgccg gtcctactgg tcctattgga agccgaggtc cttctggacc 1980
cccagggcct gatggaaaca agggtgaacc tggtgtggtt ggtgctgtgg gcactgctgg 2040
tccatctggt cctagtggac tcccaggaga gaggggtgct gctggcatac ctggaggcaa 2100
gggagaaaag ggtgaacctg gtctcagagg tgaaattggt aaccctggca gagatggtgc 2160
tcgtggtgct catggtgctg taggtgcccc tggtcctgct ggagccacag gtgaccgggg 2220
cgaagctggg gctgctggtc ctgctggtcc tgctggtcct cggggaagcc ctggtgaacg 2280
tggcgaggtc ggtcctgctg gccccaacgg atttgctggt ccggctggtg ctgctggtca 2340
accgggtgct aaaggagaaa gaggagccaa agggcctaag ggtgaaaacg gtgttgttgg 2400
tcccacaggc cccgttggag ctgctggccc agctggtcca aatggtcccc ccggtcctgc 2460
tggaagtcgt ggtgatggag gcccccctgg tatgactggt ttccctggtg ctgctggacg 2520
gactggtccc ccaggaccct ctggtatttc tggccctcct ggtccccctg gtcctgctgg 2580
gaaagaaggg cttcgtggtc ctcgtggtga ccaaggtcca gttggccgaa ctggagaagt 2640
aggtgcagtt ggtccccctg gcttcgctgg tgagaagggt ccctctggag aggctggtac 2700
tgctggacct cctggcactc caggtcctca gggtcttctt ggtgctcctg gtattctggg 2760
tctccctggc tcgagaggtg aacgtggtct acctggtgtt gctggtgctg tgggtgaacc 2820
tggtcctctt ggcattgccg gccctcctgg ggcccgtggt cctcctggtg ctgtgggtag 2880
tcctggagtc aacggtgctc ctggtgaagc tggtcgtgat ggcaaccctg ggaacgatgg 2940

```
tcccccaggt cgcgatggtc aacccggaca caagggagag cgcggttacc ctggcaatat   3000
tggtcccgtt ggtgctgcag gtgcacctgg tcctcatggc cccgtgggtc ctgctggcaa   3060
acatggaaac cgtggtgaaa ctggtccttc tggtcctgtt ggtcctgctg gtgctgttgg   3120
cccaagaggt cctagtggcc cacaaggcat tcgtggcgat aagggagagc ccggtgaaaa   3180
ggggcccaga ggtcttcctg gcttaaaggg acacaatgga ttgcaaggtc tgcctggtat   3240
cgctggtcac catggtgatc aaggtgctcc tggctccgtg ggtcctgctg gtcctagggg   3300
ccctgctggt ccttctggcc ctgctggaaa agatggtcgc actggacatc ctggtacggt   3360
tggacctgct ggcattcgag gccctcaggg tcaccaaggc cctgctggcc cccctggtcc   3420
ccctggccct cctggacctc caggtgtaag cggtggtggt tatgactttg gttacgatgg   3480
agacttctac agggctgacc agcctcgctc agcaccttct ctcagaccca aggactatga   3540
agttgatgct actctgaagt ctctcaacaa ccagattgag acccttctta ctcctgaagg   3600
ctctagaaag aacccagctc gcacatgccg tgacttgaga ctcagccacc cagagtggag   3660
cagtggttac tactggattg accctaacca aggatgcact atggatgcta tcaaagtata   3720
ctgtgatttc tctactggcg aaacctgtat ccgggcccaa cctgaaaaca tcccagccaa   3780
gaactggtat aggagctcca aggacaagaa acacgtctgg ctaggagaaa ctatcaatgc   3840
tggcagccag tttgaatata atgtagaagg agtgacttcc aaggaaatgg ctacccaact   3900
tgccttcatg cgcctgctgg ccaactatgc ctctcagaac atcacctacc actgcaagaa   3960
cagcattgca tacatggatg aggagactgg caacctgaaa aaggctgtca ttctacaggg   4020
ctctaatgat gttgaacttg ttgctgaggg caacagcagg ttcacttaca ctgttcttgt   4080
agatggctgc tctaaaaaga caaatgaatg gggaaagaca atcattgaat acaaaacaaa   4140
taagccatca cgcctgccct tccttgatat tgcacctttg gacatcggtg gtgctgacca   4200
tgaattcttt gtggacattg gcccagtctg tttcaaataa atgaactcaa tctaaattaa   4260
aaaagaaaga aatttgaaaa aactttctct ttgccatttc ttcttcttct tttttaactg   4320
aaagctgaat ccttccattt cttctgcaca tctacttgct taaattgtgg gcaaaagaga   4380
aaaagaagga ttgatcagag cattgtgcaa tacagtttca ttaactcctt cccccgctcc   4440
cccaaaaatt tgaatttttt tttcaacact cttacacctg ttatggaaaa tgtcaacctt   4500
tgtaagaaaa ccaaaataaa aattgaaaaa taaaaaccat aaacatttgc accacttgtg   4560
gcttttgaat atcttccaca gagggaagtt taaaacccaa acttccaaag gtttaaacta   4620
cctcaaaaca ctttcccatg agtgtgatcc acattgttag gtgctgacct agacagagat   4680
gaactgaggt ccttgttttg ttttgttcat aatacaaagg tgctaattaa tagtatttca   4740
gatacttgaa gaatgttgat ggtgctagaa gaatttgaga agaaatactc ctgtattgag   4800
ttgtatcgtg tggtgtattt tttaaaaaat ttgatttagc attcatattt tccatcttat   4860
tcccaattaa aagtatgcag attatttgcc caaagttgtc ctcttcttca gattcagcat   4920
ttgttctttg ccagtctcat tttcatcttc ttccatggtt ccacagaagc tttgtttctt   4980
gggcaagcag aaaaattaaa ttgtacctat tttgtatatg tgagatgttt aaataaattg   5040
tgaaaaaaat gaaataaagc atgtttggtt ttccaaaaga acatat                  5086
```

<210> 214
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 214

```
Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr
1               5                   10                  15
Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys
            20                  25                  30
Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly
        35                  40                  45
Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro
    50                  55                  60
Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln
65                  70                  75                  80
Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
                85                  90                  95
Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly
            100                 105                 110
Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
        115                 120                 125
```

Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp
130 135 140
Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly
145 150 155 160
Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
165 170 175
Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
180 185 190
Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly
195 200 205
Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg
210 215 220
Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val
225 230 235 240
Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly
245 250 255
Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn
260 265 270
Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
275 280 285
Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
290 295 300
Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
305 310 315 320
Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
325 330 335
Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly
340 345 350
Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro
355 360 365
Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
370 375 380
Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
385 390 395 400
Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val
405 410 415
Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
420 425 430
Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
435 440 445
Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
450 455 460
Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
465 470 475 480
Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
485 490 495
Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
500 505 510
Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
515 520 525
Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
530 535 540
Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
545 550 555 560
Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
565 570 575
Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
580 585 590
Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
595 600 605
Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro

610 615 620
Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
625 630 635 640
Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
645 650 655
Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
660 665 670
Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
675 680 685
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
690 695 700
Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
705 710 715 720
Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
725 730 735
Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
740 745 750
Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
755 760 765
Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
770 775 780
Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
785 790 795 800
Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
805 810 815
Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
820 825 830
Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
835 840 845
Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln
850 855 860
Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
865 870 875 880
Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
885 890 895
Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
900 905 910
Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly
915 920 925
Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His
930 935 940
Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
945 950 955 960
Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
965 970 975
Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala
980 985 990
Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys
995 1000 1005
Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly
1010 1015 1020
His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp
1025 1030 1035 1040
Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg Gly Pro Ala
1045 1050 1055
Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr Gly His Pro Gly
1060 1065 1070
Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln Gly His Gln Gly Pro
1075 1080 1085
Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser
1090 1095 1100

Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp Phe Tyr Arg Ala Asp
1105 1110 1115 1120
Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys Asp Tyr Glu Val Asp
1125 1130 1135
Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu Thr Leu Leu Thr Pro
1140 1145 1150
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Arg Leu
1155 1160 1165
Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp Ile Asp Pro Asn Gln
1170 1175 1180
Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys Asp Phe Ser Thr Gly
1185 1190 1195 1200
Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile Pro Ala Lys Asn Trp
1205 1210 1215
Tyr Arg Ser Ser Lys Asp Lys Lys His Val Trp Leu Gly Glu Thr Ile
1220 1225 1230
Asn Ala Gly Ser Gln Phe Glu Tyr Asn Val Glu Gly Val Thr Ser Lys
1235 1240 1245
Glu Met Ala Thr Gln Leu Ala Phe Met Arg Leu Leu Ala Asn Tyr Ala
1250 1255 1260
Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp
1265 1270 1275 1280
Glu Glu Thr Gly Asn Leu Lys Lys Ala Val Ile Leu Gln Gly Ser Asn
1285 1290 1295
Asp Val Glu Leu Val Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Val
1300 1305 1310
Leu Val Asp Gly Cys Ser Lys Lys Thr Asn Glu Trp Gly Lys Thr Ile
1315 1320 1325
Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg Leu Pro Phe Leu Asp Ile
1330 1335 1340
Ala Pro Leu Asp Ile Gly Gly Ala Asp His Glu Phe Phe Val Asp Ile
1345 1350 1355 1360
Gly Pro Val Cys Phe Lys
1365

<210> 215
<211> 4898
<212> DNA
<213> Homo sapiens

<400> 215
gaattccggc tgccaggggc gtccggttac atccccgcct tcctctgtcc tggccgcggg 60
accgggtttg cgggaccgca gttcgggaac atgttggcct cgagcagccg gatccgggct 120
gcgtggacgc gggcgctgct gctgccgctg ctgctggcgg ggcctgtggg ctgcctgagc 180
cgccaggagc tctttccctt cggccccgga cagggggacc tggagctgga ggacggggat 240
gacttcgtct ctcctgccct ggagctgagt ggggcgctcc gcttctacga cagatccgac 300
atcgacgcag tctacgtcac cacaaatggc atcattgcta cgagtgaacc cccggccaaa 360
gaatcccatc ccgggctctt cccaccaaca ttcggtgcag tcgccccttt cctggcggac 420
ttggacacga ccgatggcct ggggaaggtt tattatcgag aagacttatc ccccctccatc 480
actcagcgag cagcagagtg tgtccacaga gggttcccgg agatctcttt ccagcctagt 540
agcgcggtgg ttgtcacttg ggaatccgtg gccccctacc aagggcccag cagggaccca 600
gaccagaaag gcaagagaaa cacgttccag gctgttctag cctcctctga ttccagctcc 660
tatgccattt tcctttatcc tgaggatggt ctgcagttcc atacgacatt ctcaaagaag 720
gaaaacaacc aagttcctgc cgtggttgca ttcagtcaag gttcagtggg attcttatgg 780
aagagcaacg gagcttataa catatttgct aatgacaggg aatcaattga aaatttggcc 840
aagagtagta actctgggca gcagggtgtc tgggtgtttg agattgggag tccagccacc 900
accaatggcg tggtgcctgc agacgtgatc ctcggaactg aagatggggc agagtatgat 960
gatgaggatg aagattatga cctggcgacc actcgtctgg gcctggagga tgtgggcacc 1020
acgcccttct cctacaaggc tctgagaagg ggaggtgctg acacatacag tgtgcccagc 1080
gtcctctccc cgcgccgggc agctaccgaa aggcccccttg gacctcccac agagagaacc 1140
aggtctttcc agttggcagt ggagactttt caccagcagc accctcaggt catagatgtg 1200

gatgaagttg aggaaacagg agttgttttc agctataaca cggattcccg ccagacgtgt 1260
gctaacaaca gacaccagtg ctcggtgcac gcagagtgca gggactacgc cacgggcttc 1320
tgctgcagct gtgtcgctgg ctatacgggc aatggcaggc aatgtgttgc agaaggttcc 1380
ccccagcgag tcaatggcaa ggtgaaagga aggatctttg tggggagcag ccaggtcccc 1440
attgtctttg agaacactga cctccactct tacgtagtaa tgaaccacgg gcgctcctac 1500
acagccatca gcaccattcc cgagaccgtt ggatattctc tgcttccact ggccccagtt 1560
ggaggcatca ttggatggat gtttgcagtg gagcaggacg gattcaagaa tgggttcagc 1620
atcaccgggg gtgagttcac tcgccaggct gaggtgacct tcgtggggca cccgggcaat 1680
ctggtcatta agcagcggtt cagcggcatc gatgagcatg ggcacctgac catcgacacg 1740
gagctggagg gccgcgtgcc gcagattccg ttcggctcct ccgtgcacat tgagccctac 1800
acggagctgt accactactc cacctcagtg atcacttcct cctccacccg ggagtacacg 1860
gtgactgagc ccgagcgaga tggggcatct ccttcacgca tctacactta ccagtggcgc 1920
cagaccatca ccttccagga atgcgtccac gatgactccc ggccagccct gcccagcacc 1980
cagcagctct cggtggacag cgtgttcgtc ctgtacaacc aggaggagaa gatcttgcgc 2040
tacgctttca gcaactccat tgggcctgtg agggaaggct cccctgatgc tcttcagaat 2100
ccctgctaca tcggcactca tgggtgtgac accaacgcgg cctgtcgccc tggtcccagg 2160
acacagttca cctgcgagtg ctccatcggc ttccgaggag acgggcgaac ctgctatgat 2220
attgatgaat gttcagaaca accctcagtg tgtgggagcc acacaatctg caataatcac 2280
ccaggaacct tccgctgcga gtgtgtggag ggctaccagt tttcagatga gggaacgtgt 2340
gtggctgtcg tggaccagcg ccccatcaac tactgtgaaa ctggccttca taactgcgac 2400
ataccccagc gggcccagtg tatctacaca ggaggctcct cctacacctg ttcctgcttg 2460
ccaggctttt ctggggatgg ccaagcctgc caagatgtag atgaatgcca gccaagccga 2520
tgtcaccctg acgccttctg ctacaacact ccaggctctt tcacgtgcca gtgcaaacct 2580
ggttatcagg gagacggctt ccgttgcgtg cccggagagg tggagaaaac ccggtgccag 2640
cacgagcgag aacacattct cggggcagcg gggcgacag acccacagcg acccattcct 2700
ccggggctgt tcgttcctga gtgcgatgcg cacgggcact acgcgcccac ccagtgccac 2760
ggcagcaccg gctactgctg gtgcgtggat cgcgacggcc gcgaggtgga gggcaccagg 2820
accaggcccg ggatgacgcc cccgtgtctg agtacagtgg ctcccccgat tcaccaagga 2880
cctgcggtgc ctaccgccgt gatccccttg cctcctggga cccatttact ctttgcccag 2940
actgggaaga ttgagcgcct gcccctggag ggaaatacca tgaggaagac agaagcaaag 3000
gcgttccttc atgtcccggc taaagtcatc attggactgg cctttgactg cgtggacaag 3060
atggtttact ggacggacat cactgagcct tccattggga gagctagtct acatggtgga 3120
gagccaacca ccatcattag acaagatctt ggaagtccag aaggtatcgc tgttgatcac 3180
cttggccgca acatcttctg gacagactct aacctggatc gaatagaagt ggcgaagctg 3240
gacggcacgc agcgccgggt gctctttgag actgacctgg tgaatcccag aggcattgta 3300
acggattccg tgagagggaa cctttactgg acagactgga acagagataa ccccaagatt 3360
gaaacttcct acatggacgg cacgaaccgg aggatccttg tgcaggatga cctgggcttg 3420
cccaatggac tgcacttcga tgcgttctca tctcagctct gctgggtgga tgcaggcacc 3480
aatcgggcgg aatgcctgaa ccccagtcag cccagcagac gcaaggctct cgaagggctc 3540
cagtatcctt ttgctgtgac gagctacggg aagaatctgt atttcacaga ctggaagatg 3600
aattccgtgg ttgctctcga tcttgcaatt tccaaggaga cggatgcttt ccaaccccac 3660
aagcagaccc ggctgtatgg catcaccacg gccctgtctc agtgtccgca aggccataac 3720
tactgctcag tgaacaatgg cggctgcacc cacctatgct tggccacccc agggagcagg 3780
acctgccgtt gccctgacaa caccttggga gttgactgta tcgaacggaa atgaagacaa 3840
gagtgcctta tttcctttcc aagtatttca cagcaacact ctacttgaag caacttggtc 3900
cagattgaaa agtgtcctct ggctgagtgg ccactaggcc cagacccagc ccagcctgag 3960
ccccaacaac aacttttccc tcactgttcc ccaaaacatg caccctggac ttctctaata 4020
gaaaagtctc caccccctaca caaggacaga accctccacc cctaccccca accctcagac 4080
agacttatac acccctgagt gaggattaca tgcccatccc agtgtcctag gaccttttcc 4140
caatactagc cccccagtgg tgaacagaac ctcccaaatt tgagttgcac ccttccctgt 4200
ggccttatga gctcagcctc gctttgaggt acccaccgtc ctgtcagctc cttgacctat 4260
gagctggggc ctgactagga aaagttggga gttaaggagg aaattagcat tccttaatgt 4320
tttgttttgg tgctctgaat ttcttcttta ttatagtcct atagttttac tcctcagttc 4380
ctcaccatca tcatcttgtc taagaccccc attataatat tcatgcgctg ctttttcatc 4440
aaaacctacc ctgtcctaga gatctatggg catttggtgg atgataatga gcagcccctc 4500
ccagatagaa tgtcaatatt tgagcagtag gatattggca tttgttagtt aaaggcttaa 4560
atcaaaagaa tgtccaatgg taggaatttc aaggtgtagg tcagatattt gagaataggg 4620
gatttttttg atgtgcctta aattatacca aagattacta attattcctc tttgcccaaa 4680
atacttgcat ccaaggttct agtctctgtt gctgtgctgg tctttagccc cactgctggc 4740
actgatgtcc ctcctttttc acggagacct atctgaggta caggatgggg ctggcaccag 4800
atgatgtccc accacagtcc ctcacctccg gcctccacat gacagaacca atttacactc 4860

aaccatgacc tcacccctcc ttggtttctc cctccccg

<210> 216
<211> 1247
<212> PRT
<213> Homo sapiens

<400> 216
Met Leu Ala Ser Ser Ser Arg Ile Arg Ala Ala Trp Thr Arg Ala Leu
1 5 10 15
Leu Leu Pro Leu Leu Leu Ala Gly Pro Val Gly Cys Leu Ser Arg Gln
20 25 30
Glu Leu Phe Pro Phe Gly Pro Gly Gln Gly Asp Leu Glu Leu Glu Asp
35 40 45
Gly Asp Asp Phe Val Ser Pro Ala Leu Glu Leu Ser Gly Ala Leu Arg
50 55 60
Phe Tyr Asp Arg Ser Asp Ile Asp Ala Val Tyr Val Thr Thr Asn Gly
65 70 75 80
Ile Ile Ala Thr Ser Glu Pro Pro Ala Lys Glu Ser His Pro Gly Leu
85 90 95
Phe Pro Pro Thr Phe Gly Ala Val Ala Pro Phe Leu Ala Asp Leu Asp
100 105 110
Thr Thr Asp Gly Leu Gly Lys Val Tyr Tyr Arg Glu Asp Leu Ser Pro
115 120 125
Ser Ile Thr Gln Arg Ala Ala Glu Cys Val His Arg Gly Phe Pro Glu
130 135 140
Ile Ser Phe Gln Pro Ser Ser Ala Val Val Val Thr Trp Glu Ser Val
145 150 155 160
Ala Pro Tyr Gln Gly Pro Ser Arg Asp Pro Asp Gln Lys Gly Lys Arg
165 170 175
Asn Thr Phe Gln Ala Val Leu Ala Ser Ser Asp Ser Ser Ser Tyr Ala
180 185 190
Ile Phe Leu Tyr Pro Glu Asp Gly Leu Gln Phe His Thr Thr Phe Ser
195 200 205
Lys Lys Glu Asn Asn Gln Val Pro Ala Val Val Ala Phe Ser Gln Gly
210 215 220
Ser Val Gly Phe Leu Trp Lys Ser Asn Gly Ala Tyr Asn Ile Phe Ala
225 230 235 240
Asn Asp Arg Glu Ser Ile Glu Asn Leu Ala Lys Ser Ser Asn Ser Gly
245 250 255
Gln Gln Gly Val Trp Val Phe Glu Ile Gly Ser Pro Ala Thr Thr Asn
260 265 270
Gly Val Val Pro Ala Asp Val Ile Leu Gly Thr Glu Asp Gly Ala Glu
275 280 285
Tyr Asp Asp Glu Asp Glu Asp Tyr Asp Leu Ala Thr Thr Arg Leu Gly
290 295 300
Leu Glu Asp Val Gly Thr Thr Pro Phe Ser Tyr Lys Ala Leu Arg Arg
305 310 315 320
Gly Gly Ala Asp Thr Tyr Ser Val Pro Ser Val Leu Ser Pro Arg Arg
325 330 335
Ala Ala Thr Glu Arg Pro Leu Gly Pro Pro Thr Glu Arg Thr Arg Ser
340 345 350
Phe Gln Leu Ala Val Glu Thr Phe His Gln Gln His Pro Gln Val Ile
355 360 365
Asp Val Asp Glu Val Glu Glu Thr Gly Val Val Phe Ser Tyr Asn Thr
370 375 380
Asp Ser Arg Gln Thr Cys Ala Asn Asn Arg His Gln Cys Ser Val His
385 390 395 400
Ala Glu Cys Arg Asp Tyr Ala Thr Gly Phe Cys Cys Ser Cys Val Ala
405 410 415
Gly Tyr Thr Gly Asn Gly Arg Gln Cys Val Ala Glu Gly Ser Pro Gln

```
            420                 425                 430
Arg Val Asn Gly Lys Val Lys Gly Arg Ile Phe Val Gly Ser Ser Gln
        435                 440                 445
Val Pro Ile Val Phe Glu Asn Thr Asp Leu His Ser Tyr Val Val Met
    450                 455                 460
Asn His Gly Arg Ser Tyr Thr Ala Ile Ser Thr Ile Pro Glu Thr Val
465                 470                 475                 480
Gly Tyr Ser Leu Leu Pro Leu Ala Pro Val Gly Gly Ile Ile Gly Trp
                485                 490                 495
Met Phe Ala Val Glu Gln Asp Gly Phe Lys Asn Gly Phe Ser Ile Thr
            500                 505                 510
Gly Gly Glu Phe Thr Arg Gln Ala Glu Val Thr Phe Val Gly His Pro
        515                 520                 525
Gly Asn Leu Val Ile Lys Gln Arg Phe Ser Gly Ile Asp Glu His Gly
    530                 535                 540
His Leu Thr Ile Asp Thr Glu Leu Glu Gly Arg Val Pro Gln Ile Pro
545                 550                 555                 560
Phe Gly Ser Ser Val His Ile Glu Pro Tyr Thr Glu Leu Tyr His Tyr
                565                 570                 575
Ser Thr Ser Val Ile Thr Ser Ser Ser Thr Arg Glu Tyr Thr Val Thr
            580                 585                 590
Glu Pro Glu Arg Asp Gly Ala Ser Pro Ser Arg Ile Tyr Thr Tyr Gln
        595                 600                 605
Trp Arg Gln Thr Ile Thr Phe Gln Glu Cys Val His Asp Asp Ser Arg
    610                 615                 620
Pro Ala Leu Pro Ser Thr Gln Gln Leu Ser Val Asp Ser Val Phe Val
625                 630                 635                 640
Leu Tyr Asn Gln Glu Glu Lys Ile Leu Arg Tyr Ala Phe Ser Asn Ser
                645                 650                 655
Ile Gly Pro Val Arg Glu Gly Ser Pro Asp Ala Leu Gln Asn Pro Cys
            660                 665                 670
Tyr Ile Gly Thr His Gly Cys Asp Thr Asn Ala Ala Cys Arg Pro Gly
        675                 680                 685
Pro Arg Thr Gln Phe Thr Cys Glu Cys Ser Ile Gly Phe Arg Gly Asp
    690                 695                 700
Gly Arg Thr Cys Tyr Asp Ile Asp Glu Cys Ser Glu Gln Pro Ser Val
705                 710                 715                 720
Cys Gly Ser His Thr Ile Cys Asn Asn His Pro Gly Thr Phe Arg Cys
                725                 730                 735
Glu Cys Val Glu Gly Tyr Gln Phe Ser Asp Glu Gly Thr Cys Val Ala
            740                 745                 750
Val Val Asp Gln Arg Pro Ile Asn Tyr Cys Glu Thr Gly Leu His Asn
        755                 760                 765
Cys Asp Ile Pro Gln Arg Ala Gln Cys Ile Tyr Thr Gly Gly Ser Ser
    770                 775                 780
Tyr Thr Cys Ser Cys Leu Pro Gly Phe Ser Gly Asp Gly Gln Ala Cys
785                 790                 795                 800
Gln Asp Val Asp Glu Cys Gln Pro Ser Arg Cys His Pro Asp Ala Phe
                805                 810                 815
Cys Tyr Asn Thr Pro Gly Ser Phe Thr Cys Gln Cys Lys Pro Gly Tyr
            820                 825                 830
Gln Gly Asp Gly Phe Arg Cys Val Pro Gly Glu Val Glu Lys Thr Arg
        835                 840                 845
Cys Gln His Glu Arg Glu His Ile Leu Gly Ala Ala Gly Ala Thr Asp
    850                 855                 860
Pro Gln Arg Pro Ile Pro Pro Gly Leu Phe Val Pro Glu Cys Asp Ala
865                 870                 875                 880
His Gly His Tyr Ala Pro Thr Gln Cys His Gly Ser Thr Gly Tyr Cys
                885                 890                 895
Trp Cys Val Asp Arg Asp Gly Arg Glu Val Glu Gly Thr Arg Thr Arg
            900                 905                 910
```

Pro Gly Met Thr Pro Pro Cys Leu Ser Thr Val Ala Pro Pro Ile His
915 920 925
Gln Gly Pro Ala Val Pro Thr Ala Val Ile Pro Leu Pro Pro Gly Thr
930 935 940
His Leu Leu Phe Ala Gln Thr Gly Lys Ile Glu Arg Leu Pro Leu Glu
945 950 955 960
Gly Asn Thr Met Arg Lys Thr Glu Ala Lys Ala Phe Leu His Val Pro
965 970 975
Ala Lys Val Ile Ile Gly Leu Ala Phe Asp Cys Val Asp Lys Met Val
980 985 990
Tyr Trp Thr Asp Ile Thr Glu Pro Ser Ile Gly Arg Ala Ser Leu His
995 1000 1005
Gly Gly Glu Pro Thr Thr Ile Ile Arg Gln Asp Leu Gly Ser Pro Glu
1010 1015 1020
Gly Ile Ala Val Asp His Leu Gly Arg Asn Ile Phe Trp Thr Asp Ser
1025 1030 1035 1040
Asn Leu Asp Arg Ile Glu Val Ala Lys Leu Asp Gly Thr Gln Arg Arg
1045 1050 1055
Val Leu Phe Glu Thr Asp Leu Val Asn Pro Arg Gly Ile Val Thr Asp
1060 1065 1070
Ser Val Arg Gly Asn Leu Tyr Trp Thr Asp Trp Asn Arg Asp Asn Pro
1075 1080 1085
Lys Ile Glu Thr Ser Tyr Met Asp Gly Thr Asn Arg Arg Ile Leu Val
1090 1095 1100
Gln Asp Asp Leu Gly Leu Pro Asn Gly Leu His Phe Asp Ala Phe Ser
1105 1110 1115 1120
Ser Gln Leu Cys Trp Val Asp Ala Gly Thr Asn Arg Ala Glu Cys Leu
1125 1130 1135
Asn Pro Ser Gln Pro Ser Arg Arg Lys Ala Leu Glu Gly Leu Gln Tyr
1140 1145 1150
Pro Phe Ala Val Thr Ser Tyr Gly Lys Asn Leu Tyr Phe Thr Asp Trp
1155 1160 1165
Lys Met Asn Ser Val Val Ala Leu Asp Leu Ala Ile Ser Lys Glu Thr
1170 1175 1180
Asp Ala Phe Gln Pro His Lys Gln Thr Arg Leu Tyr Gly Ile Thr Thr
1185 1190 1195 1200
Ala Leu Ser Gln Cys Pro Gln Gly His Asn Tyr Cys Ser Val Asn Asn
1205 1210 1215
Gly Gly Cys Thr His Leu Cys Leu Ala Thr Pro Gly Ser Arg Thr Cys
1220 1225 1230
Arg Cys Pro Asp Asn Thr Leu Gly Val Asp Cys Ile Glu Arg Lys
1235 1240 1245

<210> 217
<211> 10558
<212> DNA
<213> Homo sapiens

<400> 217
cagtttggag ctcagtcttc caccaaaggc cgttcagttc tcctgggctc cagcctcctg 60
caaggactgc aagagttttc ctccgcagct ctgagtctcc actttttgg tggagaaagg 120
ctgcaaaaag aaaaagagac gcagtgagtg ggaaaagtat gcatcctatt caaacctaat 180
tgaatcgagg agcccaggga cacacgcctt caggtttgct caggggttca tatttggtgc 240
ttagacaaat tcaaaatgag gaaacatcgg cacttgccct tagtggccgt cttttgcctc 300
tttctctcag gctttcctac aactcatgcc cagcagcagc aagcagatgt caaaaatggt 360
gcggctgctg atataatatt tctagtggat tcctcttgga ccattggaga ggaacatttc 420
caacttgttc gagagtttct atatgatgtt gtaaaatcct tagctgtggg agaaaatgat 480
ttcçattttg ctctggtcca gttcaacgga aacccacata ccgagttcct gttaaatacg 540
tatcgtacta aacaagaagt cctttctcat atttccaaca tgtcttatat tgggggaacc 600
aatcagactg gaaaaggatt agaatacata atgcaaagcc acctcaccaa ggctgctgga 660
agccgggccg gtgacggagt ccctcaggtt atcgtagtgt taactgatgg acactcgaag 720

gatggccttg ctctgccctc agcggaactt aagtctgctg atgttaacgt gtttgcaatt 780
ggagttgagg atgcagatga aggagcgtta aaagaaatag caagtgaacc gctcaatatg 840
catatgttca acctagagaa ttttacctca cttcatgaca tagtaggaaa cttagtgtcc 900
tgtgtgcatt catccgtgag tccagaaagg gctggggaca cggaaaccct taaagacatc 960
acagcacaag actctgctga cattattttc cttattgatg gatcaaacaa caccggaagt 1020
gtcaatttcg cagtcattct cgacttcctt gtaaatctcc ttgagaaact cccaattgga 1080
actcagcaga tccgagtggg ggtggtccag tttagcgatg agcccagaac catgttttcc 1140
ttggacacct actccaccaa ggcccaggtt ctgggtgcag tgaaagccct cgggtttgct 1200
ggtggggagt tggccaatat cggcctcgcc cttgatttcg tggtggagaa ccacttcacc 1260
cgggcagggg gcagccgcgt ggaggaaggg gttccccagg tgctggtcct cataagtgcc 1320
gggccttcta gtgacgagat tcgctacggg gtggtagcac tgaagcaggc tagcgtgttc 1380
tcattcggcc ttggagccca ggccgcctcc agggcagagc ttcagcacat agctaccgat 1440
gacaacttgg tgtttactgt cccggaattc cgtagctttg gggacctcca ggagaaatta 1500
ctgccgtaca ttgttggcgt ggcccaaagg cacattgtct tgaaaccgcc aaccattgtc 1560
acacaagtca ttgaagtcaa caagagagac atagtcttcc tggtggatgg ctcatctgca 1620
ctgggactgg ccaacttcaa tgccatccga gacttcattg ctaaagtcat ccagaggctg 1680
gaaatcggac aggatcttat ccaggtggca gtggcccagt atgcagacac tgtgaggcct 1740
gaattttatt tcaataccca tccaacaaaa agggaagtca taaccgctgt gcggaaaatg 1800
aagcccctgg acggctcggc cctgtacacg ggctctgctc tagactttgt tcgtaacaac 1860
ctattcacga gttcagccgg ctaccgggct gccgagggga ttcctaagct tttggtgctg 1920
atcacaggtg gtaagtccct agatgaaatc agccagcctg cccaggagct gaagagaagc 1980
agcataatgg cctttgccat tgggaacaag ggtgccgatc aggctgagct ggaagagatc 2040
gctttcgact cctccctggt gttcatccca gctgagttcc gagccgcccc attgcaaggc 2100
atgctgcctg gcttgctggc acctctcagg accctctctg gaacccctga agttcactca 2160
aacaaaagag atatcatctt tcttttggat ggatcagcca acgttggaaa aaccaatttc 2220
ccttatgtgc gcgactttgt aatgaaccta gttaacagcc ttgatattgg aaatgacaat 2280
attcgtgttg gtttagtgca atttagtgac actcctgtaa cggagttctc tttaaacaca 2340
taccagacca agtcagatat ccttggtcat ctgaggcagc tgcagctcca gggaggttcg 2400
ggcctgaaca caggctcagc cctaagctat gtctatgcca accacttcac ggaagctggc 2460
ggcagcagga tccgtgaaca cgtgccgcag ctcctgcttc tgctcacagc tgggcagtct 2520
gaggactcct atttgcaagc tgccaacgcc ttgacacgcg cgggcatcct gactttttgt 2580
gtgggagcta gccaggcgaa taaggcagag cttgagcaga ttgcttttaa cccaagcctg 2640
gtgtatctca tggatgattt cagctccctg ccagctttgc ctcagcagct gattcagccc 2700
ctaaccacat atgttagtgg aggtgtggag gaagtaccac tcgctcagcc agagagcaag 2760
cgagacattc tgttcctctt tgacggctca gccaatcttg tgggccagtt ccctgttgtc 2820
cgtgactttc tctacaagat tatcgatgag ctcaatgtga agccagaggg gacccgaatt 2880
gcggtggctc agtacagcga tgatgtcaag gtggagtccc gttttgatga gcaccagagt 2940
aagcctgaga tcctgaatct tgtgaagaga atgaagatca agacgggcaa agccctcaac 3000
ctgggctacg cgctggacta tgcacagagg tacatttttg tgaagtctgc tggcagccgg 3060
atcgaggatg gagtgcttca gttcctggtg ctgctggtcg caggaaggtc atctgaccgt 3120
gtggatgggc cagcaagtaa cctgaagcag agtggggttg tgcctttcat cttccaagcc 3180
aagaacgcag accctgctga gttagagcag atcgtgctgt ctccagcgtt tatcctggct 3240
gcagagtcgc ttcccaagat tggagatctt catccacaga tagtgaatct cttaaaatca 3300
gtgcacaacg gagcaccagc accagtttca ggtgaaaagg acgtggtgtt tctgcttgat 3360
ggctctgagg gcgtcaggag cggcttccct ctgttgaaag agtttgtcca gagagtggtg 3420
gaaagcctgg atgtgggcca ggaccgggtc cgcgtggccg tggtgcagta cagcgaccgg 3480
accaggcccg agttctacct gaattcatac atgaacaagc aggacgtcgt caacgctgtc 3540
cgccagctga ccctgctggg agggccgacc cccaacaccg gggccgccct ggagtttgtc 3600
ctgaggaaca tcctggtcag ctctgcggga agcaggataa cagaaggtgt gccccagctg 3660
ctgatcgtcc tcacggccga caggtctggg gatgatgtgc ggaacccctc cgtggtcgtg 3720
aagaggggtg ggctgtgcc cattggcatt ggcatcggga acgctgacat cacagagatg 3780
cagaccatct ccttcatccc ggactttgcc gtggccattc ccacctttcg ccagctgggg 3840
accgtccaac aggtcatctc tgagagggtg acccagctca cccgcgagga gctgagcagg 3900
ctgcagccgg tgttgcagcc tctaccgagc ccaggtgttg gtggcaagag ggacgtggtc 3960
tttctcatcg atgggtccca aagtgccggg cctgagttcc agtacgttcg caccctcata 4020
gagaggctgg ttgactacct ggacgtgggc tttgacacca cccgggtggc tgtcatccag 4080
ttcagcgatg accccaaggc ggagttcctg ctgaacgccc attccagcaa ggatgaagtg 4140
cagaacgcgg tgcagcggct gaggcccaag ggagggcggc agatcaacgt gggcaatgcc 4200
ctggagtacg tgtccaggaa catcttcaag aggcccctgg ggagccgcat tgaagagggc 4260
gtcccacagt tcctggtcct catctcgtct ggaaagtctg acgatgaggt ggtcgtcccg 4320
gcggtggagc tcaagcagtt tggcgtggcc cctttcacga tcgccaggaa cgcagaccag 4380

gaggagctgg tgaagatctc gctgagcccc gaatatgtgt tctcggtgag caccttccgg 4440
gagctgccca gcctggagca gaaactgctg acgcccatca cgaccctgac ctcagagcag 4500
atccagaagc tcttagccag cactcgctat ccacctccag cagttgagag tgatgctgca 4560
gacattgtct ttctgatcga cagctctgag ggagttaggc cagatggctt tgcacatatt 4620
cgagattttg ttagcaggat tgttcgaaga ctcaacatcg gccccagtaa agtgagagtt 4680
ggggtcgtgc agttcagcaa tgatgtcttc ccagaattct atctgaaaac ctacagatcc 4740
caggccccgg tgctggacgc catacggcgc ctgaggctca gagggggggtc cccactgaac 4800
actggcaagg ctctcgaatt tgtggcaaga aacctctttg ttaagtctgc ggggagtcgc 4860
atagaagacg gggtgcccca acacctggtc ctggtcctgg gtggaaaatc ccaggacgat 4920
gtgtccaggt tcgcccaggt gatccgttcc tcgggcattg tgagtttagg ggtaggagac 4980
cggaacatcg acagaacaga gctgcagacc atcaccaatg accccagact ggtcttcaca 5040
gtgcgagagt tcagagagct tcccaacata gaagaaagaa tcatgaactc gtttggaccc 5100
tccgcagcca ctcctgcacc tccaggggtg gacacccctc ctccttcacg gccagagaag 5160
aagaaagcag acattgtgtt cctgttggat ggttccatca acttcaggag ggacagtttc 5220
caggaagtgc ttcgttttgt gtctgaaata gtggacacag tttatgaaga tggcgactcc 5280
atccaagtgg ggcttgtcca gtacaactct gaccccactg acgaattctt cctgaaggac 5340
ttctctacca agaggcagat tattgacgcc atcaacaaag tggtctacaa aggggggaaga 5400
cacgccaaca ctaaggtggg ccttgagcac ctgcgggtaa accactttgt gcctgaggca 5460
ggcagccgcc tggaccagcg ggtccctcag attgcctttg tgatcacggg aggaaagtcg 5520
gtggaagatg cacaggatgt gagcctggcc ctcacccaga gggggggtcaa agtgtttgct 5580
gttggagtga ggaatatcga ctcggaggag gttggaaaga tagcgtccaa cagcgccaca 5640
gcgttccgcg tgggcaacgt ccaggagctg tccgaactga gcgagcaagt tttggaaact 5700
ttgcatgatg cgatgcatga aaccctttgc cctggtgtaa ctgatgctgc caaagcttgt 5760
aatctggatg tgattctggg gtttgatggt tctagagacc agaatgtttt tgtggcccag 5820
aagggcttcg agtccaaggt ggacgccatc ttgaacagaa tcagccagat gcacagggtc 5880
agctgcagcg gtggccgctc gcccaccgtg cgtgtgtcag tggtggccaa cacgccctcg 5940
ggcccggtgg aggcctttga ctttgacgag taccagccag agatgctcga gaagttccgg 6000
aacatgcgca gccagcaccc ctacgtcctc acggaggaca ccctgaaggt ctacctgaac 6060
aagttcagac agtcctcgcc ggacagcgtg aaggtggtca ttcattttac tgatggagca 6120
gacggagatc tggctgattt acacagagca tctgagaacc tccgccaaga aggagtccgt 6180
gccttgatcc tggtgggcct tgaacgagtg gtcaacttgg agcggctaat gcatctggag 6240
tttgggcgag ggtttatgta tgacaggccc ctgaggctta acttgctgga cttggattat 6300
gaactagcgg agcagcttga caacattgcc gagaaagctt gctgtggggt tccctgcaag 6360
tgctctgggc agaggggaga ccgcgggccc atcggcagca tcgggccaaa gggtattcct 6420
ggagaagacg gctaccgagg ctatcctggt gatgagggtg gacccggtga gcgtggtccg 6480
cctggtgtga acggcactca aggtttccag ggctgccccgg gccagagagg agtaaagggc 6540
tctcggggat tcccaggaga gaagggcgaa gtaggagaaa ttggactgga tggtctggat 6600
ggtgaagatg gagacaaagg attgcctggt tcttctggag agaaagggaa tcctggaaga 6660
aggggtgata aaggacctcg aggagagaaa ggagaaagag gagatgttgg gattcgaggg 6720
gacccgggta acccaggaca agacagccag gagagaggac ccaaaggaga aaccggtgac 6780
ctcggcccca tgggtgtccc agggagagat ggagtacctg gaggacctgg agaaactggg 6840
aagaatggtg gctttggccg aaggggaccc cccggagcta agggcaacaa gggcggtcct 6900
ggccagccgg gctttgaggg agagcagggg accagaggtg cacagggccc agctggtcct 6960
gctggtcctc cagggctgat aggagaacaa ggcatttctg gacctagggg aagcggaggt 7020
gcccgtggcg ctcctggaga acgaggcaga accggtccac tgggaagaaa gggtgagccc 7080
ggagagccag gaccaaaagg aggaatcggg aacccgggcc ctcgtgggga gacgggagat 7140
gacgggagag acggagttgg cagtgaagga cgcagaggca aaaaaggaga aagaggattt 7200
cctggatacc caggaccaaa gggtaaccca ggtgaacctg ggctaaatgg aacaacagga 7260
cccaaaggca tcagaggccg aaggggaaat tcgggacctc cagggatagt tggacagaag 7320
gggagacctg gctacccagg accagctggt ccaaggggca acaggggcga ctccatcgat 7380
caatgtgccc tcatccaaag catcaaagat aaatgccctt gctgttacgg gcccctggag 7440
tgccccgtct tcccaacaga actagccttt gctttagaca cctctgaggg agtcaaccaa 7500
gacactttcg gccggatgcg agatgtggtc ttgagtattg tgaatgtcct gaccattgct 7560
gagagcaact gcccgacggg ggcccgggtg gctgtggtca cctacaacaa cgaggtgacc 7620
acggagatcc ggtttgctga ctccaagagg aagtcggtcc tcctggacaa gattaagaac 7680
cttcaggtgg ctctgacatc caaacagcag agtctggaga ctgccatgtc gtttgtggcc 7740
aggaacacat ttaagcgtgt gaggaacgga ttcctaatga ggaaagtggc tgttttcttc 7800
agcaacacac ccacaagagc atccccacag ctcagagagg ctgtgctcaa actctcagat 7860
gcggggatca ccccccttgtt ccttacaagg caggaagacc ggcagctcat caacgctttg 7920
cagatcaata acacagcagt ggggcatgcg cttgtcctgc ctgcagggag agacctcaca 7980
gacttcctgg agaatgtcct cacgtgtcat gtttgcttgg acatctgcaa catcgaccca 8040

```
tcctgtggat ttggcagttg gaggccttcc ttcagggaca ggagagcggc agggagtgat     8100
gtggacatcg acatggcttt catcttagac agcgctgaga ccaccaccct gttccagttc     8160
aatgagatga agaagtacat agcgtacctg gtcagacaac tggacatgag cccagatccc     8220
aaggcctccc agcacttcgc cagagtggca gttgtgcagc acgcgccctc tgagtccgtg     8280
gacaatgcca gcatgccacc tgtgaaggtg gaattctccc tgactgacta tggctccaag     8340
gagaagctgg tggacttcct cagcagggga atgacacagt tgcagggaac cagggcctta     8400
ggcagtgcca ttgaatacac catagagaat gtctttgaaa gtgccccaaa cccacgggac     8460
ctgaaaattg tggtcctgat gctgacgggc gaggtgccgg agcagcagct ggaggaggcc     8520
cagagagtca tcctgcaggc caaatgcaag ggctacttct tcgtggtcct gggcattggc     8580
aggaaggtga acatcaagga ggtatacacc ttcgccagtg agccaaacga cgtcttcttc     8640
aaattagtgg acaagtccac cgagctcaac gaggagcctt tgatgcgctt cgggaggctg     8700
ttgccgtcct tcgtcagcag tgaaaatgct ttttacttgt ccccagatat caggaaacag     8760
tgtgattggt tccaagggga ccaaccccaca aagaaccttg tgaagtttgg tcacaaacaa    8820
gtaaatgttc cgaataacgt tacttcaagt cctacatcca acccagtgac gacaacgaag     8880
ccggtgacta cgacgaagcc ggtgaccacc acaacaaagc ctgtaaccac cacaacaaag     8940
cctgtgacta ttataaatca gccatctgtg aagccagccg ctgcaaagcc ggcccctgcg     9000
aaacctgtgg ctgccaagcc tgtggccaca aagacggcca ctgttagacc cccagtggcg     9060
gtgaagccag caacagcagc gaagcctgta gcagcaaagc cagcagctgt aagacccccc     9120
gctgctgctg caaaaccagt ggcgaccaag cctgaggtcc ctaggccaca ggcagccaaa     9180
ccagctgcca ccaagccagc caccactaag cccgtggtta agatgctccg tgaagtccag     9240
gtgtttgaga taacagagaa cagcgccaaa ctccactggg agaggcctga gcccccccggt    9300
ccttattttt atgacctcac cgtcacctca gcccatgatc agtccctggt tctgaagcag     9360
aacctcacgg tcacggaccg cgtcattgga ggcctgctcg ctgggcagac ataccatgtg     9420
gctgtggtct gctacctgag gtctcaggtc agagccacct accacggaag tttcagtaca     9480
aagaaatctc agcccccacc tccacagcca gcaaggtcag cttctagttc aaccatcaat     9540
ctaatggtga gcacagaacc attggctctc actgaaacag atatatgcaa gttgccgaaa     9600
gacgaaggaa cttgcaggga tttcatatta aaatggtact atgatccaaa caccaaaagc     9660
tgtgcaagat tctggtatgg aggttgtggt ggaaacgaaa acaaatttgg atcacagaaa     9720
gaatgtgaaa aggtttgcgc tcctgtgctc gccaaacccg gagtcatcag tgtgatggga     9780
acctaagcgt gggtggccaa catcatatac ctcttgaaga agaaggagtc agccatcgcc     9840
aacttgtctc tgtagaagct ccgggtgtag attcccttgc actgtatcat ttcatgcttt     9900
gatttacact cgaactcggg agggaacatc ctgctgcatg acctatcagt atggtgctaa     9960
tgtgtctgtg gaccctcgct ctctgtctcc agcagttctc tcgaatactt tgaatgttgt    10020
gtaacagtta gccactgctg gtgtttatgt gaacattcct atcaatccaa attccctctg    10080
gagtttcatg ttatgcctgt tgcaggcaaa tgtaaagtct agaaaataat gcaaatgtca    10140
cggctactct atatactttt gcttggttca tttttttcc cttttagtta agcatgactt      10200
tagatgggaa gcctgtgtat cgtggagaaa caagagacca acttttttcat tccctgcccc    10260
caatttccca gactagattt caagctaatt ttctttttct gaagcctcta acaaatgatc    10320
tagttcagaa ggaagcaaaa tcccttaatc tatgtgcacc gttgggacca atgccttaat    10380
taaagaattt aaaaaagttg taatagagaa tatttttggc attcctctca atgttgtgtg    10440
tttttttttt ttgtgtgctg gagggagggg atttaatttt aattttaaaa tgtttaggaa    10500
atttatacaa agaaactttt taataaagta tattgaaagt ttaaaaaaaa aaaaaaa       10558
```

<210> 218
<211> 3173
<212> PRT
<213> Homo sapiens

<400> 218

```
Met Arg Lys His Arg His Leu Pro Leu Val Ala Val Phe Cys Leu Phe
1               5                   10                  15
Leu Ser Gly Phe Pro Thr Thr His Ala Gln Gln Gln Gln Ala Asp Val
            20                  25                  30
Lys Asn Gly Ala Ala Ala Asp Ile Ile Phe Leu Val Asp Ser Ser Trp
        35                  40                  45
Thr Ile Gly Glu Glu His Phe Gln Leu Val Arg Glu Phe Leu Tyr Asp
    50                  55                  60
Val Val Lys Ser Leu Ala Val Gly Glu Asn Asp Phe His Phe Ala Leu
65                  70                  75                  80
```

Val Gln Phe Asn Gly Asn Pro His Thr Glu Phe Leu Leu Asn Thr Tyr
85 90 95
Arg Thr Lys Gln Glu Val Leu Ser His Ile Ser Asn Met Ser Tyr Ile
100 105 110
Gly Gly Thr Asn Gln Thr Gly Lys Gly Leu Glu Tyr Ile Met Gln Ser
115 120 125
His Leu Thr Lys Ala Ala Gly Ser Arg Ala Gly Asp Gly Val Pro Gln
130 135 140
Val Ile Val Val Leu Thr Asp Gly His Ser Lys Asp Gly Leu Ala Leu
145 150 155 160
Pro Ser Ala Glu Leu Lys Ser Ala Asp Val Asn Val Phe Ala Ile Gly
165 170 175
Val Glu Asp Ala Asp Glu Gly Ala Leu Lys Glu Ile Ala Ser Glu Pro
180 185 190
Leu Asn Met His Met Phe Asn Leu Glu Asn Phe Thr Ser Leu His Asp
195 200 205
Ile Val Gly Asn Leu Val Ser Cys Val His Ser Ser Val Ser Pro Glu
210 215 220
Arg Ala Gly Asp Thr Glu Thr Leu Lys Asp Ile Thr Ala Gln Asp Ser
225 230 235 240
Ala Asp Ile Ile Phe Leu Ile Asp Gly Ser Asn Asn Thr Gly Ser Val
245 250 255
Asn Phe Ala Val Ile Leu Asp Phe Leu Val Asn Leu Leu Glu Lys Leu
260 265 270
Pro Ile Gly Thr Gln Gln Ile Arg Val Gly Val Val Gln Phe Ser Asp
275 280 285
Glu Pro Arg Thr Met Phe Ser Leu Asp Thr Tyr Ser Thr Lys Ala Gln
290 295 300
Val Leu Gly Ala Val Lys Ala Leu Gly Phe Ala Gly Gly Glu Leu Ala
305 310 315 320
Asn Ile Gly Leu Ala Leu Asp Phe Val Val Glu Asn His Phe Thr Arg
325 330 335
Ala Gly Gly Ser Arg Val Glu Glu Gly Val Pro Gln Val Leu Val Leu
340 345 350
Ile Ser Ala Gly Pro Ser Ser Asp Glu Ile Arg Tyr Gly Val Val Ala
355 360 365
Leu Lys Gln Ala Ser Val Phe Ser Phe Gly Leu Gly Ala Gln Ala Ala
370 375 380
Ser Arg Ala Glu Leu Gln His Ile Ala Thr Asp Asp Asn Leu Val Phe
385 390 395 400
Thr Val Pro Glu Phe Arg Ser Phe Gly Asp Leu Gln Glu Lys Leu Leu
405 410 415
Pro Tyr Ile Val Gly Val Ala Gln Arg His Ile Val Leu Lys Pro Pro
420 425 430
Thr Ile Val Thr Gln Val Ile Glu Val Asn Lys Arg Asp Ile Val Phe
435 440 445
Leu Val Asp Gly Ser Ser Ala Leu Gly Leu Ala Asn Phe Asn Ala Ile
450 455 460
Arg Asp Phe Ile Ala Lys Val Ile Gln Arg Leu Glu Ile Gly Gln Asp
465 470 475 480
Leu Ile Gln Val Ala Val Ala Gln Tyr Ala Asp Thr Val Arg Pro Glu
485 490 495
Phe Tyr Phe Asn Thr His Pro Thr Lys Arg Glu Val Ile Thr Ala Val
500 505 510
Arg Lys Met Lys Pro Leu Asp Gly Ser Ala Leu Tyr Thr Gly Ser Ala
515 520 525
Leu Asp Phe Val Arg Asn Asn Leu Phe Thr Ser Ser Ala Gly Tyr Arg
530 535 540
Ala Ala Glu Gly Ile Pro Lys Leu Leu Val Leu Ile Thr Gly Gly Lys
545 550 555 560
Ser Leu Asp Glu Ile Ser Gln Pro Ala Gln Glu Leu Lys Arg Ser Ser

```
                565                 570                 575
Ile Met Ala Phe Ala Ile Gly Asn Lys Gly Ala Asp Gln Ala Glu Leu
            580                 585                 590
Glu Glu Ile Ala Phe Asp Ser Ser Leu Val Phe Ile Pro Ala Glu Phe
        595                 600                 605
Arg Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro Leu
    610                 615                 620
Arg Thr Leu Ser Gly Thr Pro Glu Val His Ser Asn Lys Arg Asp Ile
625                 630                 635                 640
Ile Phe Leu Leu Asp Gly Ser Ala Asn Val Gly Lys Thr Asn Phe Pro
                645                 650                 655
Tyr Val Arg Asp Phe Val Met Asn Leu Val Asn Ser Leu Asp Ile Gly
            660                 665                 670
Asn Asp Asn Ile Arg Val Gly Leu Val Gln Phe Ser Asp Thr Pro Val
        675                 680                 685
Thr Glu Phe Ser Leu Asn Thr Tyr Gln Thr Lys Ser Asp Ile Leu Gly
    690                 695                 700
His Leu Arg Gln Leu Gln Leu Gln Gly Gly Ser Gly Leu Asn Thr Gly
705                 710                 715                 720
Ser Ala Leu Ser Tyr Val Tyr Ala Asn His Phe Thr Glu Ala Gly Gly
                725                 730                 735
Ser Arg Ile Arg Glu His Val Pro Gln Leu Leu Leu Leu Leu Thr Ala
            740                 745                 750
Gly Gln Ser Glu Asp Ser Tyr Leu Gln Ala Ala Asn Ala Leu Thr Arg
        755                 760                 765
Ala Gly Ile Leu Thr Phe Cys Val Gly Ala Ser Gln Ala Asn Lys Ala
    770                 775                 780
Glu Leu Glu Gln Ile Ala Phe Asn Pro Ser Leu Val Tyr Leu Met Asp
785                 790                 795                 800
Asp Phe Ser Ser Leu Pro Ala Leu Pro Gln Gln Leu Ile Gln Pro Leu
                805                 810                 815
Thr Thr Tyr Val Ser Gly Gly Val Glu Glu Val Pro Leu Ala Gln Pro
            820                 825                 830
Glu Ser Lys Arg Asp Ile Leu Phe Leu Phe Asp Gly Ser Ala Asn Leu
        835                 840                 845
Val Gly Gln Phe Pro Val Val Arg Asp Phe Leu Tyr Lys Ile Ile Asp
    850                 855                 860
Glu Leu Asn Val Lys Pro Glu Gly Thr Arg Ile Ala Val Ala Gln Tyr
865                 870                 875                 880
Ser Asp Asp Val Lys Val Glu Ser Arg Phe Asp Glu His Gln Ser Lys
                885                 890                 895
Pro Glu Ile Leu Asn Leu Val Lys Arg Met Lys Ile Lys Thr Gly Lys
            900                 905                 910
Ala Leu Asn Leu Gly Tyr Ala Leu Asp Tyr Ala Gln Arg Tyr Ile Phe
        915                 920                 925
Val Lys Ser Ala Gly Ser Arg Ile Glu Asp Gly Val Leu Gln Phe Leu
    930                 935                 940
Val Leu Leu Val Ala Gly Arg Ser Ser Asp Arg Val Asp Gly Pro Ala
945                 950                 955                 960
Ser Asn Leu Lys Gln Ser Gly Val Val Pro Phe Ile Phe Gln Ala Lys
                965                 970                 975
Asn Ala Asp Pro Ala Glu Leu Glu Gln Ile Val Leu Ser Pro Ala Phe
            980                 985                 990
Ile Leu Ala Ala Glu Ser Leu Pro Lys Ile Gly Asp Leu His Pro Gln
        995                 1000                1005
Ile Val Asn Leu Leu Lys Ser Val His Asn Gly Ala Pro Ala Pro Val
    1010                1015                1020
Ser Gly Glu Lys Asp Val Val Phe Leu Leu Asp Gly Ser Glu Gly Val
1025                1030                1035                1040
Arg Ser Gly Phe Pro Leu Leu Lys Glu Phe Val Gln Arg Val Val Glu
                1045                1050                1055
```

Ser Leu Asp Val Gly Gln Asp Arg Val Arg Val Ala Val Val Gln Tyr
1060 1065 1070
Ser Asp Arg Thr Arg Pro Glu Phe Tyr Leu Asn Ser Tyr Met Asn Lys
1075 1080 1085
Gln Asp Val Val Asn Ala Val Arg Gln Leu Thr Leu Leu Gly Gly Pro
1090 1095 1100
Thr Pro Asn Thr Gly Ala Ala Leu Glu Phe Val Leu Arg Asn Ile Leu
1105 1110 1115 1120
Val Ser Ser Ala Gly Ser Arg Ile Thr Glu Gly Val Pro Gln Leu Leu
1125 1130 1135
Ile Val Leu Thr Ala Asp Arg Ser Gly Asp Asp Val Arg Asn Pro Ser
1140 1145 1150
Val Val Val Lys Arg Gly Gly Ala Val Pro Ile Gly Ile Gly Ile Gly
1155 1160 1165
Asn Ala Asp Ile Thr Glu Met Gln Thr Ile Ser Phe Ile Pro Asp Phe
1170 1175 1180
Ala Val Ala Ile Pro Thr Phe Arg Gln Leu Gly Thr Val Gln Gln Val
1185 1190 1195 1200
Ile Ser Glu Arg Val Thr Gln Leu Thr Arg Glu Glu Leu Ser Arg Leu
1205 1210 1215
Gln Pro Val Leu Gln Pro Leu Pro Ser Pro Gly Val Gly Gly Lys Arg
1220 1225 1230
Asp Val Val Phe Leu Ile Asp Gly Ser Gln Ser Ala Gly Pro Glu Phe
1235 1240 1245
Gln Tyr Val Arg Thr Leu Ile Glu Arg Leu Val Asp Tyr Leu Asp Val
1250 1255 1260
Gly Phe Asp Thr Thr Arg Val Ala Val Ile Gln Phe Ser Asp Asp Pro
1265 1270 1275 1280
Lys Ala Glu Phe Leu Leu Asn Ala His Ser Ser Lys Asp Glu Val Gln
1285 1290 1295
Asn Ala Val Gln Arg Leu Arg Pro Lys Gly Gly Arg Gln Ile Asn Val
1300 1305 1310
Gly Asn Ala Leu Glu Tyr Val Ser Arg Asn Ile Phe Lys Arg Pro Leu
1315 1320 1325
Gly Ser Arg Ile Glu Glu Gly Val Pro Gln Phe Leu Val Leu Ile Ser
1330 1335 1340
Ser Gly Lys Ser Asp Asp Glu Val Val Val Pro Ala Val Glu Leu Lys
1345 1350 1355 1360
Gln Phe Gly Val Ala Pro Phe Thr Ile Ala Arg Asn Ala Asp Gln Glu
1365 1370 1375
Glu Leu Val Lys Ile Ser Leu Ser Pro Glu Tyr Val Phe Ser Val Ser
1380 1385 1390
Thr Phe Arg Glu Leu Pro Ser Leu Glu Gln Lys Leu Leu Thr Pro Ile
1395 1400 1405
Thr Thr Leu Thr Ser Glu Gln Ile Gln Lys Leu Leu Ala Ser Thr Arg
1410 1415 1420
Tyr Pro Pro Pro Ala Val Glu Ser Asp Ala Ala Asp Ile Val Phe Leu
1425 1430 1435 1440
Ile Asp Ser Ser Glu Gly Val Arg Pro Asp Gly Phe Ala His Ile Arg
1445 1450 1455
Asp Phe Val Ser Arg Ile Val Arg Arg Leu Asn Ile Gly Pro Ser Lys
1460 1465 1470
Val Arg Val Gly Val Val Gln Phe Ser Asn Asp Val Phe Pro Glu Phe
1475 1480 1485
Tyr Leu Lys Thr Tyr Arg Ser Gln Ala Pro Val Leu Asp Ala Ile Arg
1490 1495 1500
Arg Leu Arg Leu Arg Gly Gly Ser Pro Leu Asn Thr Gly Lys Ala Leu
1505 1510 1515 1520
Glu Phe Val Ala Arg Asn Leu Phe Val Lys Ser Ala Gly Ser Arg Ile
1525 1530 1535
Glu Asp Gly Val Pro Gln His Leu Val Leu Val Leu Gly Gly Lys Ser

1540 1545 1550
Gln Asp Asp Val Ser Arg Phe Ala Gln Val Ile Arg Ser Ser Gly Ile
1555 1560 1565
Val Ser Leu Gly Val Gly Asp Arg Asn Ile Asp Arg Thr Glu Leu Gln
1570 1575 1580
Thr Ile Thr Asn Asp Pro Arg Leu Val Phe Thr Val Arg Glu Phe Arg
1585 1590 1595 1600
Glu Leu Pro Asn Ile Glu Glu Arg Ile Met Asn Ser Phe Gly Pro Ser
1605 1610 1615
Ala Ala Thr Pro Ala Pro Pro Gly Val Asp Thr Pro Pro Pro Ser Arg
1620 1625 1630
Pro Glu Lys Lys Lys Ala Asp Ile Val Phe Leu Leu Asp Gly Ser Ile
1635 1640 1645
Asn Phe Arg Arg Asp Ser Phe Gln Glu Val Leu Arg Phe Val Ser Glu
1650 1655 1660
Ile Val Asp Thr Val Tyr Glu Asp Gly Asp Ser Ile Gln Val Gly Leu
1665 1670 1675 1680
Val Gln Tyr Asn Ser Asp Pro Thr Asp Glu Phe Phe Leu Lys Asp Phe
1685 1690 1695
Ser Thr Lys Arg Gln Ile Ile Asp Ala Ile Asn Lys Val Val Tyr Lys
1700 1705 1710
Gly Gly Arg His Ala Asn Thr Lys Val Gly Leu Glu His Leu Arg Val
1715 1720 1725
Asn His Phe Val Pro Glu Ala Gly Ser Arg Leu Asp Gln Arg Val Pro
1730 1735 1740
Gln Ile Ala Phe Val Ile Thr Gly Gly Lys Ser Val Glu Asp Ala Gln
1745 1750 1755 1760
Asp Val Ser Leu Ala Leu Thr Gln Arg Gly Val Lys Val Phe Ala Val
1765 1770 1775
Gly Val Arg Asn Ile Asp Ser Glu Glu Val Gly Lys Ile Ala Ser Asn
1780 1785 1790
Ser Ala Thr Ala Phe Arg Val Gly Asn Val Gln Glu Leu Ser Glu Leu
1795 1800 1805
Ser Glu Gln Val Leu Glu Thr Leu His Asp Ala Met His Glu Thr Leu
1810 1815 1820
Cys Pro Gly Val Thr Asp Ala Ala Lys Ala Cys Asn Leu Asp Val Ile
1825 1830 1835 1840
Leu Gly Phe Asp Gly Ser Arg Asp Gln Asn Val Phe Val Ala Gln Lys
1845 1850 1855
Gly Phe Glu Ser Lys Val Asp Ala Ile Leu Asn Arg Ile Ser Gln Met
1860 1865 1870
His Arg Val Ser Cys Ser Gly Gly Arg Ser Pro Thr Val Arg Val Ser
1875 1880 1885
Val Val Ala Asn Thr Pro Ser Gly Pro Val Glu Ala Phe Asp Phe Asp
1890 1895 1900
Glu Tyr Gln Pro Glu Met Leu Glu Lys Phe Arg Asn Met Arg Ser Gln
1905 1910 1915 1920
His Pro Tyr Val Leu Thr Glu Asp Thr Leu Lys Val Tyr Leu Asn Lys
1925 1930 1935
Phe Arg Gln Ser Ser Pro Asp Ser Val Lys Val Val Ile His Phe Thr
1940 1945 1950
Asp Gly Ala Asp Gly Asp Leu Ala Asp Leu His Arg Ala Ser Glu Asn
1955 1960 1965
Leu Arg Gln Glu Gly Val Arg Ala Leu Ile Leu Val Gly Leu Glu Arg
1970 1975 1980
Val Val Asn Leu Glu Arg Leu Met His Leu Glu Phe Gly Arg Gly Phe
1985 1990 1995 2000
Met Tyr Asp Arg Pro Leu Arg Leu Asn Leu Leu Asp Leu Asp Tyr Glu
2005 2010 2015
Leu Ala Glu Gln Leu Asp Asn Ile Ala Glu Lys Ala Cys Cys Gly Val
2020 2025 2030

Pro Cys Lys Cys Ser Gly Gln Arg Gly Asp Arg Gly Pro Ile Gly Ser
2035 2040 2045
Ile Gly Pro Lys Gly Ile Pro Gly Glu Asp Gly Tyr Arg Gly Tyr Pro
2050 2055 2060
Gly Asp Glu Gly Gly Pro Gly Glu Arg Gly Pro Pro Gly Val Asn Gly
2065 2070 2075 2080
Thr Gln Gly Phe Gln Gly Cys Pro Gly Gln Arg Gly Val Lys Gly Ser
2085 2090 2095
Arg Gly Phe Pro Gly Glu Lys Gly Glu Val Gly Glu Ile Gly Leu Asp
2100 2105 2110
Gly Leu Asp Gly Glu Asp Gly Asp Lys Gly Leu Pro Gly Ser Ser Gly
2115 2120 2125
Glu Lys Gly Asn Pro Gly Arg Arg Gly Asp Lys Gly Pro Arg Gly Glu
2130 2135 2140
Lys Gly Glu Arg Gly Asp Val Gly Ile Arg Gly Asp Pro Gly Asn Pro
2145 2150 2155 2160
Gly Gln Asp Ser Gln Glu Arg Gly Pro Lys Gly Glu Thr Gly Asp Leu
2165 2170 2175
Gly Pro Met Gly Val Pro Gly Arg Asp Gly Val Pro Gly Gly Pro Gly
2180 2185 2190
Glu Thr Gly Lys Asn Gly Gly Phe Gly Arg Arg Gly Pro Pro Gly Ala
2195 2200 2205
Lys Gly Asn Lys Gly Gly Pro Gly Gln Pro Gly Phe Glu Gly Glu Gln
2210 2215 2220
Gly Thr Arg Gly Ala Gln Gly Pro Ala Gly Pro Ala Gly Pro Pro Gly
2225 2230 2235 2240
Leu Ile Gly Glu Gln Gly Ile Ser Gly Pro Arg Gly Ser Gly Gly Ala
2245 2250 2255
Arg Gly Ala Pro Gly Glu Arg Gly Arg Thr Gly Pro Leu Gly Arg Lys
2260 2265 2270
Gly Glu Pro Gly Glu Pro Gly Pro Lys Gly Gly Ile Gly Asn Pro Gly
2275 2280 2285
Pro Arg Gly Glu Thr Gly Asp Asp Gly Arg Asp Gly Val Gly Ser Glu
2290 2295 2300
Gly Arg Arg Gly Lys Lys Gly Glu Arg Gly Phe Pro Gly Tyr Pro Gly
2305 2310 2315 2320
Pro Lys Gly Asn Pro Gly Glu Pro Gly Leu Asn Gly Thr Thr Gly Pro
2325 2330 2335
Lys Gly Ile Arg Gly Arg Arg Gly Asn Ser Gly Pro Pro Gly Ile Val
2340 2345 2350
Gly Gln Lys Gly Arg Pro Gly Tyr Pro Gly Pro Ala Gly Pro Arg Gly
2355 2360 2365
Asn Arg Gly Asp Ser Ile Asp Gln Cys Ala Leu Ile Gln Ser Ile Lys
2370 2375 2380
Asp Lys Cys Pro Cys Cys Tyr Gly Pro Leu Glu Cys Pro Val Phe Pro
2385 2390 2395 2400
Thr Glu Leu Ala Phe Ala Leu Asp Thr Ser Glu Gly Val Asn Gln Asp
2405 2410 2415
Thr Phe Gly Arg Met Arg Asp Val Val Leu Ser Ile Val Asn Val Leu
2420 2425 2430
Thr Ile Ala Glu Ser Asn Cys Pro Thr Gly Ala Arg Val Ala Val Val
2435 2440 2445
Thr Tyr Asn Asn Glu Val Thr Thr Glu Ile Arg Phe Ala Asp Ser Lys
2450 2455 2460
Arg Lys Ser Val Leu Leu Asp Lys Ile Lys Asn Leu Gln Val Ala Leu
2465 2470 2475 2480
Thr Ser Lys Gln Gln Ser Leu Glu Thr Ala Met Ser Phe Val Ala Arg
2485 2490 2495
Asn Thr Phe Lys Arg Val Arg Asn Gly Phe Leu Met Arg Lys Val Ala
2500 2505 2510
Val Phe Phe Ser Asn Thr Pro Thr Arg Ala Ser Pro Gln Leu Arg Glu

2515 2520 2525
Ala Val Leu Lys Leu Ser Asp Ala Gly Ile Thr Pro Leu Phe Leu Thr
2530 2535 2540
Arg Gln Glu Asp Arg Gln Leu Ile Asn Ala Leu Gln Ile Asn Asn Thr
2545 2550 2555 2560
Ala Val Gly His Ala Leu Val Leu Pro Ala Gly Arg Asp Leu Thr Asp
2565 2570 2575
Phe Leu Glu Asn Val Leu Thr Cys His Val Cys Leu Asp Ile Cys Asn
2580 2585 2590
Ile Asp Pro Ser Cys Gly Phe Gly Ser Trp Arg Pro Ser Phe Arg Asp
2595 2600 2605
Arg Arg Ala Ala Gly Ser Asp Val Asp Ile Asp Met Ala Phe Ile Leu
2610 2615 2620
Asp Ser Ala Glu Thr Thr Thr Leu Phe Gln Phe Asn Glu Met Lys Lys
2625 2630 2635 2640
Tyr Ile Ala Tyr Leu Val Arg Gln Leu Asp Met Ser Pro Asp Pro Lys
2645 2650 2655
Ala Ser Gln His Phe Ala Arg Val Ala Val Val Gln His Ala Pro Ser
2660 2665 2670
Glu Ser Val Ser Met Pro Pro Val Lys Val Glu Phe Ser Leu Thr Asp
2675 2680 2685
Tyr Gly Ser Lys Glu Lys Leu Val Asp Phe Leu Ser Arg Gly Met Thr
2690 2695 2700
Gln Leu Gln Gly Thr Arg Ala Leu Gly Ser Ala Ile Glu Tyr Thr Ile
2705 2710 2715 2720
Glu Asn Val Phe Glu Ser Ala Pro Asn Pro Arg Asp Leu Lys Ile Val
2725 2730 2735
Val Leu Met Leu Thr Gly Glu Val Pro Glu Gln Gln Leu Glu Glu Ala
2740 2745 2750
Gln Arg Val Ile Leu Gln Ala Lys Cys Lys Gly Tyr Phe Phe Val Val
2755 2760 2765
Leu Gly Ile Gly Arg Lys Val Asn Ile Lys Glu Val Tyr Thr Phe Ala
2770 2775 2780
Ser Glu Pro Asn Asp Val Phe Phe Lys Leu Val Asp Lys Ser Thr Glu
2785 2790 2795 2800
Leu Asn Glu Glu Pro Leu Met Arg Phe Gly Arg Leu Leu Pro Ser Phe
2805 2810 2815
Val Ser Ser Glu Asn Ala Phe Tyr Leu Ser Pro Asp Ile Arg Lys Gln
2820 2825 2830
Cys Asp Trp Phe Gln Gly Asp Gln Pro Thr Lys Asn Leu Val Lys Phe
2835 2840 2845
Gly His Lys Gln Val Asn Val Pro Asn Asn Val Thr Ser Ser Pro Thr
2850 2855 2860
Ser Asn Pro Val Thr Thr Thr Lys Pro Val Thr Thr Thr Lys Pro Val
2865 2870 2875 2880
Thr Thr Thr Thr Lys Pro Val Thr Thr Thr Thr Lys Pro Val Thr Ile
2885 2890 2895
Ile Asn Gln Pro Ser Val Lys Pro Ala Ala Ala Lys Pro Ala Pro Ala
2900 2905 2910
Lys Pro Val Ala Ala Lys Pro Val Ala Thr Lys Thr Ala Thr Val Arg
2915 2920 2925
Pro Pro Val Ala Val Lys Pro Ala Thr Ala Ala Lys Pro Val Ala Ala
2930 2935 2940
Lys Pro Ala Ala Val Arg Pro Pro Ala Ala Ala Lys Pro Val Ala
2945 2950 2955 2960
Thr Lys Pro Glu Val Pro Arg Pro Gln Ala Ala Lys Pro Ala Ala Thr
2965 2970 2975
Lys Pro Ala Thr Thr Lys Pro Val Val Lys Met Leu Arg Glu Val Gln
2980 2985 2990
Val Phe Glu Ile Thr Glu Asn Ser Ala Lys Leu His Trp Glu Arg Pro
2995 3000 3005

Glu Pro Pro Gly Pro Tyr Phe Tyr Asp Leu Thr Val Thr Ser Ala His
3010 3015 3020
Asp Gln Ser Leu Val Leu Lys Gln Asn Leu Thr Val Thr Asp Arg Val
3025 3030 3035 3040
Ile Gly Gly Leu Leu Ala Gly Gln Thr Tyr His Val Ala Val Val Cys
3045 3050 3055
Tyr Leu Arg Ser Gln Val Arg Ala Thr Tyr His Gly Ser Phe Ser Thr
3060 3065 3070
Lys Lys Ser Gln Pro Pro Pro Pro Gln Pro Ala Arg Ser Ala Ser Ser
3075 3080 3085
Ser Thr Ile Asn Leu Met Val Ser Thr Glu Pro Leu Ala Leu Thr Glu
3090 3095 3100
Thr Asp Ile Cys Lys Leu Pro Lys Asp Glu Gly Thr Cys Arg Asp Phe
3105 3110 3115 3120
Ile Leu Lys Trp Tyr Tyr Asp Pro Asn Thr Lys Ser Cys Ala Arg Phe
3125 3130 3135
Trp Tyr Gly Gly Cys Gly Gly Asn Glu Asn Lys Phe Gly Ser Gln Lys
3140 3145 3150
Glu Cys Glu Lys Val Cys Ala Pro Val Leu Ala Lys Pro Gly Val Ile
3155 3160 3165
Ser Val Met Gly Thr
3170

<210> 219
<211> 2806
<212> DNA
<213> Homo sapiens

<400> 219
ggatccagga ctgagatccc agaaccatga acctggccat cagcatcgct ctcctgctaa 60
caggtacccg gcatggggca ggactggggc tccaggcgcc ctggcttcct tccctccaga 120
gaagcagctt ctccctcaca gtctcagaaa agcgcaggtg acaaagagag ggctcttttt 180
catcctgaag tcagccgatc caccgcgctg atattctgac ggcctgaggt ggtttttgga 240
aacacagttt gctgagccct ccttcacact attgaactag aatccccaac tgagaaccca 300
ggaaccagca tcaactccct aagatctcct gtccttgaaa cacattgata ggatccaagg 360
ctcaagcaga gtggggaggg aggctggggt ctgcaaagga gaagtgggat ccctggggtg 420
gggaaaggca ctcagagagc agaccccggt cccctcccta gccaggccca tctctccact 480
tcaggtgggt gggaggcccc tgtgccgcag gcccctccag tttgaaggag gcactgctgg 540
tgccagtctt gcaggtctcc cgagggcaga aggtgaccag cctaacggcc tgcctagtgg 600
accagagcct tcgtctggac tgccgccatg agaataccag cagttcaccc atccagtacg 660
agttcagcct gacccgtgag acaaagaagc acgtgctctt tggcactgtg ggggtgcctg 720
agcacacata ccgctcccga accaacttca ccagcaaata ccacatgaag gtcctctact 780
tatccgcctt cactagcaag gacgagggca cctacacgtg tgcactccac cactctggcc 840
attccccacc catctcctcc cagaacgtca cagtgctcag aggtgagaca agcccctaac 900
aaggtcaagt gagctgggag agccaggctc ggggacagca ggcagttccc ttggctggac 960
tagagaggag aatagcccca taacgctctc accctctccc aactgctgcc tggtcaactg 1020
gggaaccatt gccttcggtg tgaatggggt gaagagctca gggccagaca ggcagagcag 1080
tgtggttcca ccagaactgt gggcaaggcc tttggcccct aatcttcctt ctcccagcgg 1140
gaaacaggga tgacaccacc tccctcagcc agttttcttg tcatgatgtt tagtaaggtt 1200
ttcataagat gatatgtgtg caagagatca gtaatctgca aatgggaaag atggctggtt 1260
ctgtgagacc aggctgttcc tggtcccagc taagacattg cagtacccac ctcccaaagg 1320
gagtacaccc ttgctttggg cctgtgcctg cctgagtcct gatccgtctt ccttcctacc 1380
ctgcccccgg ccccctctc tttctgcaga caaactggtc aagtgtgagg gcatcagcct 1440
gctggctcag aacacctcgt ggctgctgct gctcctgctg tccctctccc tcctccaggc 1500
cacggatttc atgtccctgt gactggtggg gcccatggag gagacaggaa gcctcaagtt 1560
ccagtgcaga gatcctactt ctctgagtca gctgaccccc tccccccaat ccctcaaacc 1620
ttgaggagaa gtggggaccc cacccctcat caggagttcc agtgctgcat gcgattatct 1680
acccacgtcc acgcggccac ctcaccctct ccgcacacct ctggctgtct ttttgtactt 1740
tttgttccag agctgcttct gtctggttta tttaggtttt atccttcctt ttctttgaga 1800
gttcgtgaag agggaagcca ggattgggga cctgatggag agtgagagca tgtgaggggt 1860
agtgggatgg tggggtacca gccactggag gggtcatcct tgcccatcgg gaccagaaac 1920

```
ctgggagaga cttggatgag gagtggttgg gctgtgctgg gcctagcacg gacatggtct    1980
gtcctgacag cactcctcgg caggcatggc tggtgcctga agaccccaga tgtgagggca    2040
ccaccaagaa tttgtggcct accttgtgag ggagagaact gaggatctcc agcattctca    2100
gccacaacca aaaaaaaata aaaagggcag ccctccttac cactgtggaa gtccctcaga    2160
ggccttgggg catgacccag tgaagatgca ggtttgacca ggaaagcagc gctagtggag    2220
ggttggagaa ggaggtaaag gatgagggtt catcatccct ccctgcctaa ggaagctaaa    2280
agcatggccc tgctgcccct ccctgcctcc acccacagtg gagagggcta caaaggagga    2340
caagaccctc tcaggctgtc ccaagctccc aagagcttcc agagctctga cccacagcct    2400
ccaagtcagg tggggtggag tcccagagct gcacagggtt tggcccaagt ttctaaggga    2460
ggcacttcct cccctcgccc atcagtgcca gcccctgctg gctggtgcct gagcccctca    2520
gacagccccc tgccccgcag gcctgccttc tcagggactt ctgcggggcc tgaggcaagc    2580
catggagtga gacccaggag ccggacactt ctcaggaaat ggcttttccc aacccccagc    2640
ccccacccgg tggttcttcc tgttctgtga ctgtgtatag tgccaccaca gcttatggca    2700
tctcattgag gacaaagaaa actgcacaat aaaaccaagc ctctggaatc tgtcctcgtg    2760
tccacctggc cttcgctcct ccagcagtgc ctgcctgccc ccgctt                   2806
```

<210> 220
<211> 161
<212> PRT
<213> Homo sapiens

<400> 220

```
Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Leu Thr Val Leu Gln Val
1               5                   10                  15
Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln
            20                  25                  30
Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile
        35                  40                  45
Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe
    50                  55                  60
Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe
65                  70                  75                  80
Thr Ser Lys Tyr His Met Lys Val Leu Tyr Leu Ser Ala Phe Thr Ser
                85                  90                  95
Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His Ser Gly His Ser
            100                 105                 110
Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg Asp Lys Leu Val
        115                 120                 125
Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr Ser Trp Leu Leu
    130                 135                 140
Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr Asp Phe Met Ser
145                 150                 155                 160
Leu
```

<210> 221
<211> 736
<212> DNA
<213> Homo sapiens

<400> 221

```
ggctctcacc ctcctctcct gcagctccag ctctgtgctc tgcctctgag gagaccatgg     60
cccggcctct gtgtaccctg ctactcctga tggctaccct ggctggggct ctggcctcga    120
gctccaagga ggagaatagg ataatcccag gtggcatcta tgatgcagac ctcaatgatg    180
agtgggtaca gcgtgccctt cacttcgcca tcagcgagta caacaaggcc accgaagatg    240
agtactacag acgcccgctg caggtgctgc gagccaggga gcagaccttt ggggggggtga    300
attacttctt cgacgtagag gtgggccgca ccatatgtac caagtcccag cccaacttgg    360
acacctgtgc cttccatgaa cagccagaac tgcagaagaa acagttatgc tctttcgaga    420
tctacgaagt tccctgggag gacagaatgt ccctggtgaa ttccaggtgt caagaagcct    480
aggggtctgt gccaggccag tcacaccgac caccacccac tcccaccccc tgtagtgctc    540
ccacccctgg actggtggcc cccaccctgc gggaggcctc cccatgtgcc tgtgccaaga    600
```

gacagacaga gaaggctgca ggagtccttt gttgctcagc agggcgctct gccctccctc 660
cttccttctt gcttctaata gacctggtac atggtacaca caccccacc tcctgcaatt 720
aaacagtagc atcgcc 736

<210> 222
<211> 594
<212> DNA
<213> Homo sapiens

<400> 222
cccaccctgg gacaggctct caccctcctc tcctgcagct ccagctttgt gctctgcctc 60
tgaggagacc atggcccagc atctgagtac cctgctgctc ctgctggcca ccctagctgt 120
ggccctggcc tggagcccca aggaggagga taggataatc ccgggtggca tctataacgc 180
agacctcaat gatgagtggg tacagcgtgc ccttcacttc gccatcagcg agtataacaa 240
ggccaccaaa gatgactact acagacgtcc gctgcgggta ctaagagcca ggcaacagac 300
cgttgggggg gtgaattact tcttcgacgt agaggtgggc cgaaccatat gtaccaagtc 360
ccagcccaac ttggacacct gtgccttcca tgaacagcca gaactgcaga agaaacagtt 420
gtgctctttc gagatctacg aagttccctg ggagaacaga aggtccctgg tgaaatccag 480
gtgtcaagaa tcctagggat ctgtgccagg ccattcgcac cagccaccac ccactcccac 540
cccctgtagt gctcccaccc ctgggggcca atgggactgt gcaggagaca gcgg 594

<210> 223
<211> 141
<212> PRT
<213> Homo sapiens

<400> 223
Met Ala Arg Pro Leu Cys Thr Leu Leu Leu Leu Met Ala Thr Leu Ala
1 5 10 15
Gly Ala Leu Ala Ser Ser Ser Lys Glu Glu Asn Arg Ile Ile Pro Gly
20 25 30
Gly Ile Tyr Asp Ala Asp Leu Asn Asp Glu Trp Val Gln Arg Ala Leu
35 40 45
His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Glu Asp Glu Tyr Tyr
50 55 60
Arg Arg Pro Leu Gln Val Leu Arg Ala Arg Glu Gln Thr Phe Gly Gly
65 70 75 80
Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
85 90 95
Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
100 105 110
Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
115 120 125
Asp Arg Met Ser Leu Val Asn Ser Arg Cys Gln Glu Ala
130 135 140

<210> 224
<211> 141
<212> PRT
<213> Homo sapiens

<400> 224
Met Ala Gln His Leu Ser Thr Leu Leu Leu Leu Leu Ala Thr Leu Ala
1 5 10 15
Val Ala Leu Ala Trp Ser Pro Lys Glu Glu Asp Arg Ile Ile Pro Gly
20 25 30
Gly Ile Tyr Asn Ala Asp Leu Asn Asp Glu Trp Val Gln Arg Ala Leu
35 40 45
His Phe Ala Ile Ser Glu Tyr Asn Lys Ala Thr Lys Asp Asp Tyr Tyr
50 55 60
Arg Arg Pro Leu Arg Val Leu Arg Ala Arg Gln Gln Thr Val Gly Gly

```
65                  70                  75                  80
Val Asn Tyr Phe Phe Asp Val Glu Val Gly Arg Thr Ile Cys Thr Lys
                85                  90                  95
Ser Gln Pro Asn Leu Asp Thr Cys Ala Phe His Glu Gln Pro Glu Leu
            100                 105                 110
Gln Lys Lys Gln Leu Cys Ser Phe Glu Ile Tyr Glu Val Pro Trp Glu
        115                 120                 125
Asn Arg Arg Ser Leu Val Lys Ser Arg Cys Gln Glu Ser
    130                 135                 140

      <210> 225
      <211> 5460
      <212> DNA
      <213> Homo sapiens

      <400> 225
cgggcccggt gctgaagggc agggaacaac ttgatggtgc tactttgaac tgcttttctt      60
ttctcctttt tgcacaaaga gtctcatgtc tgatatttag acatgatgag ctttgtgcaa     120
aaggggagct ggctacttct cgctctgctt catcccacta ttattttggc acaacaggaa     180
gctgttgaag gaggatgttc ccatcttggt cagtcctatg cggatagaga tgtctggaag     240
ccagaaccat gccaaatatg tgtctgtgac tcaggatccg ttctctgcga tgacataata     300
tgtgacgatc aagaattaga ctgccccaac ccagaaattc catttggaga atgttgtgca     360
gtttgcccac agcctccaac tgctcctact cgccctccta atggtcaagg acctcaaggc     420
cccaagggag atccaggccc tcctggtatt cctgggagaa atggtgaccc tggtattcca     480
ggacaaccag ggtcccctgg ttctcctggc cccccctggaa tctgtgaatc atgccctact     540
ggtcctcaga actattctcc ccagtatgat tcatatgatg tcaagtctgg agtagcagta     600
ggaggactcg caggctatcc tggaccagct ggccccccag gccctcccgg tccccctggt     660
acatctggtc atcctggttc ccctggatct ccaggatacc aaggaccccc tggtgaacct     720
gggcaagctg gtccttcagg ccctccagga cctcctggtg ctataggtcc atctggtcct     780
gctggaaaag atggagaatc aggtagaccc ggacgacctg gagagcgagg attgcctgga     840
cctccaggta tcaaaggtcc agctgggata cctggattcc ctggtatgaa aggacacaga     900
ggcttcgatg gacgaaatgg agaaaagggt gaaacaggtg ctcctggatt aaagggtgaa     960
aatggtcttc caggcgaaaa tggagctcct ggacccatgg gtccaagagg ggctcctggt    1020
gagcgaggac ggccaggact tcctggggct gcaggtgctc ggggtaatga cggtgctcga    1080
ggcagtgatg gtcaaccagg ccctcctggt cctcctggaa ctgccggatt ccctggatcc    1140
cctggtgcta agggtgaagt tggacctgca gggtctcctg gttcaaatgg tgcccctgga    1200
caaagaggag aacctggacc tcagggacac gctggtgctc aaggtcctcc tggccctcct    1260
gggattaatg gtagtcctgg tggtaaaggc gaaatgggtc ccgctggcat tcctggagct    1320
cctggactga tgggagcccg gggtcctcca ggaccagccg gtgctaatgg tgctcctgga    1380
ctgcgaggtg gtgcaggtga gcctggtaag aatggtgcca aggagagccc ggaccacgt     1440
ggtgaacgcg gtgaggctgg tattccaggt gttccaggag ctaaaggcga agatggcaag    1500
gatggatcac ctggagaacc tggtgcaaat gggcttccag gagctgcagg agaaaggggt    1560
gcccctgggt tccgaggacc tgctggacca aatggcatcc caggagaaaa gggtcctgct    1620
ggagagcgtg gtgctccagg ccctgcaggg cccagaggag ctgctggaga acctggcaga    1680
gatggcgtcc ctggaggtcc aggaatgagg ggcatgcccg gaagtccagg aggaccagga    1740
agtgatggga aaccagggcc tcccggaagt caaggagaaa gtggtcgacc aggtcctcct    1800
gggccatctg gtccccgagg tcagcctggt gtcatgggct tccccggtcc taaaggaaat    1860
gatggtgctc ctggtaagaa tggagaacga ggtggccctg gaggacctgg ccctcagggt    1920
cctcctggaa agaatggtga aactggacct caaggacccc cagggcctac tgggcctggt    1980
ggtgacaaag gagacacagg acccccctggt ccacaaggat tacaaggctt gcctggtaca    2040
ggtggtcctc caggagaaaa tggaaaacct ggggaaccag gtccaaaggg tgatgccggt    2100
gcacctggag ctccaggagg caagggtgat gctggtgccc ctggtgaacg tggacctcct    2160
ggattggcag gggccccagg acttagaggt ggagctggtc cccctggtcc cgaaggagga    2220
aagggtgctg ctggtcctcc tgggccacct ggtgctgctg gtactcctgg tctgcaagga    2280
atgcctggag aaagaggagg tcttggaagt cctggtccaa agggtgacaa gggtgaacca    2340
ggcggcccag gtgctgatgg tgtcccaggg aaagatggcc caaggggtcc tactggtcct    2400
attggtcctc ctggcccagc tggccagcct ggagataagg gtgaaggtgg tgcccccgga    2460
cttccaggta tagctggacc tcgtggtagc cctggtgaga gaggtgaaac tggccctcca    2520
ggacctgctg gtttccctgg tgctcctgga cagaatggtg aacctggtgg taaaggagaa    2580
agaggggctc cgggtgagaa aggtgaagga ggccctcctg gagttgcagg acccccctgga    2640
ggttctggac ctgctggtcc tcctggtccc caaggtgtca aaggtgaacg tggcagtcct    2700
```

```
ggtggacctg gtgctgctgg cttccctggt gctcgtggtc ttcctggtcc tcctggtagt   2760
aatggtaacc caggaccccc aggtcccagc ggttctccag gcaaggatgg gcccccaggt   2820
cctgcgggta acactggtgc tcctggcagc cctggagtgt ctggaccaaa aggtgatgct   2880
ggccaaccag gagagaaggg atcgcctggt gcccagggcc caccaggagc tccaggccca   2940
cttgggattg ctgggatcac tggagcacgg ggtcttgcag gaccaccagg catgccaggt   3000
cctaggggaa gccctggccc tcagggtgtc aagggtgaaa gtgggaaacc aggagctaac   3060
ggtctcagtg gagaacgtgg tccccctgga ccccagggtc ttcctggtct ggctggtaca   3120
gctggtgaac ctggaagaga tggaaaccct ggatcagatg gtcttccagg ccgagatgga   3180
tctcctggtg gcaagggtga tcgtggtgaa aatggctctc ctggtgcccc tggcgctcct   3240
ggtcatccag gcccacctgg tcctgtcggt ccagctggaa agagtggtga cagaggagaa   3300
agtggccctg ctggccctgc tggtgctccc ggtcctgctg gttcccgagg tgctcctggt   3360
cctcaaggcc cacgtggtga caaaggtgaa acaggtgaac gtggagctgc tggcatcaaa   3420
ggacatcgag gattccctgg taatccaggt gccccaggtt ctccaggccc tgctggtcag   3480
cagggtgcaa tcggcagtcc aggacctgca ggccccagag gacctgttgg acccagtgga   3540
cctcctggca aagatggaac cagtggacat ccaggtccca ttggaccacc agggcctcga   3600
ggtaacagag gtgaaagagg atctgagggc tccccaggcc acccagggca accaggccct   3660
cctggacctc ctggtgcccc tggtccttgc tgtggtggtg ttggagccgc tgccattgct   3720
gggattggag gtgaaaaagc tggcggtttt gccccgtatt atggagatga accaatggat   3780
ttcaaaatca acaccgatga gattatgact tcactcaagt ctgttaatgg acaaatagaa   3840
agcctcatta gtcctgatgg ttctcgtaaa aaccccgcta gaaactgcag agacctgaaa   3900
ttctgccatc ctgaactcaa gagtggagaa tactgggttg accctaacca aggatgcaaa   3960
ttggatgcta tcaaggtatt ctgtaatatg gaaactgggg aaacatgcat aagtgccaat   4020
cctttgaatg ttccacggaa acactggtgg acagattcta gtgctgagaa gaaacacgtt   4080
tggtttggag agtccatgga tggtggtttt cagtttagct acggcaatcc tgaacttcct   4140
gaagatgtcc ttgatgtgca gctggcattc cttcgacttc tctccagccg agcttcccag   4200
aacatcacat atcactgcaa aaatagcatt gcatacatgg atcaggccag tggaaatgta   4260
aagaaggccc tgaagctgat ggggtcaaat gaaggtgaat tcaaggctga aggaaatagc   4320
aaattcacct acacagttct ggaggatggt tgcacgaaac acactgggga atggagcaaa   4380
acagtctttg aatatcgaac acgcaaggct gtgagactac ctattgtaga tattgcaccc   4440
tatgacattg gtggtcctga tcaagaattt ggtgtggacg ttggccctgt ttgcttttta   4500
taaaccaaac tctatctgaa atcccaacaa aaaaaattta actccatatg tgttcctctt   4560
gttctaatct tgtcaaccag tgcaagtgac cgacaaaatt ccagttattt atttccaaaa   4620
tgtttggaaa cagtataatt tgacaaagaa aaatgatact tctctttttt tgctgttcca   4680
ccaaatacaa ttcaaatgct tttgtttta ttttttacc aattccaatt tcaaaatgtc   4740
tcaatggtgc tataataaat aaacttcaac actctttatg ataacaacac tgtgttatat   4800
tctttgaatc ctagcccatc tgcagagcaa tgactgtgct caccagtaaa agataacctt   4860
tctttctgaa atagtcaaat acgaaattag aaaagccctc cctattttaa ctacctcaac   4920
tggtcagaaa cacagattgt attctatgag tcccagaaga tgaaaaaaat tttatacgtt   4980
gataaaactt ataaatttca ttgattaatc tcctggaaga ttggtttaaa aagaaaagtg   5040
taatgcaaga atttaaagaa atattttaa agccacaatt attttaatat tggatatcaa   5100
ctgcttgtaa aggtgctcct cttttttctt gtcattgctg gtcaagatta ctaatatttg   5160
ggaaggcttt aaagacgcat gttatggtgc taatgtactt tcacttttaa actctagatc   5220
agaattgttg acttgcattc agaacataaa tgcacaaaat ctgtacatgt ctcccatcag   5280
aaagattcat tggcatgcca cagggattct cctccttcat cctgtaaagg tcaacaataa   5340
aaaccaaatt atggggctgc ttttgtcaca ctagcataga gaatgtgttg aaatttaact   5400
ttgtaagctt gtatgtggtt gttgatcttt tttttcctta cagacaccca taataaaata   5460
```

<210> 226
<211> 1466
<212> PRT
<213> Homo sapiens

<400> 226

```
Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala Leu Leu
1               5                   10                  15
His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly Gly Cys
            20                  25                  30
Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys Pro Glu
```

```
        35                  40                  45
Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys Asp Asp
    50                  55                  60
Ile Ile Cys Asp Asp Gln Glu Leu Asp Cys Pro Asn Pro Glu Ile Pro
65                  70                  75                  80
Phe Gly Glu Cys Cys Ala Val Cys Pro Gln Pro Pro Thr Ala Pro Thr
                85                  90                  95
Arg Pro Pro Asn Gly Gln Gly Pro Gln Gly Pro Lys Gly Asp Pro Gly
            100                 105                 110
Pro Pro Gly Ile Pro Gly Arg Asn Gly Asp Pro Gly Ile Pro Gly Gln
        115                 120                 125
Pro Gly Ser Pro Gly Ser Pro Gly Pro Pro Gly Ile Cys Glu Ser Cys
    130                 135                 140
Pro Thr Gly Pro Gln Asn Tyr Ser Pro Gln Tyr Asp Ser Tyr Asp Val
145                 150                 155                 160
Lys Ser Gly Val Ala Val Gly Gly Leu Ala Gly Tyr Pro Gly Pro Ala
                165                 170                 175
Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Thr Ser Gly His Pro Gly
            180                 185                 190
Ser Pro Gly Ser Pro Gly Tyr Gln Gly Pro Pro Gly Glu Pro Gly Gln
        195                 200                 205
Ala Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly Ala Ile Gly Pro Ser
    210                 215                 220
Gly Pro Ala Gly Lys Asp Gly Glu Ser Gly Arg Pro Gly Arg Pro Gly
225                 230                 235                 240
Glu Arg Gly Leu Pro Gly Pro Pro Gly Ile Lys Gly Pro Ala Gly Ile
                245                 250                 255
Pro Gly Phe Pro Gly Met Lys Gly His Arg Gly Phe Asp Gly Arg Asn
            260                 265                 270
Gly Glu Lys Gly Glu Thr Gly Ala Pro Gly Leu Lys Gly Glu Asn Gly
        275                 280                 285
Leu Pro Gly Glu Asn Gly Ala Pro Gly Pro Met Gly Pro Arg Gly Ala
    290                 295                 300
Pro Gly Glu Arg Gly Arg Pro Gly Leu Pro Gly Ala Ala Gly Ala Arg
305                 310                 315                 320
Gly Asn Asp Gly Ala Arg Gly Ser Asp Gly Gln Pro Gly Pro Pro Gly
                325                 330                 335
Pro Pro Gly Thr Ala Gly Phe Pro Gly Ser Pro Gly Ala Lys Gly Glu
            340                 345                 350
Val Gly Pro Ala Gly Ser Pro Gly Ser Asn Gly Ala Pro Gly Gln Arg
        355                 360                 365
Gly Glu Pro Gly Pro Gln Gly His Ala Gly Ala Gln Gly Pro Pro Gly
    370                 375                 380
Pro Pro Gly Ile Asn Gly Ser Pro Gly Gly Lys Gly Glu Met Gly Pro
385                 390                 395                 400
Ala Gly Ile Pro Gly Ala Pro Gly Leu Met Gly Ala Arg Gly Pro Pro
                405                 410                 415
Gly Pro Ala Gly Ala Asn Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly
            420                 425                 430
Glu Pro Gly Lys Asn Gly Ala Lys Gly Glu Pro Gly Pro Arg Gly Glu
        435                 440                 445
Arg Gly Glu Ala Gly Ile Pro Gly Val Pro Gly Ala Lys Gly Glu Asp
    450                 455                 460
Gly Lys Asp Gly Ser Pro Gly Glu Pro Gly Ala Asn Gly Leu Pro Gly
465                 470                 475                 480
Ala Ala Gly Glu Arg Gly Ala Pro Gly Phe Arg Gly Pro Ala Gly Pro
                485                 490                 495
Asn Gly Ile Pro Gly Glu Lys Gly Pro Ala Gly Glu Arg Gly Ala Pro
            500                 505                 510
Gly Pro Ala Gly Pro Arg Gly Ala Ala Gly Glu Pro Gly Arg Asp Gly
        515                 520                 525
```

Val Pro Gly Gly Pro Gly Met Arg Gly Met Pro Gly Ser Pro Gly Gly
530 535 540
Pro Gly Ser Asp Gly Lys Pro Gly Pro Pro Gly Ser Gln Gly Glu Ser
545 550 555 560
Gly Arg Pro Gly Pro Pro Gly Pro Ser Gly Pro Arg Gly Gln Pro Gly
565 570 575
Val Met Gly Phe Pro Gly Pro Lys Gly Asn Asp Gly Ala Pro Gly Lys
580 585 590
Asn Gly Glu Arg Gly Gly Pro Gly Gly Pro Gly Pro Gln Gly Pro Pro
595 600 605
Gly Lys Asn Gly Glu Thr Gly Pro Gln Gly Pro Pro Gly Pro Thr Gly
610 615 620
Pro Gly Gly Asp Lys Gly Asp Thr Gly Pro Pro Gly Pro Gln Gly Leu
625 630 635 640
Gln Gly Leu Pro Gly Thr Gly Gly Pro Pro Gly Glu Asn Gly Lys Pro
645 650 655
Gly Glu Pro Gly Pro Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly
660 665 670
Gly Lys Gly Asp Ala Gly Ala Pro Gly Glu Arg Gly Pro Pro Gly Leu
675 680 685
Ala Gly Ala Pro Gly Leu Arg Gly Gly Ala Gly Pro Pro Gly Pro Glu
690 695 700
Gly Gly Lys Gly Ala Ala Gly Pro Pro Gly Pro Pro Gly Ala Ala Gly
705 710 715 720
Thr Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Gly Leu Gly Ser
725 730 735
Pro Gly Pro Lys Gly Asp Lys Gly Glu Pro Gly Gly Pro Gly Ala Asp
740 745 750
Gly Val Pro Gly Lys Asp Gly Pro Arg Gly Pro Thr Gly Pro Ile Gly
755 760 765
Pro Pro Gly Pro Ala Gly Gln Pro Gly Asp Lys Gly Glu Gly Gly Ala
770 775 780
Pro Gly Leu Pro Gly Ile Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg
785 790 795 800
Gly Glu Thr Gly Pro Pro Gly Pro Ala Gly Phe Pro Gly Ala Pro Gly
805 810 815
Gln Asn Gly Glu Pro Gly Gly Lys Gly Glu Arg Gly Ala Pro Gly Glu
820 825 830
Lys Gly Glu Gly Gly Pro Pro Gly Val Ala Gly Pro Pro Gly Gly Ser
835 840 845
Gly Pro Ala Gly Pro Pro Gly Pro Gln Gly Val Lys Gly Glu Arg Gly
850 855 860
Ser Pro Gly Gly Pro Gly Ala Ala Gly Phe Pro Gly Ala Arg Gly Leu
865 870 875 880
Pro Gly Pro Pro Gly Ser Asn Gly Asn Pro Gly Pro Pro Gly Pro Ser
885 890 895
Gly Ser Pro Gly Lys Asp Gly Pro Pro Gly Pro Ala Gly Asn Thr Gly
900 905 910
Ala Pro Gly Ser Pro Gly Val Ser Gly Pro Lys Gly Asp Ala Gly Gln
915 920 925
Pro Gly Glu Lys Gly Ser Pro Gly Ala Gln Gly Pro Pro Gly Ala Pro
930 935 940
Gly Pro Leu Gly Ile Ala Gly Ile Thr Gly Ala Arg Gly Leu Ala Gly
945 950 955 960
Pro Pro Gly Met Pro Gly Pro Arg Gly Ser Pro Gly Pro Gln Gly Val
965 970 975
Lys Gly Glu Ser Gly Lys Pro Gly Ala Asn Gly Leu Ser Gly Glu Arg
980 985 990
Gly Pro Pro Gly Pro Gln Gly Leu Pro Gly Leu Ala Gly Thr Ala Gly
995 1000 1005
Glu Pro Gly Arg Asp Gly Asn Pro Gly Ser Asp Gly Leu Pro Gly Arg

1010 1015 1020
Asp Gly Ser Pro Gly Gly Lys Gly Asp Arg Gly Glu Asn Gly Ser Pro
1025 1030 1035 1040
Gly Ala Pro Gly Ala Pro Gly His Pro Gly Pro Pro Gly Pro Val Gly
1045 1050 1055
Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Ser Gly Pro Ala Gly Pro
1060 1065 1070
Ala Gly Ala Pro Gly Pro Ala Gly Ser Arg Gly Ala Pro Gly Pro Gln
1075 1080 1085
Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Arg Gly Ala Ala Gly
1090 1095 1100
Ile Lys Gly His Arg Gly Phe Pro Gly Asn Pro Gly Ala Pro Gly Ser
1105 1110 1115 1120
Pro Gly Pro Ala Gly Gln Gln Gly Ala Ile Gly Ser Pro Gly Pro Ala
1125 1130 1135
Gly Pro Arg Gly Pro Val Gly Pro Ser Gly Pro Pro Gly Lys Asp Gly
1140 1145 1150
Thr Ser Gly His Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Asn
1155 1160 1165
Arg Gly Glu Arg Gly Ser Glu Gly Ser Pro Gly His Pro Gly Gln Pro
1170 1175 1180
Gly Pro Pro Gly Pro Pro Gly Ala Pro Gly Pro Cys Cys Gly Gly Val
1185 1190 1195 1200
Gly Ala Ala Ala Ile Ala Gly Ile Gly Gly Glu Lys Ala Gly Gly Phe
1205 1210 1215
Ala Pro Tyr Tyr Gly Asp Glu Pro Met Asp Phe Lys Ile Asn Thr Asp
1220 1225 1230
Glu Ile Met Thr Ser Leu Lys Ser Val Asn Gly Gln Ile Glu Ser Leu
1235 1240 1245
Ile Ser Pro Asp Gly Ser Arg Lys Asn Pro Ala Arg Asn Cys Arg Asp
1250 1255 1260
Leu Lys Phe Cys His Pro Glu Leu Lys Ser Gly Glu Tyr Trp Val Asp
1265 1270 1275 1280
Pro Asn Gln Gly Cys Lys Leu Asp Ala Ile Lys Val Phe Cys Asn Met
1285 1290 1295
Glu Thr Gly Glu Thr Cys Ile Ser Ala Asn Pro Leu Asn Val Pro Arg
1300 1305 1310
Lys His Trp Trp Thr Asp Ser Ser Ala Glu Lys Lys His Val Trp Phe
1315 1320 1325
Gly Glu Ser Met Asp Gly Gly Phe Gln Phe Ser Tyr Gly Asn Pro Glu
1330 1335 1340
Leu Pro Glu Asp Val Leu Asp Val Gln Leu Ala Phe Leu Arg Leu Leu
1345 1350 1355 1360
Ser Ser Arg Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile
1365 1370 1375
Ala Tyr Met Asp Gln Ala Ser Gly Asn Val Lys Lys Ala Leu Lys Leu
1380 1385 1390
Met Gly Ser Asn Glu Gly Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe
1395 1400 1405
Thr Tyr Thr Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp
1410 1415 1420
Ser Lys Thr Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro
1425 1430 1435 1440
Ile Val Asp Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu Phe
1445 1450 1455
Gly Val Asp Val Gly Pro Val Cys Phe Leu
1460 1465

<210> 227
<211> 6663
<212> DNA

<213> Homo sapiens

<400> 227
ccccgactag cccgacagtc cccgactagc ccgacagccc cagcaggatc tgcatcgtca 60
tcgagccggc ccagcttctg aagggagatg tcatggtgaa atgctaccac aagaaatacc 120
gctcggccac ccgtgacgtc attttccgcc tgcagtttca cactggggct gtgcagggct 180
acggctggt gtttgggaag gaggatctgg acaatgccag caaagatgac cgttttcctg 240
actatgggaa ggttgaatta gtcttctctg ccacgcctga gaagattcaa gggtccgaac 300
acttgtacaa cgaccacggt gtgattgtgg actacaacac aacagaccca ctgatacgct 360
gggactcgta cgagaacctc agtgcagatg gagaagtgct acacacgcag ggccctgtcg 420
atggcagcct ttacgcgaag gtgaggaaga aaagctcctc ggatcctggc atcccaggtg 480
gccccccaggc aatcccggcc accaacagcc cagaccacag tgaccacacc ttgtctgtca 540
gcagtgactc cggccactct acagcctctg ccaggacgga taagacggaa gagcgcctgg 600
ccccaggaac caggaggggc ctgagtgccc aggagaaggc agagttggac cagctgctca 660
gtggctttgg cctggaagat cctggaagct ccctcaagga aatgactgat gctcgaagca 720
agtacagtgg gacccgccac gtggtgccag cccaggttca cgtgaatgga gacgctgctc 780
tgaaggatcg ggagacagac attctggatg acgagatgcc ccaccacgac ctgcacagtg 840
tggacagcct tgggaccctg tcctcctcgg aagggcctca gtcggcccac ctgggtccct 900
tcacctgcca caagagcagc cagaactcac tcctatctga cggttttggc agcaacgttg 960
gtgaagatcc gcagggcacc ctcgttccgg acctgggcct tggcatggac ggcccctatg 1020
agcgggagcg gacttttggg agtcgagagc ccaagcagcc ccagcccctg ctgagaaagc 1080
cctcagtgtc cgcccagatg caggcctatg ggcagagcag ctactccaca cagacctggg 1140
tgcgccagca gcagatggtt gtagctcacc agtatagctt cgccccagat ggggaggccc 1200
ggctggtgag ccgctgccct gcagacaatc ctggcctcgt ccaggcccag cccagagtgc 1260
cactcacccc cacccgaggg accagcagta gggtggctgt ccagaggggt gtaggcagtg 1320
ggccacatcc ccctgacaca cagcagccct ctcccagcaa agcgttcaaa cccaggtttc 1380
caggagacca ggttgtgaat ggagccggcc cagagctgag cacaggcccc tccccaggct 1440
cgcccaccct ggacatcgac cagtccatcg agcagctcaa caggctgatc ctggagctgg 1500
atcccacctt cgagcccatc cctacccaca tgaacgccct cggtagccag gccaatggct 1560
ctgtgtctcc agacagcgtg ggaggtgggc tccgggcaag cagcaggctg cctgacacag 1620
gagagggccc cagcagggcc accgggcggc aaggctcctc tgctgaacag cccctgggcg 1680
ggagactcag gaagctgagc ctggggcagt acgacaacga tgctgggggg cagctgccct 1740
tctccaaatg tgcatgggga aaggctggtg tggactatgc ccccaaacctg ccgccattcc 1800
cctcaccagc ggacgtcaaa gagacgatga ccccctggcta tccccaggac ctcgatatta 1860
tcgatggcag aattttaagt agcaaggagt ccatgtgttc aactccagca tttcctgtgt 1920
ctccagagac accgtatgtg aaaacagcgc tgcgccatcc tccgttcagc ccacctgagc 1980
ccccgctgag cagcccagcc agtcagcaca aaggaggacg tgaaccacga agctgccctg 2040
agacgctcac tcacgctgtg gggatgtcag agagccccat cggacccaaa tccacgatgc 2100
tccgggctga tgcgtcctcg acgccctcct ttcagcaggc ttttgcttct tcctgcacca 2160
tttccagcaa cggccctggg cagaggagag agagctcctc ttctgcagaa cgccagtggg 2220
tggagagcag ccccaagccc atggtttccc tgctggggag cggccggccc acggaagtc 2280
ccctcagcgc tgagttctcc ggtaccagga aggactcccc agtgctgtcc tgcttcccgc 2340
cgtcagagct ccaggctcct ttccacagcc atgagctgtc cctagcagag ccaccggact 2400
ccctggcgcc tcccagcagc caggccttcc tgggcttcgg caccgcccca gtgggaagtg 2460
gccttccgcc cgaggaggac ctggggggcct tgctggccaa ttctcatgga gcgtcaccga 2520
cccccagcat cccgctgaca gcgacagggg ctgccgacaa tggcttcctg tcccacaact 2580
ttctcacggt ggcgcctgga cacagcagcc accacagtcc aggcctgcag ggccagggtg 2640
tgaccctgcc cgggcagcca cccctccctg agaagaagcg ggcctcggag ggggatcgtt 2700
ctttgggctc agtctctccc tcctccagtg gcttctccag cccgcacagc gggagcacca 2760
tcagtatccc cttcccaaat gtccttcccg acttttccaa ggcttcagaa gcggcctcac 2820
ctctgccaga tagtccaggt gataaacttg tgatcgtgaa atttgttcaa gacacttcca 2880
agttctggta caaggcggat atttcaagag aacaagccat cgccatgttg aaggacaagg 2940
agccgggctc attcattgtt cgagacagcc attccttccg aggggcctat ggcctggcca 3000
tgaaggtggc cacgccccca ccttcagtcc tgcagctgaa caagaaagct ggagatttgg 3060
ccaatgaact cgtccggcac tttttgatcg agtgtacccc gaagggagtg cggttgaaag 3120
ggtgctcgaa tgaaccatat ttcgggagcc tgacggcctt ggtgtgccag cattccatca 3180
cgccccttggc cttgccgtgc aagctgctta tcccagagag agatccattg gaggaaatag 3240
cagaaagttc tccccagacg gcagccaatt cagcagctga gctgttgaag caggggggcag 3300
cctgcaacgt gtggtacttg aactctgtgg agatggagtc cctcaccggc caccaggcga 3360
tccagaaggc cctgagcatc accctggtcc aggagcctcc acctgtgtcc acagttgtgc 3420
acttcaaggt gtcagcccag ggcatcaccc tgacagacaa tcagaggaag ctcttcttcc 3480

```
ggaggcatta ccccgtgaac agtgtgattt tctgtgcctt ggacccacaa gacaggaagt   3540
ggatcaaaga tggcccttcc tcaaaagtct ttggatttgt ggcccggaag cagggcagtg   3600
ccacggataa tgtgtgccac ctgtttgcag agcatgaccc tgagcagcct gccagtgcca   3660
ttgtcaactt cgtatcaaag gtcatgattg gttccccaaa gaaggtctga gaactcccct   3720
ccctccctgg acccaccgat gcctctcgaa gccctggaga cagccgttgg gtgagggtgg   3780
ggcccccact ttttaccaaa ctagtaaacc tgacattcca ggcccatgag gggaaagagg   3840
atcttccagc tctgcaaaaa caagaacaaa caacatcacc gtgaattggc ctttcctgaa   3900
agtgacttat ctgacacatc tctgtagcca catgcttttt gggtagaaga agctgggcat   3960
gggtgcaccc caccccctag ggtccccatg ggaaagggac atgcaaggaa acagcacaga   4020
acacgaggtg gtccccatgt ccctggcaca ctagcattcc gggggatgag gaatccccag   4080
cccttgaggc agaggtgccg agtgactgcc atgcttcgcc cgtccgcatg ggcgcttctg   4140
tccagctgca cccgaggccg gggtttccc tcacctcggt cttcccaaga tggagatgct   4200
aacgaaactg agaaggggc gtatgtttga cgaaggtttg tgcaagtcag gcccttctgg   4260
aacacagcag ggcctacaac gaggggcctt tgcgatgggc tgtgaggatg gggtggtgg   4320
gaagaattgg ccacgttaga gaccccatgc caccccacca tggtgagtgc tctgtgcctc   4380
ctgctcacct gtggtgagct gggcgagctg ggcgagctgg gcgagctggg ctggggagag   4440
cctgtgagga ccgagaggag aaatgagaag aaggaacaaa aatattattt ctatgtaatt   4500
tatattttac ttatgccaaa ttatttatga taatttgcca ttgctatact gtaccagtgt   4560
caaatgctgc agcctgccaa gctgtgattt tgtgaggctt gtccctatgt aggatgcacc   4620
gcaggcccct ggccactgaa agagtgtgca gtggactgtg ggtctcccat atgcggtgcc   4680
gcccaaaggt ggctttgcct caagcaacct accctgatgt tttactcatt ggaatgtttt   4740
tccccgattg tggatgactt cttttctgat ggagagagtc caggagggat ggaaaactcc   4800
tggatttaag ctcagcatcc cccacatggg cttttcgatc atcttcaggc ctgaagctgc   4860
acgacctgaa gttcgcctgc atttatcagc cctctttgtg ctgctccttg ccaccttggg   4920
gttcctgctg gggaccatgt gtggttgtgg catgtgtgag cagaagggag gatgaggaaa   4980
aagagaagaa accccggtac tgacaagctg tttttgagtg ccactgtttg ccatcatcta   5040
agccactgaa tcaagtgtat ttcaggctta tttcaacatt ccaatgccct ggttttcctg   5100
cttgaatctg ttcgtggtca aaggtttggg ggaatttgtg accctggaac atccccagag   5160
tgaaagatgg agctgggcca catcagaata aggccttggc cccatcctct cacagcctag   5220
gtgctctgca ggcatgctga ctgtcctgat tgcgatccag cccgaaattc cctcctctgc   5280
tttcaaaagt caaatccccc attcttaggc cacactggtg tcacaagctc ctgtcaggga   5340
gctggggttt gggaatgtgc tttgtgaact ctgctttaaa gtgaggggcc gaggaaaact   5400
tagaaacagg cagagttgga agcagccaaa tcacagtggg tgttgtgtgt gtgtgcgtgt   5460
gtgcatgcgt gcgtgtatgc gtgtgtgaaa gcaggtggac cattccactt tttagctcct   5520
attgatgcac caaaccaagt gcctcatttc tgtgccaaat gtttgccttg gtcgttgtgg   5580
acctccttct ctaacttgcg gtggcatgac tgtcaggagg tgctggcatt ttcagcagat   5640
cctcatgtgt tgaccctgat gtctttagca gaggcctcta gcatctcggt ttttcatcca   5700
ctgcaggaat gtggccacag ggagcagagg tttgtacttt ccccaagagg tcctcatcct   5760
gagacggtct ctacccatgt ttaacccaaa gagtgcaggc caggttcctt atccttctga   5820
tgaaggatga gagagctcat ttagaagtca gagcaaacta gggtctcagt attgagaaac   5880
gcagcctgcc agggaatcac agagacatcg gggtgcccgc gatggccctc atgaagccat   5940
gcctcgacgg cattcaggaa gccctgcaaa cgtgcttttt gaactcattg gccaggtgtg   6000
atttttacac aaggtaaacg tggtcaaggg catcggggaa tttgctccaa gcagatagct   6060
ccctctgagg aaccaaagga agcaagtttc cacgatttct gaagagctgg tataggaagt   6120
ttctttcttc cttttgtgtt acatgtgcat taaacagaac aagctgtgtg tcatcacaga   6180
ttgtactgtg ggctcagaaa ccgtgagaga gcccccaccg tggacaccgg ctctagggcc   6240
acaggaaaag gaacgtttcc aggcattttg tctccagggc tcccgctgga caggcacgta   6300
ctgccctggg gagtaaatgc ggagagttca cgaactgtgc ccaacgcatg ttatagccag   6360
ggtcctacta actactcagt aaaagaacgt attgttgtat tcctccagtg ttaagctata   6420
gccatgttaa aagtcactgt gcatttattc tcagcatcaa ataccttgta acgtcttctc   6480
tgccttgtta gtgcatattt ttacttttct gatactgtaa agaatatatc cagtatgtaa   6540
atgaatgttc tataaatctt ttgtatagtc attttctctg ctccttaaat atcatctcta   6600
ttcagagtat aataaaatta tgaacttggt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   6660
aaa                                                                 6663
```

<210> 228
<211> 1202
<212> PRT
<213> Homo sapiens

<400> 228

Met Val Lys Cys Tyr His Lys Lys Tyr Arg Ser Ala Thr Arg Asp Val
1 5 10 15
Ile Phe Arg Leu Gln Phe His Thr Gly Ala Val Gln Gly Tyr Gly Leu
20 25 30
Val Phe Gly Lys Glu Asp Leu Ser Lys Asp Asp Arg Phe Pro Asp Tyr
35 40 45
Gly Lys Val Glu Leu Val Phe Ser Ala Thr Pro Glu Lys Ile Gln Gly
50 55 60
Ser Glu His Leu Tyr Asn Asp His Gly Val Ile Val Asp Tyr Asn Thr
65 70 75 80
Thr Asp Pro Leu Ile Arg Trp Asp Ser Tyr Glu Asn Leu Ser Ala Asp
85 90 95
Gly Glu Val Leu His Thr Gln Gly Pro Val Asp Gly Ser Leu Tyr Ala
100 105 110
Lys Val Arg Lys Lys Ser Ser Ser Asp Pro Gly Ile Pro Gly Gly Pro
115 120 125
Gln Ala Ile Pro Ala Thr Asn Ser Pro Asp His Ser Asp His Thr Leu
130 135 140
Ser Val Ser Ser Asp Ser Gly His Ser Thr Ala Ser Ala Arg Thr Asp
145 150 155 160
Lys Thr Glu Glu Arg Leu Ala Pro Gly Thr Arg Arg Gly Leu Ser Ala
165 170 175
Gln Glu Lys Ala Glu Leu Asp Gln Leu Leu Ser Gly Phe Gly Leu Glu
180 185 190
Asp Pro Gly Ser Ser Leu Lys Glu Met Thr Asp Ala Arg Ser Lys Tyr
195 200 205
Ser Gly Thr Arg His Val Val Pro Ala Gln Val His Val Asn Gly Asp
210 215 220
Ala Ala Leu Lys Asp Arg Glu Thr Asp Ile Leu Asp Asp Glu Met Pro
225 230 235 240
His His Asp Leu His Ser Val Asp Ser Leu Gly Thr Leu Ser Ser Ser
245 250 255
Glu Gly Pro Gln Ser Ala His Leu Gly Pro Phe Thr Cys His Lys Ser
260 265 270
Ser Gln Asn Ser Leu Leu Ser Asp Gly Phe Gly Ser Asn Val Gly Glu
275 280 285
Asp Pro Gln Gly Thr Leu Val Pro Asp Leu Gly Leu Gly Met Asp Gly
290 295 300
Pro Tyr Glu Arg Glu Arg Thr Phe Gly Ser Arg Glu Pro Lys Gln Pro
305 310 315 320
Gln Pro Leu Leu Arg Lys Pro Ser Val Ser Ala Gln Met Gln Ala Tyr
325 330 335
Gly Gln Ser Ser Tyr Ser Thr Gln Thr Trp Val Arg Gln Gln Gln Met
340 345 350
Val Val Ala His Gln Tyr Ser Phe Ala Pro Asp Gly Glu Ala Arg Leu
355 360 365
Val Ser Arg Cys Pro Ala Asp Asn Pro Gly Leu Val Gln Ala Gln Pro
370 375 380
Arg Val Pro Leu Thr Pro Thr Arg Gly Thr Ser Ser Arg Val Ala Val
385 390 395 400
Gln Arg Gly Val Gly Ser Gly Pro His Pro Pro Asp Thr Gln Gln Pro
405 410 415
Ser Pro Ser Lys Ala Phe Lys Pro Arg Phe Pro Gly Asp Gln Val Val
420 425 430
Asn Gly Ala Gly Pro Glu Leu Ser Thr Gly Pro Ser Pro Gly Ser Pro
435 440 445
Thr Leu Asp Ile Asp Gln Ser Ile Glu Gln Leu Asn Arg Leu Ile Leu
450 455 460
Glu Leu Asp Pro Thr Phe Glu Pro Ile Pro Thr His Met Asn Ala Leu

465 470 475 480
Gly Ser Gln Ala Asn Gly Ser Val Ser Pro Asp Ser Val Gly Gly Gly
485 490 495
Leu Arg Ala Ser Ser Arg Leu Pro Asp Thr Gly Glu Gly Pro Ser Arg
500 505 510
Ala Thr Gly Arg Gln Gly Ser Ser Ala Glu Gln Pro Leu Gly Gly Arg
515 520 525
Leu Arg Lys Leu Ser Leu Gly Gln Tyr Asp Asn Asp Ala Gly Gly Gln
530 535 540
Leu Pro Phe Ser Lys Cys Ala Trp Gly Lys Ala Gly Val Asp Tyr Ala
545 550 555 560
Pro Asn Leu Pro Pro Phe Pro Ser Pro Ala Asp Val Lys Glu Thr Met
565 570 575
Thr Pro Gly Tyr Pro Gln Asp Leu Asp Ile Ile Asp Gly Arg Ile Leu
580 585 590
Ser Ser Lys Glu Ser Met Cys Ser Thr Pro Ala Phe Pro Val Ser Pro
595 600 605
Glu Thr Pro Tyr Val Lys Thr Ala Leu Arg His Pro Pro Phe Ser Pro
610 615 620
Pro Glu Pro Pro Leu Ser Ser Pro Ala Ser Gln His Lys Gly Gly Arg
625 630 635 640
Glu Pro Arg Ser Cys Pro Glu Thr Leu Thr His Ala Val Gly Met Ser
645 650 655
Glu Ser Pro Ile Gly Pro Lys Ser Thr Met Leu Arg Ala Asp Ala Ser
660 665 670
Ser Thr Pro Ser Phe Gln Gln Ala Phe Ala Ser Ser Cys Thr Ile Ser
675 680 685
Ser Asn Gly Pro Gly Gln Arg Arg Glu Ser Ser Ser Ser Ala Glu Arg
690 695 700
Gln Trp Val Glu Ser Ser Pro Lys Pro Met Val Ser Leu Leu Gly Ser
705 710 715 720
Gly Arg Pro Thr Gly Ser Pro Leu Ser Ala Glu Phe Ser Gly Thr Arg
725 730 735
Lys Asp Ser Pro Val Leu Ser Cys Phe Pro Pro Ser Glu Leu Gln Ala
740 745 750
Pro Phe His Ser His Glu Leu Ser Leu Ala Glu Pro Pro Asp Ser Leu
755 760 765
Ala Pro Pro Ser Ser Gln Ala Phe Leu Gly Phe Gly Thr Ala Pro Val
770 775 780
Gly Ser Gly Leu Pro Pro Glu Glu Asp Leu Gly Ala Leu Leu Ala Asn
785 790 795 800
Ser His Gly Ala Ser Pro Thr Pro Ser Ile Pro Leu Thr Ala Thr Gly
805 810 815
Ala Ala Asp Asn Gly Phe Leu Ser His Asn Phe Leu Thr Val Ala Pro
820 825 830
Gly His Ser Ser His His Ser Pro Gly Leu Gln Gly Gln Gly Val Thr
835 840 845
Leu Pro Gly Gln Pro Pro Leu Pro Glu Lys Lys Arg Ala Ser Glu Gly
850 855 860
Asp Arg Ser Leu Gly Ser Val Ser Pro Ser Ser Ser Gly Phe Ser Ser
865 870 875 880
Pro His Ser Gly Ser Thr Ile Ser Ile Pro Phe Pro Asn Val Leu Pro
885 890 895
Asp Phe Ser Lys Ala Ser Glu Ala Ala Ser Pro Leu Pro Asp Ser Pro
900 905 910
Gly Asp Lys Leu Val Ile Val Lys Phe Val Gln Asp Thr Ser Lys Phe
915 920 925
Trp Tyr Lys Ala Asp Ile Ser Arg Glu Gln Ala Ile Ala Met Leu Lys
930 935 940
Asp Lys Glu Pro Gly Ser Phe Ile Val Arg Asp Ser His Ser Phe Arg
945 950 955 960

Gly Ala Tyr Gly Leu Ala Met Lys Val Ala Thr Pro Pro Pro Ser Val
965 970 975
Leu Gln Leu Asn Lys Lys Ala Gly Asp Leu Ala Asn Glu Leu Val Arg
980 985 990
His Phe Leu Ile Glu Cys Thr Pro Lys Gly Val Arg Leu Lys Gly Cys
995 1000 1005
Ser Asn Glu Pro Tyr Phe Gly Ser Leu Thr Ala Leu Val Cys Gln His
1010 1015 1020
Ser Ile Thr Pro Leu Ala Leu Pro Cys Lys Leu Leu Ile Pro Glu Arg
1025 1030 1035 1040
Asp Pro Leu Glu Glu Ile Ala Glu Ser Ser Pro Gln Thr Ala Ala Asn
1045 1050 1055
Ser Ala Ala Glu Leu Leu Lys Gln Gly Ala Ala Cys Asn Val Trp Tyr
1060 1065 1070
Leu Asn Ser Val Glu Met Glu Ser Leu Thr Gly His Gln Ala Ile Gln
1075 1080 1085
Lys Ala Leu Ser Ile Thr Leu Val Gln Glu Pro Pro Pro Val Ser Thr
1090 1095 1100
Val Val His Phe Lys Val Ser Ala Gln Gly Ile Thr Leu Thr Asp Asn
1105 1110 1115 1120
Gln Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Val Asn Ser Val Ile
1125 1130 1135
Phe Cys Ala Leu Asp Pro Gln Asp Arg Lys Trp Ile Lys Asp Gly Pro
1140 1145 1150
Ser Ser Lys Val Phe Gly Phe Val Ala Arg Lys Gln Gly Ser Ala Thr
1155 1160 1165
Asp Asn Val Cys His Leu Phe Ala Glu His Asp Pro Glu Gln Pro Ala
1170 1175 1180
Ser Ala Ile Val Asn Phe Val Ser Lys Val Met Ile Gly Ser Pro Lys
1185 1190 1195 1200
Lys Val

<210> 229
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 229
gcggccgcag cctgagccag ggccccctcc ctcgtcagga ccggggcagc aagcaggccg 60
ggggcaggtc cgggcaccca ccatgcgagg cgagctctgg ctcctggtgc tggtgctcag 120
ggaggctgcc cgggcgctga gcccccagcc cggagcaggt cacgatgagg gcccaggctc 180
tggatgggct gccaaaggga ccgtgcgggg ctggaaccgg agagcccgag agagccctgg 240
gcatgtgtca gagccggaca ggacccagct gagccaggac ctgggtgggg gcaccctggc 300
catggacacg ctgccagata acaggaccag ggtggtggag gacaaccaca gctattatgt 360
gtcccgtctc tatggcccca gcgagcccca cagccgggaa ctgtgggtag atgtggccga 420
ggccaaccgg agccaagtga agatccacac aatactctcc aacacccacc ggcaggcttc 480
gagagtggtc ttgtcctttg atttcccttt ctacgggcat cctctgcggc agatcaccat 540
agcaactgga ggcttcatct tcatggggga cgtgatccat cggatgctca cagctactca 600
gtatgtggcg cccctgatgg ccaacttcaa ccctggctac tccgacaact ccacagttgt 660
ttactttgac aatggacag tctttgtggt tcagtgggac cacgtttatc tccaaggctg 720
ggaagacaag ggcagtttca ccttccaggc agctctgcac catgacggcc gcattgtctt 780
tgcctataaa gagatcccta tgtctgtccc ggaaatcagc tcctcccagc atcctgtcaa 840
aaccggccta tcggatgcct tcatgattct caatccatcc ccggatgtgc cagaatctcg 900
gcgaaggagc atctttgaat accaccgcat agagctggac cccagcaagg tcaccagcat 960
gtcggccgtg gagttcaccc cattgccgac ctgcctgcag cataggagct gtgacgcctg 1020
catgtcctca gacctgacct tcaactgcag ctggtgccat gtcctccaga gatgctccag 1080
tggctttgac cgctatcgcc aggagtggat ggactatggc tgtgcacagg aggcagaggg 1140
caggatgtgc gaggacttcc aggatgagga ccacgactca gcctcccctg acacttcctt 1200
cagcccctat gatggagacc tcaccactac ctcctcctcc ctcttcatcg acagcctcac 1260
cacagaagat gacaccaagt tgaatcccta tgcaggagga gacggccttc agaacaacct 1320

```
gtcccccaag acaaagggca ctcctgtgca cctgggcacc atcgtgggca tcgtgctggc    1380
agtcctcctc gtggcggcca tcatcctggc tggaatttac atcaatggcc accccacatc    1440
caatgctgcg ctcttcttca tcgagcgtag acctcaccac tggccagcca tgaagtttcg    1500
cagccacccct gaccattcca cctatgcgga ggtggagccc tcgggccatg agaaggaggg    1560
cttcatggag gctgagcagt gctgagaaca ccaagtctcc cctttgaaga ctttgaggcc    1620
acagaaaaga cagttaaagc aaagaagaga agtgactttt cctggcctct cccagcatgc    1680
cctgggctga gatgagatgg tggtttatgg ctccagagct gctgttcgct tcgtcagcac    1740
accccgaata ttgaagaggg ggccaaaaaa caaccacatg gattttttat aggaacaaca    1800
acctaatctc atcctgtttt gatgcaaggg ttctcttctg tgtcttgtaa ccatgaaaca    1860
gcagaagaac taacataact aactccattt ttgtttaagg ggcctttacc tattcctgca    1920
cctaggctag gataacttta gagcactgac ataaaacgca aaaacaggaa tcatgccgtt    1980
tgcaaaacta actctgggat taaaggggaa gcatgtaaac agctaactgt ttttgttaaa    2040
gatttatagg aatgaggagg tttggctatt gtcacatgac agactgttag ccaaggacaa    2100
agaagttctg caaacctccc ctggaccctt gctggtgtcc agatgtctgc ggttgtcagc    2160
cccttccttt cccccgacct aaacataaaa gacaaggcaa agcccgcata attttaagac    2220
ggttctttag gacattagtc caccatcttc ttggtttgct ggctctccga aataaagtcc    2280
ctttccttgc tccaaaaaaa aaaaaaaaaa aaaaaaaaaa                          2320
```

<210> 230
<211> 500
<212> PRT
<213> Homo sapiens

<400> 230

```
Met Arg Gly Glu Leu Trp Leu Leu Val Leu Val Leu Arg Glu Ala Ala
1               5                   10                  15
Arg Ala Leu Ser Pro Gln Pro Gly Ala Gly His Asp Glu Gly Pro Gly
            20                  25                  30
Ser Gly Trp Ala Ala Lys Gly Thr Val Arg Gly Trp Asn Arg Arg Ala
        35                  40                  45
Arg Glu Ser Pro Gly His Val Ser Glu Pro Asp Arg Thr Gln Leu Ser
    50                  55                  60
Gln Asp Leu Gly Gly Gly Thr Leu Ala Met Asp Thr Leu Pro Asp Asn
65                  70                  75                  80
Arg Thr Arg Val Val Glu Asp Asn His Ser Tyr Tyr Val Ser Arg Leu
                85                  90                  95
Tyr Gly Pro Ser Glu Pro His Ser Arg Glu Leu Trp Val Asp Val Ala
            100                 105                 110
Glu Ala Asn Arg Ser Gln Val Lys Ile His Thr Ile Leu Ser Asn Thr
        115                 120                 125
His Arg Gln Ala Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe Tyr
    130                 135                 140
Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile Phe
145                 150                 155                 160
Met Gly Asp Val Ile His Arg Met Leu Thr Ala Thr Gln Tyr Val Ala
                165                 170                 175
Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr Val
            180                 185                 190
Val Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His Val
        195                 200                 205
Tyr Leu Gln Gly Trp Glu Asp Lys Gly Ser Phe Thr Phe Gln Ala Ala
    210                 215                 220
Leu His His Asp Gly Arg Ile Val Phe Ala Tyr Lys Glu Ile Pro Met
225                 230                 235                 240
Ser Val Pro Glu Ile Ser Ser Ser Gln His Pro Val Lys Thr Gly Leu
                245                 250                 255
Ser Asp Ala Phe Met Ile Leu Asn Pro Ser Pro Asp Val Pro Glu Ser
            260                 265                 270
Arg Arg Arg Ser Ile Phe Glu Tyr His Arg Ile Glu Leu Asp Pro Ser
        275                 280                 285
Lys Val Thr Ser Met Ser Ala Val Glu Phe Thr Pro Leu Pro Thr Cys
```

290 295 300
Leu Gln His Arg Ser Cys Asp Ala Cys Met Ser Ser Asp Leu Thr Phe
305 310 315 320
Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe Asp
325 330 335
Arg Tyr Arg Gln Glu Trp Met Asp Tyr Gly Cys Ala Gln Glu Ala Glu
340 345 350
Gly Arg Met Cys Glu Asp Phe Gln Asp Glu Asp His Asp Ser Ala Ser
355 360 365
Pro Asp Thr Ser Phe Ser Pro Tyr Asp Gly Asp Leu Thr Thr Thr Ser
370 375 380
Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu
385 390 395 400
Asn Pro Tyr Ala Gly Gly Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys
405 410 415
Thr Lys Gly Thr Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu
420 425 430
Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Asn
435 440 445
Gly His Pro Thr Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro
450 455 460
His His Trp Pro Ala Met Lys Phe Arg Ser His Pro Asp His Ser Thr
465 470 475 480
Tyr Ala Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Met Glu
485 490 495
Ala Glu Gln Cys
500

<210> 231
<211> 5540
<212> DNA
<213> Homo sapiens

<400> 231
aattgcttcc ggggagttgc gagggagcga gggggaataa aggacccgcg aggaagggcc 60
cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtgggaa ggagcggacc 120
ctgctctccc cgggctgcgg gccatggcca cggcggagcg gagagccctc ggcatcggct 180
tccagtggct ctctttggcc actctggtgc tcatctgcgc cgggcaaggg ggacgcaggg 240
aggatggggg tccagcctgc tacggcggat ttgacctgta cttcattttg gacaaatcag 300
gaagtgtgct gcaccactgg aatgaaatct attactttgt ggaacagttg gctcacaaat 360
tcatcagccc acagttgaga atgtccttta ttgttttctc cacccgagga acaaccttaa 420
tgaaactgac agaagacaga gaacaaatcc gtcaaggcct agaagaactc cagaaagttc 480
tgccaggagg agacacttac atgcatgaag gatttgaaag ggccagtgag cagatttatt 540
atgaaaacag acaagggtac aggacagcca gcgtcatcat tgctttgact gatggagaac 600
tccatgaaga tctcttttc tattcagaga gggaggctaa taggtctcga gatcttggtg 660
caattgttta ctgtgttggt gtgaaagatt tcaatgagac acagctggcc cggattgcgg 720
acagtaagga tcatgtgttt cccgtgaatg acggctttca ggctctgcaa ggcatcatcc 780
actcaatttt gaagaagtcc tgcatcgaaa ttctagcagc tgaaccatcc accatatgtg 840
caggagagtc atttcaagtt gtcgtgagag gaaacggctt ccgacatgcc cgcaacgtgg 900
acagggtcct ctgcagcttc aagatcaatg actcggtcac actcaatgag aagccctttt 960
ctgtggaaga tacttattta ctgtgtccag cgcctatctt aaaagaagtt ggcatgaaag 1020
ctgcactcca ggtcagcatg aacgatggcc tctcttttat ctccagttct gtcatcatca 1080
ccaccacaca ctgttctgac ggttccatcc tggccatcgc cctgctgatc ctgttcctgc 1140
tcctagccct ggctctcctc tggtggttct ggcccctctg ctgcactgtg attatcaagg 1200
aggtccctcc accccctgcc gaggagagtg aggaagaaga tgatgatggt ctgcctaaga 1260
aaaagtggcc aacggtagac gcctcttatt atggtgggag aggcgttgga ggcattaaaa 1320
gaatggaggt tcgttgggga gaaaagggct ccacagaaga aggtgctaag ttggaaaagg 1380
caaagaatgc aagagtcaag atgccggagc aggaatatga attccctgag ccgcgaaatc 1440
tcaacaacaa tatgcgtcgg ccttcttccc ccccggaagtg gtactctcca atcaagggaa 1500
aactcgatgc cttgtgggtc ctactgagga aaggatatga tcgtgtgtct gtgatgcgtc 1560
cacagccagg agacacgggg cgctgcatca acttcaccag ggtcaagaac aaccagccag 1620

ccaagtaccc actcaacaac gcctaccaca cctcctcgcc gcctcctgcc cccatctaca 1680
ctcccccacc tcctgcgccc cactgccctc ccccgccccc cagcgcccct acccctccca 1740
tcccgtcccc accttccacc cttccccctc ctccccaggc tccacctccc aacagggcac 1800
ctcctccctc ccgccctcct ccaaggcctt ctgtctagag cccaaagttc ctgctctggg 1860
ctctctcaga aacttcagga gatgttagaa caagtctttc cagttagaga agaggagtgg 1920
tgataaagcc cactgacctt cacacattct aaaaattggt tggcaatgcc agtataccaa 1980
caatcatgat cagctgaaag aaacagatat tttaaattgc cagaaaacaa atgatgaggc 2040
aactacagtc agatttatag ccagccatct atcacctcta gaaggttcca gagacagtga 2100
aactgcaaga tgctctcaac aggattatgt ctcatggaga ccagtaagaa aatcatttat 2160
ctgaaggtga aatgcagagt tggataagaa atacattgct gggtttctaa aatgctgcct 2220
tcctgcctct actccacctc catccctgga ctttggaccc ttggcctagg agcctaagga 2280
ccttcacccc tgtgcaccac ccaagaaaga ggaaaacttt gcctacaact ttggaaatgc 2340
tggggtccct ggtgtggtaa gaaactcaac atcagacggg tatgcagaag gatgttcttc 2400
tgggatttgc aggtacataa aaaatgtatg gcatcttttc cttgcaaatt cttccagttt 2460
ccaagtgaga aggggagcag gtgtttactg atggaaaagg tatgttgcta tgttgatgtg 2520
taagtgaaat cagttgtgtg caatagacag gggcgtattc atgggagcat cagccagttt 2580
ctaaaaccca caggccatca gcagctagag gtggctggct ttggccagac atggacccta 2640
aatcaacaga caatggcatt gtcgaagagc aacctgttaa tgaatcatgt taaaaatcaa 2700
ggtttggctt cagtttaaat cacttgaggt atgaagttta tcctgttttc cagagataaa 2760
cataagttga tcttcccaaa ataccatcat taggacctat cacacaatat cactagtttt 2820
ttttgtttgt ttgttttttg tttttttct tggtaaagcc atgcaccaca gacttctggg 2880
cagagctgag agacaatggt cctgacataa taaggatctt tgattaaccc ccataaggca 2940
tgtgtgtgta tacaaatata cttctctttg gcttttcgac atagaacctc agctgttaac 3000
caaggggaaa tacatcagat ctgcaacaca gaaatgctct gcctgaaatt tccaccatgc 3060
ctaggactca ccccatttat ccaggtcttt ctggatctgt ttaatcaata agccctataa 3120
tcacttgcta aacactgggc ttcatcaccc agggataaaa acagagatca ttgtcttgga 3180
cctcctgcat cagcctattc aaaattatct ctctctctag ctttccacaa atcctaaaat 3240
tcctgtccca agccacccaa attctcagat cttttctgga acaaggcaga atataaaata 3300
aatatacatt tagtggcttg ggctatggtc tccaaagatc cttcaaaaat acatcaagcc 3360
agcttcattc actcacttta cttagaacag agatataagg gcctgggatg catttatttt 3420
atcaatacca atttttgtgg ccatggcaga cattgctaat caatcacagc actatttcct 3480
attaagccca ctgatttctt cacaatcctt ctcaaattac aattccaaag agccgccact 3540
caacagtcag atgaacccaa cagtcagatg agagaaatga accctacttg ctatctctat 3600
cttagaaagc aaaaacaaac aggagtttcc agggagaatg ggaaagccag ggggcataaa 3660
aggtacagtc aggggaaaat agatctaggc agagtgcctt agtcagggac cacgggcgct 3720
gaatctgcag tgccaacacc aaactgacac atctccaggt gtacctccaa ccctagcctt 3780
ctcccacagc tgcctacaac agagtctccc agccttctca gagagctaaa accagaaatt 3840
tccagactca tgaaagcaac cccccagcct ctccccaacc ctgccgcatt gtctaatttt 3900
tagaacacta ggcttcttct ttcatgtagt tcctcataag caggggccag aatatctcag 3960
ccacctgcag tgacattgct ggacccctga aaaccattcc ataggagaat gggttcccca 4020
ggctcacagt gtagagacat tgagcccatc acaactgttt tgactgctgg cagtctaaaa 4080
cagtccaccc accccatggc actgccgcgt gattcccgcg gccattcaga agttcaagcc 4140
gagatgctga cgttgctgag caacgagatg gtgagcatca gtgcaaatgc accattcagc 4200
acatcagtca tatgcccagt gcagttacaa gatgttgttt cggcaaagca ttttgatgga 4260
atagggaact gcaaatgtat gatgattttg aaaaggctca gcaggatttg ttcttaaacc 4320
gactcagtgt gtcatccccg gttatttaga attacagtta agaaggagaa acttctataa 4380
gactgtatga acaaggtgat atcttcatag tgggctatta caggcaggaa aatgttttaa 4440
ctggtttaca aaatccatca atacttgtgt cattccctgt aaaaggcagg agacatgtga 4500
ttatgatcag gaaactgcac aaaattattg ttttcagccc ccgtgttatt gtccttttga 4560
actgtttttt ttttattaaa gccaaatttg tgttgtatat attcgtattc catgtgttag 4620
atggaagcat ttcctatcca gtgtgaataa aaagaacagt tgtagtaaat tattataaag 4680
ccgatgatat ttcatggcag gttattctac caagctgtgc ttgttggttt ttcccatgac 4740
tgtattgctt ttataaatgt acaaatagtt actgaaatga cgagacccct gtttgcacag 4800
cattaataag aaccttgata agaaccatat tctgttgaca gccagctcac agtttcttgc 4860
ctgaagcttg gtgcaccctc cagtgagaca caagatctct cttttaccaa agttgagaac 4920
agagctggtg gattaattaa tagtcttcga tatctggcca tgggtaacct cattgtaact 4980
atcatcagaa tgggcagaga tgatcttgaa gtgtcacata cactaaagtc caaacactat 5040
gtcagatggg ggtaaaatcc attaaagaac aggaaaaaat aattataaga tgataagcaa 5100
atgtttcagc ccaatgtcaa cccagttaaa aaaaaaatta atgctgtgta aaatggttga 5160
attagtttgc aaactatata aagacatatg cagtaaaaag tctgttaatg cacatcctgt 5220
gggaatggag tgttctaacc aattgccttt tcttgttatc tgagctctcc tatattatca 5280

```
tactcagata accaaattaa aagaattaga atatgatttt taatacactt aacattaaac    5340
tcttctaact ttcttctttc tgtgataatt cagaagatag ttatggatct tcaatgcctc    5400
tgagtcattg ttataaaaaa tcagttatca ctataccatg ctataggaga ctgggcaaaa    5460
cctgtacaat gacaaccctg gaagttgctt tttttaaaaa aataataaat ttcttaaatc    5520
aaaaaaaaaa aaaaaaaaaa                                                 5540
```

```
<210> 232
<211> 564
<212> PRT
<213> Homo sapiens

<400> 232
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu
1               5                   10                  15
Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg
            20                  25                  30
Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile
        35                  40                  45
Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr
    50                  55                  60
Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met
65                  70                  75                  80
Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr
                85                  90                  95
Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val
            100                 105                 110
Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser
        115                 120                 125
Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val
    130                 135                 140
Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145                 150                 155                 160
Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
                165                 170                 175
Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
            180                 185                 190
Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
        195                 200                 205
Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
    210                 215                 220
Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225                 230                 235                 240
Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
                245                 250                 255
Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
            260                 265                 270
Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
        275                 280                 285
Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
    290                 295                 300
Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305                 310                 315                 320
Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
                325                 330                 335
Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
            340                 345                 350
Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Glu Asp Asp Asp
        355                 360                 365
Gly Leu Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly
```

```
    370                 375                 380
Gly Arg Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu
385                 390                 395                 400
Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala
                405                 410                 415
Arg Val Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn
            420                 425                 430
Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser
        435                 440                 445
Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly
    450                 455                 460
Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg
465                 470                 475                 480
Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro
                485                 490                 495
Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr
            500                 505                 510
Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala
        515                 520                 525
Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro
    530                 535                 540
Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro
545                 550                 555                 560
Arg Pro Ser Val
```

<210> 233
<211> 5086
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(5086)
<223> n = A,T,C or G

<400> 233

```
agcaccacgg cagcaggagg tttcggncta agttggaggt actggnccac gactgcatgc      60
ccgcgcccgc caggtgatac ctccgccggt gacccagggg ctctgcgaca caaggagtct     120
gcatgtctaa gtgctagaca tgctcagctt tgtggatacg cggactttgt tgctgcttgc     180
agtaacctta tgcctagcaa catgccaatc tttacaagag gaaactgtaa gaaagggccc     240
agccggagat agaggaccac gtggagaaag gggtccacca ggccccccag gcagagatgg     300
tgaagatggt cccacaggcc ctcctggtcc acctggtcct cctggccccc ctggtctcgg     360
tgggaacttt gctgctcagt atgatggaaa aggagttgga cttggccctg gaccaatggg     420
cttaatggga cctagaggcc cacctggtgc agctggagcc ccaggccctc aaggtttcca     480
aggacctgct ggtgagcctg gtgaacctgg tcaaactggt cctgcaggtg ctcgtggtcc     540
agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaacccg gacgacctgg     600
tgagagagga gttgttggac cacagggtgc tcgtggtttc cctggaactc ctggacttcc     660
tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaagggac agcccggtgc     720
tcctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg     780
agcccgtggg cttcctggtg agagaggacg tgttggtgcc cctggcccag ctggtgcccg     840
tggcagtgat ggaagtgtgg gtcccgtggg tcctgctggt cccattgggt ctgctggccc     900
tccaggcttc ccaggtgccc ctggccccaa gggtgaaatt ggagctgttg gtaacgctgg     960
tcctgctggt cccgccggtc cccgtggtga agtgggtctt ccaggcctct ccggcccccgt    1020
tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccaagggtg ctgctggcct    1080
tcccggcgtt gctggggctc ccggcctccc tggaccccgc ggtattcctg gccctgttgg    1140
tgctgccggt gctactggtg ccagaggact tgttggtgag cctggtccag ctggctccaa    1200
aggagagagc ggtaacaagg gtgagcccgg ctctgctggg ccccaaggtc ctcctggtcc    1260
cagtggtgaa gaaggaaaga gaggccctaa tggggaagct ggatctgccg gccctccagg    1320
acctcctggg ctgagaggta gtcctggttc tcgtggtctt cctggagctg atggcagagc    1380
tggcgtcatg ggccctcctg gtagtcgtgg tgcaagtggc cctgctggag tccgaggacc    1440
```

taatggagat gctggtcgcc ctggggagcc tggtctcatg ggacccagag gtcttcctgg 1500
ttcccctgga aatatcggcc ccgctggaaa agaaggtcct gtcggcctcc ctggcatcga 1560
cggcaggcct ggcccaattg gcccagctgg agcaagagga gagcctggca acattggatt 1620
ccctggaccc aaaggcccca ctggtgatcc tggcaaaaac ggtgataaag gtcatgctgg 1680
tcttgctggt gctcggggtg ctccaggtcc tgatggaaac aatggtgctc agggacctcc 1740
tggaccacag ggtgttcaag gtggaaaagg tgaacagggt cccgctggtc ctccaggctt 1800
ccagggtctg cctggcccct caggtcccgc tggtgaagtt ggcaaaccag gagaaagggg 1860
tctccatggt gagtttggtc tccctggtcc tgctggtcca agaggggaac gcggtccccc 1920
aggtgagagt ggtgctgccg gtcctactgg tcctattgga agccgaggtc cttctggacc 1980
cccagggcct gatggaaaca agggtgaacc tggtgtggtt ggtgctgtgg gcactgctgg 2040
tccatctggt cctagtggac tcccaggaga gaggggtgct gctggcatac ctggaggcaa 2100
gggagaaaag ggtgaacctg gtctcagagg tgaaattggt aaccctggca gagatggtgc 2160
tcgtggtgct catggtgctg taggtgcccc tggtcctgct ggagccacag gtgaccgggg 2220
cgaagctggg gctgctggtc ctgctggtcc tgctggtcct cggggaagcc ctggtgaacg 2280
tggcgaggtc ggtcctgctg gccccaacgg atttgctggt ccggctggtg ctgctggtca 2340
accgggtgct aaaggagaaa gaggagccaa agggcctaag ggtgaaaacg gtgttgttgg 2400
tcccacaggc cccgttggag ctgctggccc agctggtcca aatggtcccc ccggtcctgc 2460
tggaagtcgt ggtgatggag gcccccctgg tatgactggt ttccctggtg ctgctggacg 2520
gactggtccc ccaggaccct ctggtatttc tggccctcct ggtccccctg gtcctgctgg 2580
gaaagaaggg cttcgtggtc ctcgtggtga ccaaggtcca gttggccgaa ctggagaagt 2640
aggtgcagtt ggtccccctg gcttcgctgg tgagaagggt ccctctggag aggctggtac 2700
tgctggacct cctggcactc caggtcctca gggtcttctt ggtgctcctg gtattctggg 2760
tctccctggc tcgagaggtg aacgtggtct acctggtgtt gctggtgctg tgggtgaacc 2820
tggtcctctt ggcattgccg gccctcctgg ggcccgtggt cctcctggtg ctgtgggtag 2880
tcctggagtc aacggtgctc ctggtgaagc tggtcgtgat ggcaaccctg ggaacgatgg 2940
tcccccaggt cgcgatggtc aacccggaca caagggagag cgcggttacc ctggcaatat 3000
tggtcccgtt ggtgctgcag gtgcacctgg tcctcatggc cccgtgggtc ctgctggcaa 3060
acatggaaac cgtggtgaaa ctggtccttc tggtcctgtt ggtcctgctg gtgctgttgg 3120
cccaagaggt cctagtggcc cacaaggcat tcgtggcgat aagggagagc ccggtgaaaa 3180
ggggcccaga ggtcttcctg gcttaaaggg acacaatgga ttgcaaggtc tgcctggtat 3240
cgctggtcac catggtgatc aaggtgctcc tggctccgtg ggtcctgctg gtcctagggg 3300
ccctgctggt ccttctggcc ctgctggaaa agatggtcgc actggacatc ctggtacggt 3360
tggacctgct ggcattcgag gccctcaggg tcaccaaggc cctgctggcc cccctggtcc 3420
ccctggccct cctggacctc caggtgtaag cggtggtggt tatgactttg gttacgatgg 3480
agacttctac agggctgacc agcctcgctc agcaccttct ctcagaccca aggactatga 3540
agttgatgct actctgaagt ctctcaacaa ccagattgag acccttctta ctcctgaagg 3600
ctctagaaag aacccagctc gcacatgccg tgacttgaga ctcagccacc cagagtggag 3660
cagtggttac tactggattg accctaacca aggatgcact atggatgcta tcaaagtata 3720
ctgtgatttc tctactggcg aaacctgtat ccgggcccaa cctgaaaaca tcccagccaa 3780
gaactggtat aggagctcca aggacaagaa acacgtctgg ctaggagaaa ctatcaatgc 3840
tggcagccag tttgaatata atgtagaagg agtgacttcc aaggaaatgg ctacccaact 3900
tgccttcatg cgcctgctgg ccaactatgc ctctcagaac atcacctacc actgcaagaa 3960
cagcattgca tacatggatg aggagactgg caacctgaaa aaggctgtca ttctacaggg 4020
ctctaatgat gttgaacttg ttgctgaggg caacagcagg ttcacttaca ctgttcttgt 4080
agatggctgc tctaaaaaga caaatgaatg gggaaagaca atcattgaat acaaaacaaa 4140
taagccatca cgcctgccct tccttgatat tgcacctttg gacatcggtg gtgctgacca 4200
tgaattcttt gtggacattg gcccagtctg tttcaaataa atgaactcaa tctaaattaa 4260
aaaagaaaga aatttgaaaa aactttctct ttgccatttc ttcttcttct tttttaactg 4320
aaagctgaat ccttccattt cttctgcaca tctacttgct taaattgtgg gcaaaagaga 4380
aaaagaagga ttgatcagag cattgtgcaa tacagtttca ttaactcctt cccccgctcc 4440
cccaaaaatt tgaatttttt tttcaacact cttacacctg ttatggaaaa tgtcaacctt 4500
tgtaagaaaa ccaaaataaa aattgaaaaa taaaaaccat aaacatttgc accacttgtg 4560
gcttttgaat atcttccaca gagggaagtt taaaacccaa acttccaaag gtttaaacta 4620
cctcaaaaca ctttcccatg agtgtgatcc acattgttag gtgctgacct agacagagat 4680
gaactgaggt ccttgttttg ttttgttcat aatacaaagg tgctaattaa tagtatttca 4740
gatacttgaa gaatgttgat ggtgctagaa gaatttgaga agaaatactc ctgtattgag 4800
ttgtatcgtg tggtgtattt tttaaaaaat ttgatttagc attcatattt tccatcttat 4860
tcccaattaa aagtatgcag attatttgcc caaagttgtc ctcttcttca gattcagcat 4920
ttgttctttg ccagtctcat tttcatcttc ttccatggtt ccacagaagc tttgtttctt 4980
gggcaagcag aaaaattaaa ttgtacctat tttgtatatg tgagatgttt aaataaattg 5040

tgaaaaaaat gaaataaagc atgtttggtt ttccaaaaga acatat 5086

<210> 234
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 234
Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr
1 5 10 15
Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys
20 25 30
Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly
35 40 45
Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro
50 55 60
Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln
65 70 75 80
Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
85 90 95
Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly
100 105 110
Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
115 120 125
Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp
130 135 140
Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly
145 150 155 160
Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
165 170 175
Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
180 185 190
Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly
195 200 205
Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg
210 215 220
Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val
225 230 235 240
Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly
245 250 255
Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn
260 265 270
Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
275 280 285
Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
290 295 300
Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
305 310 315 320
Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
325 330 335
Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly
340 345 350
Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro
355 360 365
Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
370 375 380
Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
385 390 395 400
Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val

```
                405                 410                 415
Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
            420                 425                 430
Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
        435                 440                 445
Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
    450                 455                 460
Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
465                 470                 475                 480
Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
                485                 490                 495
Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
            500                 505                 510
Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
        515                 520                 525
Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
    530                 535                 540
Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
545                 550                 555                 560
Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
                565                 570                 575
Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
            580                 585                 590
Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
        595                 600                 605
Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
    610                 615                 620
Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
625                 630                 635                 640
Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
                645                 650                 655
Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
            660                 665                 670
Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
        675                 680                 685
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
    690                 695                 700
Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
705                 710                 715                 720
Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
                725                 730                 735
Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
            740                 745                 750
Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
        755                 760                 765
Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
    770                 775                 780
Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
785                 790                 795                 800
Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
                805                 810                 815
Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
            820                 825                 830
Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
        835                 840                 845
Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln
    850                 855                 860
Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
865                 870                 875                 880
Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
                885                 890                 895
```

Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
900 905 910
Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly
915 920 925
Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His
930 935 940
Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
945 950 955 960
Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
965 970 975
Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala
980 985 990
Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys
995 1000 1005
Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly
1010 1015 1020
His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp
1025 1030 1035 1040
Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg Gly Pro Ala
1045 1050 1055
Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr Gly His Pro Gly
1060 1065 1070
Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln Gly His Gln Gly Pro
1075 1080 1085
Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser
1090 1095 1100
Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp Phe Tyr Arg Ala Asp
1105 1110 1115 1120
Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys Asp Tyr Glu Val Asp
1125 1130 1135
Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu Thr Leu Leu Thr Pro
1140 1145 1150
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Arg Leu
1155 1160 1165
Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp Ile Asp Pro Asn Gln
1170 1175 1180
Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys Asp Phe Ser Thr Gly
1185 1190 1195 1200
Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile Pro Ala Lys Asn Trp
1205 1210 1215
Tyr Arg Ser Ser Lys Asp Lys Lys His Val Trp Leu Gly Glu Thr Ile
1220 1225 1230
Asn Ala Gly Ser Gln Phe Glu Tyr Asn Val Glu Gly Val Thr Ser Lys
1235 1240 1245
Glu Met Ala Thr Gln Leu Ala Phe Met Arg Leu Leu Ala Asn Tyr Ala
1250 1255 1260
Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp
1265 1270 1275 1280
Glu Glu Thr Gly Asn Leu Lys Lys Ala Val Ile Leu Gln Gly Ser Asn
1285 1290 1295
Asp Val Glu Leu Val Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Val
1300 1305 1310
Leu Val Asp Gly Cys Ser Lys Lys Thr Asn Glu Trp Gly Lys Thr Ile
1315 1320 1325
Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg Leu Pro Phe Leu Asp Ile
1330 1335 1340
Ala Pro Leu Asp Ile Gly Gly Ala Asp His Glu Phe Phe Val Asp Ile
1345 1350 1355 1360
Gly Pro Val Cys Phe Lys
1365

<210> 235
<211> 4168
<212> DNA
<213> Homo sapiens

<400> 235
atgggcaacc tggagagcgc cgagggggtc ccgggagagc ccccctctgt cccgttgttg 60
ctgccgcccg gcaagatgcc gatgcctgag ccctgtgagc tggaggaaag gttcgccctg 120
gtgctgagct ccatgaacct gcctccagac aaggcccggc tcctgcggca gtatgacaat 180
gagaagaaat gggatctgat ctgtgaccag gaacgattcc aggtgaagaa tcctccccac 240
acttacattc agaaactcca gagcttcttg gaccccagtg taactcggaa gaagttcagg 300
aggagggtgc aggagtcaac caaagtacta agggagctgg agatctctct tcgcaccaac 360
cacattgggt gggtgcggga atttctgaat gatgaaaaca aaggcctgga tgtactggtg 420
gattacctgt cctttgccca gtgttctgtc atgtttgact ttgagggtct ggaaagtggt 480
gacgatggtg catttgacaa actccggtcc tggagcaggt caatcgagga cctgcagcca 540
cccagcgccc tgtcggcccc cttcaccaac agcctcgctc gctctgcgcg ccagtctgtg 600
ctccggtata gcactctccc tgggcgcagg gccctgaaga actcccgcct agtgagccag 660
aaggatgacg tccacgtctg tatcctttgt ctcagagcca tcatgaacta tcagtacgga 720
ttcaacctgg tcatgtccca cccccatgct gtcaatgaga ttgcacttag cctcaataac 780
aagaatccaa ggaccaaagc ccttgtctta gagcttctgg cagctgtgtg tttggtgcga 840
ggaggtcacg aaatcatcct tgctgccttt gacaatttca aagaggtatg caaggagctg 900
caccgctttg agaagctgat ggagtatttc cggaatgagg acagcaatat tgacttcatg 960
gtggcctgca tgcagttcat caacatcgtg gtgcactcgg tggaggacat gaacttccgg 1020
gtccacctgc agtatgagtt taccaagctg ggctagagg agttcctgca gaagtcaagg 1080
cacacagaga gcgagaagct gcaggtgcag attcaggcat atctggacaa cgtgtttgat 1140
gtcgggggtt tgttggagga tgctgagacc aagaatgtag ccctggagaa ggtggaggag 1200
ttggaggagc atgtgtccca tctcacagag aagcttctgg acctagagaa tgaaaacatg 1260
atgcgggtgg cagaactaga gaagcagctg ctacagcggg agaaggaact agagagcatc 1320
aaggagacat atgagaacac aagccaccag gtgcacaccc tgcggaggct cattaaagag 1380
aaggaggagg cctttcagcg tcgatgtcat ttggagccaa atgtccgggg cctggagtct 1440
gtggacagtg aggccctggc cagagtaggc cctgcagagc tgagtgaggg catgccaccc 1500
tccgacctgg accttctggc tccagcccca cccccctgagg aggtcctgcc tcttcctcca 1560
ccaccagctc cgcccttgcc ccctccacct cccccattac cagacaagtg tcccccagcc 1620
ccacctctcc ctggtgctgc accctctgtg gtgttgacag tgggcctgtc agccattcga 1680
attaagaaac ctatcaagac caagttccgg ctgcctgtct tcaactggac agcactgaaa 1740
cccaaccaga tcagtggcac tgtcttcagc gaacttgatg atgagaagat cttggaggac 1800
ctggatcttg ataagtttga agaattattc aagacaaaag cgcagggccc tgcccttgac 1860
ctcatctgct ccaaaaacaa gacagcgcaa aaagctgcca gcaaggtgac tctgttggaa 1920
gccaatcgtg ccaagaacct ggccatcacc ctacgcaagg ctggccgctc ggctgaggag 1980
atctgcaggg ccattcatac gtttgacttg cagacactac ctgtggactt cgtggagtgc 2040
ctgatgcgct tcctgcccac agaggctgag gtaaagctgc tgcggcaata tgagcgggag 2100
cggcagcccc tggaggagtt ggcagctgag gaccgcttca tgctgctctt cagcaaggtg 2160
gaacggttga cccagcgaat ggctggcatg gccttcctgg ggaacttcca ggataacctg 2220
cagatgctca caccgcaact caatgccatc attgcggcgt ccgcttccgt caagtcttca 2280
cagaagctga agcagatgtt ggagatcata cttgcactgg ggaactacat gaacagcagc 2340
aagcggggag ctgtgtatgg cttcaagctc cagagcctgg atctgctgct ggataccaag 2400
tccactgacc ggaagatgac actgcttcat ttcatcgcct tgacagtgaa ggagaaatac 2460
ccagacctgg ctaacttctg gcatgagctg cactttgttg agaaggctgc agcagtgtcc 2520
ctggagaacg tgctgctgga cgtgaaggag ctgggccggg gcatggagct gattcggcgt 2580
gagtgcagca tccatgacaa cagcgtcctc cggaacttcc tcagtaccaa tgaaggcaaa 2640
ctagacaagc tccagcggga cgccaagacg gctgaggagg cctacaatgc agttgtgcgc 2700
tactttggcg agagtcccaa gactacacct ccttctgtat tcttcccagt atttgtccga 2760
ttcattcgtt cttacaagga agcagaacaa gagaatgaag cccgcaagaa gcaggaggag 2820
gtaatgcggg agaagcagct ggctcaggaa gccaagaaac tggatgccaa gaccccatcc 2880
cagcggaaca agtggcaaca gcaggagtta atagcagagt tgaggcggcg ccaggccaag 2940
gaacaccggc ctgtttatga ggggaaggat ggtaccatcg aggacatcat cacagtgctg 3000
aagagtgtcc ctttcacggc ccgtactgcc aagcggggct cacgcttctt ctgtgatgca 3060
gcccaccatg atgagtcaaa ctgttagccc ccaaggttgg ggcccgacag gcctccactg 3120
ccagcctatg gttgttcgcc accaagccag gagtgctgca ccgcccagtg gtccccctcg 3180
ggctccaggc ccccactgag accctctcgg aggcagaagc acttcacccc tcagagtcct 3240
acaagtccaa ccagtggacc tggaattggc caagggctca ggagagggct gtgttgctct 3300

```
ctcaaccatg tccgccccag ctcttgaggc tggatctttc tacttgtgcc actatgggca   3360
ctaggtctgt aggtccctgg tgcttccagt actgcacttt gcccccaagg tctttgactt   3420
catttcctga agggtcacca agggtcagct cagggctagg aaaaaccatt tccagcctta   3480
gcctaaacag ggcacataga tctctcccac tagagcccag agggatgaga ggagagagca   3540
actgttcttt cttttttttt cccttccttt ttgcaggccc atggtcagct ctggtctaga   3600
tgtatctagg cttagggagc cctgggaccc tgccagtctc agttcatctc ttaccaggag   3660
caaggccctc tgaagcatgg gccgtgccag ctgtgcccta gtgataaggg taagaggaga   3720
gatgtcaggc tcactgccct tatttctctg cccatttcat tctaggctca cactgtcctt   3780
gtcaaggtgg gcagaagagc agaggtcttc tctgcaccaa ccactctctg cagatggctg   3840
gagaaagggt gtgccaactc ttcaccttct ttcctcagct acggtttttt tttttttttt   3900
tttttttggc aggggacaag gagcatggtg gtcttggcta tttgcttacc ttcccgtttc   3960
tcctctgccc ctggaaggga atgtgggggc ccactttttt gtacatgtac cacctccctt   4020
tcctcttact gtacataaac ctcagactct ccccctctca acaaaggctt gatgcaccaa   4080
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   4140
aaaaaaaaaa aaaaaaaaaa aaaaaaa                                       4168
```

<210> 236
<211> 1028
<212> PRT
<213> Homo sapiens

<400> 236

```
Met Gly Asn Leu Glu Ser Ala Glu Gly Val Pro Gly Glu Pro Pro Ser
1               5                   10                  15
Val Pro Leu Leu Leu Pro Pro Gly Lys Met Pro Met Pro Glu Pro Cys
            20                  25                  30
Glu Leu Glu Glu Arg Phe Ala Leu Val Leu Ser Ser Met Asn Leu Pro
        35                  40                  45
Pro Asp Lys Ala Arg Leu Leu Arg Gln Tyr Asp Asn Glu Lys Lys Trp
    50                  55                  60
Asp Leu Ile Cys Asp Gln Glu Arg Phe Gln Val Lys Asn Pro Pro His
65                  70                  75                  80
Thr Tyr Ile Gln Lys Leu Gln Ser Phe Leu Asp Pro Ser Val Thr Arg
                85                  90                  95
Lys Lys Phe Arg Arg Arg Val Gln Glu Ser Thr Lys Val Leu Arg Glu
            100                 105                 110
Leu Glu Ile Ser Leu Arg Thr Asn His Ile Gly Trp Val Arg Glu Phe
        115                 120                 125
Leu Asn Asp Glu Asn Lys Gly Leu Asp Val Leu Val Asp Tyr Leu Ser
    130                 135                 140
Phe Ala Gln Cys Ser Val Met Phe Asp Phe Glu Gly Leu Glu Ser Gly
145                 150                 155                 160
Asp Asp Gly Ala Phe Asp Lys Leu Arg Ser Trp Ser Arg Ser Ile Glu
                165                 170                 175
Asp Leu Gln Pro Pro Ser Ala Leu Ser Ala Pro Phe Thr Asn Ser Leu
            180                 185                 190
Ala Arg Ser Ala Arg Gln Ser Val Leu Arg Tyr Ser Thr Leu Pro Gly
        195                 200                 205
Arg Arg Ala Leu Lys Asn Ser Arg Leu Val Ser Gln Lys Asp Asp Val
    210                 215                 220
His Val Cys Ile Leu Cys Leu Arg Ala Ile Met Asn Tyr Gln Tyr Gly
225                 230                 235                 240
Phe Asn Leu Val Met Ser His Pro His Ala Val Asn Glu Ile Ala Leu
                245                 250                 255
Ser Leu Asn Asn Lys Asn Pro Arg Thr Lys Ala Leu Val Leu Glu Leu
            260                 265                 270
Leu Ala Ala Val Cys Leu Val Arg Gly Gly His Glu Ile Ile Leu Ala
        275                 280                 285
Ala Phe Asp Asn Phe Lys Glu Val Cys Lys Glu Leu His Arg Phe Glu
    290                 295                 300
Lys Leu Met Glu Tyr Phe Arg Asn Glu Asp Ser Asn Ile Asp Phe Met
```

305 310 315 320
Val Ala Cys Met Gln Phe Ile Asn Ile Val Val His Ser Val Glu Asp
325 330 335
Met Asn Phe Arg Val His Leu Gln Tyr Glu Phe Thr Lys Leu Gly Leu
340 345 350
Glu Glu Phe Leu Gln Lys Ser Arg His Thr Glu Ser Glu Lys Leu Gln
355 360 365
Val Gln Ile Gln Ala Tyr Leu Asp Asn Val Phe Asp Val Gly Gly Leu
370 375 380
Leu Glu Asp Ala Glu Thr Lys Asn Val Ala Leu Glu Lys Val Glu Glu
385 390 395 400
Leu Glu Glu His Val Ser His Leu Thr Glu Lys Leu Leu Asp Leu Glu
405 410 415
Asn Glu Asn Met Met Arg Val Ala Glu Leu Glu Lys Gln Leu Leu Gln
420 425 430
Arg Glu Lys Glu Leu Glu Ser Ile Lys Glu Thr Tyr Glu Asn Thr Ser
435 440 445
His Gln Val His Thr Leu Arg Arg Leu Ile Lys Glu Lys Glu Glu Ala
450 455 460
Phe Gln Arg Arg Cys His Leu Glu Pro Asn Val Arg Gly Leu Glu Ser
465 470 475 480
Val Asp Ser Glu Ala Leu Ala Arg Val Gly Pro Ala Glu Leu Ser Glu
485 490 495
Gly Met Pro Pro Ser Asp Leu Asp Leu Leu Ala Pro Ala Pro Pro Pro
500 505 510
Glu Glu Val Leu Pro Leu Pro Pro Pro Pro Ala Pro Pro Leu Pro Pro
515 520 525
Pro Pro Pro Pro Leu Pro Asp Lys Cys Pro Pro Ala Pro Pro Leu Pro
530 535 540
Gly Ala Ala Pro Ser Val Val Leu Thr Val Gly Leu Ser Ala Ile Arg
545 550 555 560
Ile Lys Lys Pro Ile Lys Thr Lys Phe Arg Leu Pro Val Phe Asn Trp
565 570 575
Thr Ala Leu Lys Pro Asn Gln Ile Ser Gly Thr Val Phe Ser Glu Leu
580 585 590
Asp Asp Glu Lys Ile Leu Glu Asp Leu Asp Leu Asp Lys Phe Glu Glu
595 600 605
Leu Phe Lys Thr Lys Ala Gln Gly Pro Ala Leu Asp Leu Ile Cys Ser
610 615 620
Lys Asn Lys Thr Ala Gln Lys Ala Ala Ser Lys Val Thr Leu Leu Glu
625 630 635 640
Ala Asn Arg Ala Lys Asn Leu Ala Ile Thr Leu Arg Lys Ala Gly Arg
645 650 655
Ser Ala Glu Glu Ile Cys Arg Ala Ile His Thr Phe Asp Leu Gln Thr
660 665 670
Leu Pro Val Asp Phe Val Glu Cys Leu Met Arg Phe Leu Pro Thr Glu
675 680 685
Ala Glu Val Lys Leu Leu Arg Gln Tyr Glu Arg Glu Arg Gln Pro Leu
690 695 700
Glu Glu Leu Ala Ala Glu Asp Arg Phe Met Leu Leu Phe Ser Lys Val
705 710 715 720
Glu Arg Leu Thr Gln Arg Met Ala Gly Met Ala Phe Leu Gly Asn Phe
725 730 735
Gln Asp Asn Leu Gln Met Leu Thr Pro Gln Leu Asn Ala Ile Ile Ala
740 745 750
Ala Ser Ala Ser Val Lys Ser Ser Gln Lys Leu Lys Gln Met Leu Glu
755 760 765
Ile Ile Leu Ala Leu Gly Asn Tyr Met Asn Ser Ser Lys Arg Gly Ala
770 775 780
Val Tyr Gly Phe Lys Leu Gln Ser Leu Asp Leu Leu Leu Asp Thr Lys
785 790 795 800

Ser Thr Asp Arg Lys Met Thr Leu Leu His Phe Ile Ala Leu Thr Val
805 810 815
Lys Glu Lys Tyr Pro Asp Leu Ala Asn Phe Trp His Glu Leu His Phe
820 825 830
Val Glu Lys Ala Ala Ala Val Ser Leu Glu Asn Val Leu Leu Asp Val
835 840 845
Lys Glu Leu Gly Arg Gly Met Glu Leu Ile Arg Arg Glu Cys Ser Ile
850 855 860
His Asp Asn Ser Val Leu Arg Asn Phe Leu Ser Thr Asn Glu Gly Lys
865 870 875 880
Leu Asp Lys Leu Gln Arg Asp Ala Lys Thr Ala Glu Glu Ala Tyr Asn
885 890 895
Ala Val Val Arg Tyr Phe Gly Glu Ser Pro Lys Thr Thr Pro Pro Ser
900 905 910
Val Phe Phe Pro Val Phe Val Arg Phe Ile Arg Ser Tyr Lys Glu Ala
915 920 925
Glu Gln Glu Asn Glu Ala Arg Lys Lys Gln Glu Glu Val Met Arg Glu
930 935 940
Lys Gln Leu Ala Gln Glu Ala Lys Lys Leu Asp Ala Lys Thr Pro Ser
945 950 955 960
Gln Arg Asn Lys Trp Gln Gln Gln Glu Leu Ile Ala Glu Leu Arg Arg
965 970 975
Arg Gln Ala Lys Glu His Arg Pro Val Tyr Glu Gly Lys Asp Gly Thr
980 985 990
Ile Glu Asp Ile Ile Thr Val Leu Lys Ser Val Pro Phe Thr Ala Arg
995 1000 1005
Thr Ala Lys Arg Gly Ser Arg Phe Phe Cys Asp Ala Ala His His Asp
1010 1015 1020
Glu Ser Asn Cys
1025

<210> 237
<211> 5641
<212> DNA
<213> Homo sapiens

<400> 237
cggaggagga cgcgagcccc ttgcgggcgg tcatcacagc ccagcctcgg ggctgccaca 60
gcgcgttgcg cctgtgcgcc ctcggtcccc gcgtccactg agcgccgcgc tcggggatgg 120
ggcccggccg gccggccccc gcgccctggc ctcgtcacct gctgcgctgc gtcctgctcc 180
tcgggtgcct gcacctcggc cgtcccggcg cccctgggga cgccgccctc ccggaaccca 240
acgtcttcct catcttcagc catggactgc agggctgcct ggaggcccag ggcgggcagg 300
tcagagtcac cccggcttgc aataccagcc tccctgccca gcgctggaag tgggtctccc 360
gaaaccggct attcaacctg ggtaccatgc agtgcctggg cacaggctgg ccaggcacca 420
acaccacggc ctccctgggc atgtatgagt gtgaccggga agcactgaat cttcgctggc 480
attgtcgtac actgggtgac cagctgtcct tgctcctggg ggcccgcacc agcaacatat 540
ccaagcctgg caccccttgag cgtggtgacc agacccgcag tggccagtgg cgcatctacg 600
gcagcgagga ggacctatgt gctctgccct accacgaggt ctacaccatc cagggaaact 660
cccacggaaa gccgtgcacc atccccttca aatatgacaa ccagtggttc cacggctgca 720
ccagcacggg ccgcgaggat ggtcacctgt ggtgtgccac cacccaggac tacggcaaag 780
acgagcgctg gggcttctgc cccatcaaga gtaacgactg cgagaccttc tgggacaagg 840
accagctgac tgacagctgc taccagttta acttccagtc cacgctgtcg tggagggagg 900
cctgggccag ctgcgagcag cagggtgcgg atctgctgag catcacggag atccacgagc 960
agacctacat caacggcctc ctcactgggt acagctccac cctgtggatc ggcttgaatg 1020
acttggacac gagcggaggc tggcagtggt cggacaactc gcccctcaag tacctcaact 1080
gggagagtga ccagccggac aaccccagtg aggagaactg tggagtgatc cgcactgagt 1140
cctcgggcgg ctggcagaac cgtgactgca gcatcgcgct gccctatgtg tgcaagaaga 1200
agcccaacgc cacggccgag cccacccctc cagacaggtg ggccaatgtg aaggtggagt 1260
gcgagccgag ctggcagccc ttccagggcc actgctaccg cctgcaggcc gagaagcgca 1320
gctggcagga gtccaagaag gcatgtctac ggggcggtgg cgacctggtc agcatccaca 1380
gcatggcgga gctggaattc atcaccaagc agatcaagca agaggtggag gagctgtgga 1440

```
tcggcctcaa cgatttgaaa ctgcagatga attttgagtg gtctgacggg agccttgtga    1500
gcttcaccca ctggcacccc tttgagccca acaacttccg ggacagtctg gaggactgtg    1560
tcaccatctg ggcccggaa ggccgctgga acgacagtcc ctgtaaccag tccttgccat    1620
ccatctgcaa gaaggcaggc cagctgagcc agggggccgc cgaggaggac catggctgcc    1680
ggaagggttg gacgtggcac agcccatcct gctactggct gggagaagac caagtgacct    1740
acagtgaggc ccggcgcctg tgcactgacc atggctctca gctggtcacc atcaccaaca    1800
ggttcgagca ggccttcgtc agcagcctca tctacaactg ggagggcgag tacttctgga    1860
cggccctgca ggacctcaac agcaccggct ccttcttctg gctcagtggg gatgaagtca    1920
tgtacaccca ctggaaccgg gaccagcccg ggtacagccg tgggggctgc gtggcgctgg    1980
ccactggcag cgccatgggg ctgtgggagg tgaagaactg tacctcgttc cgggcccgct    2040
acatctgccg gcagagcctg ggcactccag tgacgccgga gctgccgggg ccagatccca    2100
cgcccagcct cactggctcc tgtccccagg gctgggcctc ggacaccaaa ctccggtatt    2160
gctataaggt gttcagctca gagcggctgc aggacaagaa gagctgggtc caggcccagg    2220
gggcctgcca ggagctgggg gcccagctgc tgagcctggc cagctacgag gaggagcact    2280
ttgtggccaa catgctcaac aagatcttcg gtgaatcaga acccgagatc cacgagcagc    2340
actggttctg gatcggcctg aaccgtcggg atcccagagg gggtcagagt tggcgctgga    2400
gcgacggcgt agggttctct taccacaatt tcgaccggag ccggcacgac gacgacgaca    2460
tccgaggctg tgcggtgctg gacctggcct ccctgcagtg ggtggccatg cagtgcgaca    2520
cacagctgga ctggatctgc aagatcccca gaggtacgga cgtgcgggag cccgacgaca    2580
gccctcaagg ccgacgggaa tggctgcgct tccaggaggc cgagtacaag ttctttgagc    2640
accactccac gtgggcgcag gcgcagcgca tctgcacgtg gttccaggcc gagctgacct    2700
ccgtgcacag ccaggcagag ctagacttcc tgagccacaa cttgcagaag ttctcccggg    2760
cccaggagca gcactggtgg atcggcctgc acacctctga gagcgatggg cgcttcagat    2820
ggacagatgg ttccattata aacttcatct cctgggcacc aggcaaacct cggcctgtcg    2880
gcaaggacaa gaagtgcgtg tacatgacag ccagccgaga ggactggggg gaccagaggt    2940
gcctgacagc cttgccctac atctgcaagc gcagcaacgt caccaaagaa acgcagcccc    3000
cagacctgcc aactacagcc ctgggggct gcccctctga ctggatccag ttcctcaaca    3060
agtgttttca ggtccagggc caggaacccc agagccgggt gaagtggtca gaggcacagt    3120
tctcctgtga acagcaagag gcccagctgg tcaccatcac aaaccccta gagcaagcat    3180
tcatcacagc cagcctgccc aatgtgacct ttgacctttg gattggcctc catgcctcgc    3240
agagggactt ccagtgggtg gagcaggagc ctttgatgta tgccaactgg gcacctgggg    3300
agccctctgg ccctagccct gctcccagtg gcaacaaacc gaccagctgt gcggtggtcc    3360
tgcacagccc ctcagcccac ttcactggcc gctgggacga tcggagctgc acggaggaga    3420
cccatggctt catctgccag aagggcacgg acccctccct gagcccgtcc ccagcagcgc    3480
tgccccccgc cccgggcact gagctctcct acctcaacgg caccttccgg ctgcttcaga    3540
agccgctgcg ctggcacgat gccctcctgc tgtgtgagag ccacaatgcc agcctggcct    3600
acgtgcccga cccctacacc caggccttcc tcacgcaggc tgcccgaggg ctgcgcacgc    3660
cgctctggat tgggctggct ggcgaggagg gctctcggcg gtactcctgg gtctcagagg    3720
agccgctgaa ctacgtgggc tggcaggacg gggagccgca gcagccgggg ggctgtacct    3780
acgtagatgt ggacggggcc tggcgcacca ccagctgtga caccaagctg caggggggctg    3840
tgtgtggggt tagcagtggg ccccctcctc cccgaagaat aagctaccat ggcagctgtc    3900
cccagggact ggcagactcc gcgtggattc ccttccggga gcactgctat tctttccaca    3960
tggagctgct gctgggccac aaggaggcgc gacagcgctg ccagagagcg ggtggggccg    4020
tcctgtctat cctggatgag atggagaatg tgtttgtctg ggagcacctg cagagctatg    4080
agggccagag tcggggcgcc tggctgggca tgaacttcaa ccccaaagga ggcactctgg    4140
tctggcagga caacacagct gtgaactact ccaactgggg gcccccgggc ttgggcccca    4200
gcatgctgag ccacaacagc tgctactgga ttcagagcaa cagcgggcta tggcgccccg    4260
gcgcttgcac caacatcacc atgggtgtcg tctgcaagct tcctcgtgct gagcagagca    4320
gcttctcccc atcagcgctt ccagagaacc cagcggccct ggtggtggtg ctgatggcgg    4380
tgctgctgct cctggccttg ctgaccgcag ccctcatcct ttaccggagg cgccagagca    4440
tcgagcgcgg ggcctttgag ggtgcccgct acagccgcag cagctccagc cccaccgagg    4500
ccactgagaa gaacatcctg gtgtcagaca tggaaatgaa tgagcaacaa gaatagagcc    4560
aggcgcgtgg gcagggccag ggcgggagga gctggggagc tggggccctg ggtcagtctg    4620
gcccccccacc agctgcctgt ccagttggcc tatggaaggg tgcccttggg agtcgctgtt    4680
gggagccgga gctgggcaga gcctgggctg gtggggtgcc accctcccac aagggctggg    4740
ctgagaccca gctgagtgca gcgtggcgtt tccctttctg gggggcctg aggtcttgtc    4800
acctggtcct gtgcccccac aggaaccaga ggtaggatgg gagggggaac gagagcctct    4860
ttctccccag agcccccggc ccaggcctgt tgatccgcgc cccaggaccc ccttctttgc    4920
agagcccgag gagcctcccc tgtcccctcg ggcagatctg ttgtgtctct cttcccacct    4980
ggcagcctca gctctgtgcc cctcaccctg ctccctctcg cccctctct cccacccctt    5040
ccttctgagc cgggccctgg ggattgggga gccctcttgt tcctgatgag ggtcagctga    5100
```

```
gggggctgag catccatcac tcctgtgcct gctggggtgg ctgtggggcg tggcaggagg    5160
ggcctaggtg ggttgggcct gagaaccagg gcacgggtgt ggtgtctgct gggctggaga    5220
taagactggg gagagacacc ccaacctccc agggtgggag ctgggccggg ctgggatgtc    5280
atctcctgcc gggcgggggga gggctctgcc cctggaagag tcccctgtgg ggaccaaaat   5340
aagttcccta acatctccag ctcctggctc tggtttggag caaggggaag ggttgccaga    5400
gtcctggggg ccccagagga gcaggagtct gggagggccc agagttcacc ctctagtgga    5460
tccaggagga gcagcacccg agccctggag tggcccagta cccttccaag aggccacagt    5520
cccagccagg acaaagtatg cggcccatcc tggtgcgaca gcgtgggaca atgtgaacat    5580
ggactcgaag acatggccct ttctctgtag ttgatttttt aaatgtgcca ttattgtttt    5640
t                                                                    5641
```

<210> 238
<211> 1479
<212> PRT
<213> Homo sapiens

<400> 238

```
Met Gly Pro Gly Arg Pro Ala Pro Ala Pro Trp Pro Arg His Leu Leu
1               5                   10                  15
Arg Cys Val Leu Leu Leu Gly Cys Leu His Leu Gly Arg Pro Gly Ala
            20                  25                  30
Pro Gly Asp Ala Ala Leu Pro Glu Pro Asn Val Phe Leu Ile Phe Ser
        35                  40                  45
His Gly Leu Gln Gly Cys Leu Glu Ala Gln Gly Gly Gln Val Arg Val
    50                  55                  60
Thr Pro Ala Cys Asn Thr Ser Leu Pro Ala Gln Arg Trp Lys Trp Val
65                  70                  75                  80
Ser Arg Asn Arg Leu Phe Asn Leu Gly Thr Met Gln Cys Leu Gly Thr
                85                  90                  95
Gly Trp Pro Gly Thr Asn Thr Thr Ala Ser Leu Gly Met Tyr Glu Cys
            100                 105                 110
Asp Arg Glu Ala Leu Asn Leu Arg Trp His Cys Arg Thr Leu Gly Asp
        115                 120                 125
Gln Leu Ser Leu Leu Leu Gly Ala Arg Thr Ser Asn Ile Ser Lys Pro
    130                 135                 140
Gly Thr Leu Glu Arg Gly Asp Gln Thr Arg Ser Gly Gln Trp Arg Ile
145                 150                 155                 160
Tyr Gly Ser Glu Glu Asp Leu Cys Ala Leu Pro Tyr His Glu Val Tyr
                165                 170                 175
Thr Ile Gln Gly Asn Ser His Gly Lys Pro Cys Thr Ile Pro Phe Lys
            180                 185                 190
Tyr Asp Asn Gln Trp Phe His Gly Cys Thr Ser Thr Gly Arg Glu Asp
        195                 200                 205
Gly His Leu Trp Cys Ala Thr Thr Gln Asp Tyr Gly Lys Asp Glu Arg
    210                 215                 220
Trp Gly Phe Cys Pro Ile Lys Ser Asn Asp Cys Glu Thr Phe Trp Asp
225                 230                 235                 240
Lys Asp Gln Leu Thr Asp Ser Cys Tyr Gln Phe Asn Phe Gln Ser Thr
                245                 250                 255
Leu Ser Trp Arg Glu Ala Trp Ala Ser Cys Glu Gln Gln Gly Ala Asp
            260                 265                 270
Leu Leu Ser Ile Thr Glu Ile His Glu Gln Thr Tyr Ile Asn Gly Leu
        275                 280                 285
Leu Thr Gly Tyr Ser Ser Thr Leu Trp Ile Gly Leu Asn Asp Leu Asp
    290                 295                 300
Thr Ser Gly Gly Trp Gln Trp Ser Asp Asn Ser Pro Leu Lys Tyr Leu
305                 310                 315                 320
Asn Trp Glu Ser Asp Gln Pro Asp Asn Pro Ser Glu Glu Asn Cys Gly
                325                 330                 335
```

Val Ile Arg Thr Glu Ser Ser Gly Gly Trp Gln Asn Arg Asp Cys Ser
340 345 350
Ile Ala Leu Pro Tyr Val Cys Lys Lys Lys Pro Asn Ala Thr Ala Glu
355 360 365
Pro Thr Pro Pro Asp Arg Trp Ala Asn Val Lys Val Glu Cys Glu Pro
370 375 380
Ser Trp Gln Pro Phe Gln Gly His Cys Tyr Arg Leu Gln Ala Glu Lys
385 390 395 400
Arg Ser Trp Gln Glu Ser Lys Lys Ala Cys Leu Arg Gly Gly Gly Asp
405 410 415
Leu Val Ser Ile His Ser Met Ala Glu Leu Glu Phe Ile Thr Lys Gln
420 425 430
Ile Lys Gln Glu Val Glu Glu Leu Trp Ile Gly Leu Asn Asp Leu Lys
435 440 445
Leu Gln Met Asn Phe Glu Trp Ser Asp Gly Ser Leu Val Ser Phe Thr
450 455 460
His Trp His Pro Phe Glu Pro Asn Asn Phe Arg Asp Ser Leu Glu Asp
465 470 475 480
Cys Val Thr Ile Trp Gly Pro Glu Gly Arg Trp Asn Asp Ser Pro Cys
485 490 495
Asn Gln Ser Leu Pro Ser Ile Cys Lys Lys Ala Gly Gln Leu Ser Gln
500 505 510
Gly Ala Ala Glu Glu Asp His Gly Cys Arg Lys Gly Trp Thr Trp His
515 520 525
Ser Pro Ser Cys Tyr Trp Leu Gly Glu Asp Gln Val Thr Tyr Ser Glu
530 535 540
Ala Arg Arg Leu Cys Thr Asp His Gly Ser Gln Leu Val Thr Ile Thr
545 550 555 560
Asn Arg Phe Glu Gln Ala Phe Val Ser Ser Leu Ile Tyr Asn Trp Glu
565 570 575
Gly Glu Tyr Phe Trp Thr Ala Leu Gln Asp Leu Asn Ser Thr Gly Ser
580 585 590
Phe Phe Trp Leu Ser Gly Asp Glu Val Met Tyr Thr His Trp Asn Arg
595 600 605
Asp Gln Pro Gly Tyr Ser Arg Gly Gly Cys Val Ala Leu Ala Thr Gly
610 615 620
Ser Ala Met Gly Leu Trp Glu Val Lys Asn Cys Thr Ser Phe Arg Ala
625 630 635 640
Arg Tyr Ile Cys Arg Gln Ser Leu Gly Thr Pro Val Thr Pro Glu Leu
645 650 655
Pro Gly Pro Asp Pro Thr Pro Ser Leu Thr Gly Ser Cys Pro Gln Gly
660 665 670
Trp Ala Ser Asp Thr Lys Leu Arg Tyr Cys Tyr Lys Val Phe Ser Ser
675 680 685
Glu Arg Leu Gln Asp Lys Lys Ser Trp Val Gln Ala Gln Gly Ala Cys
690 695 700
Gln Glu Leu Gly Ala Gln Leu Leu Ser Leu Ala Ser Tyr Glu Glu Glu
705 710 715 720
His Phe Val Ala Asn Met Leu Asn Lys Ile Phe Gly Glu Ser Glu Pro
725 730 735
Glu Ile His Glu Gln His Trp Phe Trp Ile Gly Leu Asn Arg Arg Asp
740 745 750
Pro Arg Gly Gly Gln Ser Trp Arg Trp Ser Asp Gly Val Gly Phe Ser
755 760 765
Tyr His Asn Phe Asp Arg Ser Arg His Asp Asp Asp Asp Ile Arg Gly
770 775 780
Cys Ala Val Leu Asp Leu Ala Ser Leu Gln Trp Val Ala Met Gln Cys
785 790 795 800
Asp Thr Gln Leu Asp Trp Ile Cys Lys Ile Pro Arg Gly Thr Asp Val
805 810 815
Arg Glu Pro Asp Asp Ser Pro Gln Gly Arg Arg Glu Trp Leu Arg Phe

```
            820                 825                 830
Gln Glu Ala Glu Tyr Lys Phe Phe Glu His His Ser Thr Trp Ala Gln
        835                 840                 845
Ala Gln Arg Ile Cys Thr Trp Phe Gln Ala Glu Leu Thr Ser Val His
    850                 855                 860
Ser Gln Ala Glu Leu Asp Phe Leu Ser His Asn Leu Gln Lys Phe Ser
865                 870                 875                 880
Arg Ala Gln Glu Gln His Trp Trp Ile Gly Leu His Thr Ser Glu Ser
                885                 890                 895
Asp Gly Arg Phe Arg Trp Thr Asp Gly Ser Ile Ile Asn Phe Ile Ser
            900                 905                 910
Trp Ala Pro Gly Lys Pro Arg Pro Val Gly Lys Asp Lys Lys Cys Val
        915                 920                 925
Tyr Met Thr Ala Ser Arg Glu Asp Trp Gly Asp Gln Arg Cys Leu Thr
    930                 935                 940
Ala Leu Pro Tyr Ile Cys Lys Arg Ser Asn Val Thr Lys Glu Thr Gln
945                 950                 955                 960
Pro Pro Asp Leu Pro Thr Thr Ala Leu Gly Gly Cys Pro Ser Asp Trp
                965                 970                 975
Ile Gln Phe Leu Asn Lys Cys Phe Gln Val Gln Gly Gln Glu Pro Gln
            980                 985                 990
Ser Arg Val Lys Trp Ser Glu Ala Gln Phe Ser Cys Glu Gln Gln Glu
        995                 1000                1005
Ala Gln Leu Val Thr Ile Thr Asn Pro Leu Glu Gln Ala Phe Ile Thr
    1010                1015                1020
Ala Ser Leu Pro Asn Val Thr Phe Asp Leu Trp Ile Gly Leu His Ala
1025                1030                1035                1040
Ser Gln Arg Asp Phe Gln Trp Val Glu Gln Glu Pro Leu Met Tyr Ala
                1045                1050                1055
Asn Trp Ala Pro Gly Glu Pro Ser Gly Pro Ser Pro Ala Pro Ser Gly
            1060                1065                1070
Asn Lys Pro Thr Ser Cys Ala Val Val Leu His Ser Pro Ser Ala His
        1075                1080                1085
Phe Thr Gly Arg Trp Asp Asp Arg Ser Cys Thr Glu Glu Thr His Gly
    1090                1095                1100
Phe Ile Cys Gln Lys Gly Thr Asp Pro Ser Leu Ser Pro Ser Pro Ala
1105                1110                1115                1120
Ala Leu Pro Pro Ala Pro Gly Thr Glu Leu Ser Tyr Leu Asn Gly Thr
                1125                1130                1135
Phe Arg Leu Leu Gln Lys Pro Leu Arg Trp His Asp Ala Leu Leu Leu
            1140                1145                1150
Cys Glu Ser His Asn Ala Ser Leu Ala Tyr Val Pro Asp Pro Tyr Thr
        1155                1160                1165
Gln Ala Phe Leu Thr Gln Ala Ala Arg Gly Leu Arg Thr Pro Leu Trp
    1170                1175                1180
Ile Gly Leu Ala Gly Glu Glu Gly Ser Arg Arg Tyr Ser Trp Val Ser
1185                1190                1195                1200
Glu Glu Pro Leu Asn Tyr Val Gly Trp Gln Asp Gly Glu Pro Gln Gln
                1205                1210                1215
Pro Gly Gly Cys Thr Tyr Val Asp Val Asp Gly Ala Trp Arg Thr Thr
            1220                1225                1230
Ser Cys Asp Thr Lys Leu Gln Gly Ala Val Cys Gly Val Ser Ser Gly
        1235                1240                1245
Pro Pro Pro Pro Arg Arg Ile Ser Tyr His Gly Ser Cys Pro Gln Gly
    1250                1255                1260
Leu Ala Asp Ser Ala Trp Ile Pro Phe Arg Glu His Cys Tyr Ser Phe
1265                1270                1275                1280
His Met Glu Leu Leu Leu Gly His Lys Glu Ala Arg Gln Arg Cys Gln
                1285                1290                1295
Arg Ala Gly Gly Ala Val Leu Ser Ile Leu Asp Glu Met Glu Asn Val
            1300                1305                1310
```

Phe Val Trp Glu His Leu Gln Ser Tyr Glu Gly Gln Ser Arg Gly Ala
1315 1320 1325
Trp Leu Gly Met Asn Phe Asn Pro Lys Gly Gly Thr Leu Val Trp Gln
1330 1335 1340
Asp Asn Thr Ala Val Asn Tyr Ser Asn Trp Gly Pro Pro Gly Leu Gly
1345 1350 1355 1360
Pro Ser Met Leu Ser His Asn Ser Cys Tyr Trp Ile Gln Ser Asn Ser
1365 1370 1375
Gly Leu Trp Arg Pro Gly Ala Cys Thr Asn Ile Thr Met Gly Val Val
1380 1385 1390
Cys Lys Leu Pro Arg Ala Glu Gln Ser Ser Phe Ser Pro Ser Ala Leu
1395 1400 1405
Pro Glu Asn Pro Ala Ala Leu Val Val Val Leu Met Ala Val Leu Leu
1410 1415 1420
Leu Leu Ala Leu Leu Thr Ala Ala Leu Ile Leu Tyr Arg Arg Arg Gln
1425 1430 1435 1440
Ser Ile Glu Arg Gly Ala Phe Glu Gly Ala Arg Tyr Ser Arg Ser Ser
1445 1450 1455
Ser Ser Pro Thr Glu Ala Thr Glu Lys Asn Ile Leu Val Ser Asp Met
1460 1465 1470
Glu Met Asn Glu Gln Gln Glu
1475

<210> 239
<211> 6127
<212> DNA
<213> Homo sapiens

<400> 239
ctgctccttg caccccgctc cctgcctgga cacaggctca ctcgctgcct tcttctgggg 60
gaaaccagct tcttgccagc cacagctgct gcctccgcca ctggccaccg cccctgtcct 120
gggagtccct tggcccagac acccacctga cttagtggct cctctgcagg aaaggtggct 180
gccccctgcg ttcctccatc caaccatgag ctggtgccca tcaccactga gaatgcacca 240
aagaatgtag tggacaaggg agaaggagcc tcccggggtg gaaacacacg gaaaagcctc 300
gaggacaacg gctccaccag ggtcaccccg agtgtccagc cccacctcca gcccatcaga 360
aacatgagtg tgagccggac catggaggac agctgtgagc tggacctggt gtacgtcaca 420
gagaggatca tcgctgtctc cttccccagc acagccaatg aggagaactt ccggagcaac 480
ctccgtgagg tggcgcagat gctcaagtcc aaacatggag gcaactacct gctgttcaac 540
ctctctgagc ggagacctga catcacgaag ctccatgcca aggtactgga atttggctgg 600
cccgacctcc acaccccagc cctggagaag atctgcagca tctgtaaggc catggacaca 660
tggctcaatg cagaccctca caatgtcgtt gttctacaca acaagggaaa ccgaggcagg 720
ataggagttg tcatcgcggc ttacatgcac tacagcaaca tttctgccag tgcggaccag 780
gctctggacc ggtttgcaat gaagcggttc tatgaggata agattgtgcc cattggccag 840
ccatcccaaa gaaggtacgt gcattacttc agtggcctgc tctccggctc catcaaaata 900
aacaacaagc ccttgtttct gcaccacgtg atcatgcacg gcatccccaa ctttgagtct 960
aaaggaggat gtcggccatt tctccgcatc taccaggcca tgcaacctgt gtacacatct 1020
ggcatctaca acatcccagg agacagccag actagcgtct gcatcaccat cgagccagga 1080
ctgctcttga agggagacat cttgctgaag tgctaccaca agaagttccg aagcccagcc 1140
cgagacgtca tcttccgtgt gcagttccac acctgtgcca tccatgacct gggggttgtc 1200
tttgggaagg aggaccttga tgatgctttc aaagatgatc gatttccaga gtatggcaaa 1260
gtggagtttg tattttctta tgggccagag aaaattcaag gcatggagca cctggagaac 1320
gggccgagcg tgtctgtgga ctataacacc tctgaccccc tcatccgctg ggactcctac 1380
gacaacttca gtgggcatcg agatgacggc atggaggagg tggtgggaca cacgcagggg 1440
ccactagatg ggagcctgta tgctaaggtg aagaagaaag actccctgca cggcagcacc 1500
ggggctgtta atgccacacg tcctacactg tcggccaccc ccaaccacgt ggaacacacg 1560
ctttctgtga gcagcgactc gggcaactcc acagcctcca ccaagaccga caagaccgac 1620
gagcctgtcc ccggggcctc cagtgccact gctgccttga gtccccagga gaagcgggag 1680
ctggaccgcc tgctgagtgg ctttggctta gagcgagaga agcaaggcgc catgtaccac 1740
acccagcacc tcaggtcccg cccagcaggg ggctcggctg tgccctcctc tggacgccac 1800
gttgtcccag cccaggttca tgtcaatggt ggggcgttag catctgagcg ggagacagac 1860
atcctggacg atgaattgcc aaaccaggat ggtcacagtg cgggcagcat gggcacactc 1920

tcttctctgg acggggtcac caacaccagt gagggggct acccagaggc cctgtcccca 1980
ctgaccaacg gtctggacaa gtcctacccc atggagccta tggtcaatgg aggaggctac 2040
ccctacgagt ctgccagccg ggcggggcct gcccatgctg gccacacggc cccatgcgg 2100
ccctcctact ctgcacagga gggtttagct ggctaccaga gggagggcc ccacccagcc 2160
tggccacagc cagtgaccac ctcccactat gcccatgacc ccagcggtat gttccgctct 2220
caatcctttt cggaagctga accccagctg cccccagctc cggtccgagg gggaagcagc 2280
cgggaggctg tgcaaagggg actgaattcg tggcagcagc agcagcagca gcagcagcag 2340
cctcgcccac ctccacgcca gcaggaaaga gcccacttgg agagtcttgt agccagcagg 2400
cccagccctc agccattggc agagaccccc atccccagtc tccctgagtt cccgcgagca 2460
gcctcccagc aggagattga acagtccatc gaaacactca atatgctgat gctggacctg 2520
gagccagcct ccgctgctgc cccactacac aagtcccaga gtgtccccgg ggcctggcca 2580
ggggcttctc cactctcctc ccagcccctc tctggatcct cccgtcagtc ccatccactg 2640
acccagtcca gatctggcta tatccccagt gggcattcgt tgggaacccc tgagccagcc 2700
ccacgggcct ctctggagtc tgtccctcct ggcaggtctt actcacctta tgactatcag 2760
ccatgtttgg ctgggcctaa ccaggatttc cattcaaaga gcccagcctc ttcctccttg 2820
cctgccttcc ttccgaccac ccacagccct ccagggcctc agcaaccccc agcctctctc 2880
cctggcctca ctgctcagcc tctgctctca ccaaaggaag cgacttcaga cccctcccgg 2940
actccagagg aggagccatt gaatttagaa gggctggtgg cccacagggt agcaggggta 3000
caggctcggg agaagcagcc tgcagagccc ccagcccctc tgcggaggcg ggcggccagt 3060
gatggacagt atgagaacca gtctccagaa gccacatccc ctcgtagccc tggggttcgc 3120
tcccctgtcc agtgtgtctc ccccggagctg gctcttacca tcgctctcaa tcctggaggg 3180
cggcccaaag agccccattt gcacagctac aaggaggcct tcgaggagat ggagggaacc 3240
tccccgagca gcccaccacc cagtggggtg cggtcccccc cgggtctggc caagacaccc 3300
ctgtctgctc tgggcctgaa acctcacaac ccagcggaca tcctgttgca ccccacagga 3360
gttaccagaa gacggatcca gccagaggaa gatgagggga aggtggtggt caggctgtca 3420
gaagagcccc ggagctatgt ggagtctgtg gcacggacag cggtggctgg accccgagct 3480
caggactctg agcccaagag ctttagtgct ccagccaccc aggcctatgg ccatgagata 3540
cccctgagga acgggaccct gggtggctcc tttgtctccc ccagcccccct ctccaccagc 3600
agccccatcc tcagtgctga cagcacttca gtggggagtt tcccgtcggg agagagcagt 3660
gaccagggtc cccggacgcc cacccagcct ctgttggagt ctggcttccg ctcaggcagc 3720
ctgggacagc ccagcccatc tgcccagaga aactaccaga gctcttctcc tctcccgact 3780
gtgggcagta gctacagcag ccccgactac tcacttcagc atttcagctc ctctccggaa 3840
agccaggccc gagctcagtt cagtgtggct ggcgtccaca cggtgcctgg gagccctcag 3900
gcgcgccaca gaacagtggg caccaacact ccccctagtc ctggcttcgg ccggcgggcc 3960
atcaatccca gcatggctgc cccccagcagt cccagtttga gccatcacca gatgatgggt 4020
ccaccaggca ctggcttcca tggtagcact gtctccagcc cccagagcag tgcagcgacc 4080
accccgggga gccccagcct gtgtcggcac ccagcagggg tctaccaggt ttctggcctc 4140
cacaacaaag tggccaccac cccgggggagt cccagcctgg gccggcaccc tggggctcac 4200
caaggcaacc tggcctccgg tcttcatagc aatgcaatag ccagccctgg aagccccagc 4260
ctgggccgtc acctcggagg gtctggatct gtggttcccg gcagcccctg cttggaccgg 4320
catgtggcct atggcggcta ttctaccccg gaggatcgga gacccacact gtcccggcag 4380
agcagtgcct ctggctacca ggctccttcc acgccctcct tccctgtctc ccctgcctac 4440
taccctggcc tgagcagccc tgccacctcc ccgtcaccag actccgcagc cttccggcaa 4500
gggagcccaa caccagcctt gccagagaag cgaaggatgt cagtgggaga ccgggcaggc 4560
agcctcccca actatgccac catcaatggg aaggttgctt cgcctgtgcc cagcggcatg 4620
tccagtccca gcgggggcag caccgtctcc ttctcccaca ctctgcccga cttctccaag 4680
tactccatgc cagacaacag cccggagacg cgggctaaag tgaagtttgt ccaggacact 4740
tctaagtatt ggtacaagcc tgagatctcc agggagcagg ccatcgcgct cctcaaggac 4800
caggagccgg gggccttcat catccgcgac agtcactcct tccgaggcgc gtacgggctg 4860
gccatgaagg tgtcttcgcc acctccaacc atcatgcagc agaataaaaa aggagacatg 4920
acccatgagc tggtcaggca ttttctgata gagactggcc ccagaggagt caagctcaag 4980
ggctgcccca atgagccaaa cttcggatcg ctgtctgccc tggtctacca gcactccatc 5040
atcccattgg ccctgccttg caagctggtc attccaaacc gagaccccac agatgaatcg 5100
aaagatagct ccggccctgc caactcaact gcagacctgc tgaaacaagg ggcagcctgc 5160
aatgtgctct tcatcaactc tgtggacatg gagtcactca ctgggccaca ggccatctct 5220
aaagccacat ctgagacgtt ggctgcagac cccacgccag ctgccaccat cgttcacttc 5280
aaagtctctg cccagggaat cactctgact gacaaccaga gaaagctctt tttcagacgc 5340
cactaccctc tcaacactgt caccttctgt gacctggatc cacaggaaag aaagtggatg 5400
aaaacagagg gtggtgcccc tgctaagctc ttcggcttcg tggcccggaa gcagggcagc 5460
accacggaca acgcctgcca cctctttgct gagcttgacc ccaaccagcc ggcctctgcc 5520
atcgtcaact tcgtctccaa ggtcatgctg aatgccggcc aaaagagatg aaccctgccc 5580

```
cttgcccagg gccagtgcca tggggaaggg gcttgtgggg aggggaccca tgaatcctga      5640
ccactcttga acccagaagg aggactttgg gccaatttcg gaggagagaa gaaagtgcaa      5700
cgtggggaga gggaagtgaa ttgcagaggg gagggggaaa agagagagag agagagagag      5760
agagagagag agagagagaa agatggagga gaagaacttg gattcccctg ggtagatgga      5820
aactgcaaaa acccaaagcc tccaaaacta accaggtcca cctaacaccc cctccctccc      5880
ctaagaagat ggatgtcctc aaaagagaag gaacaaacct ccttgggaat ccacattttt      5940
tgggggaatg gaaaagctct gtctccctaa ctcaactgct ttgcaagggg aaatcaagct      6000
gggagaatct ttttctggcc acctgtaggg taggttgtca aaccaaacag agccaccgtg      6060
ggacatcaag tggaagaact tgtttgcttg aaagtatctc agacccaagg cacctcaggt      6120
ctctttg                                                                 6127
```

<210> 240
<211> 1732
<212> PRT
<213> Homo sapiens

<400> 240

```
Met Ser Val Ser Arg Thr Met Glu Asp Ser Cys Glu Leu Asp Leu Val
1               5                   10                  15
Tyr Val Thr Glu Arg Ile Ile Ala Val Ser Phe Pro Ser Thr Ala Asn
            20                  25                  30
Glu Glu Asn Phe Arg Ser Asn Leu Arg Glu Val Ala Gln Met Leu Lys
        35                  40                  45
Ser Lys His Gly Gly Asn Tyr Leu Leu Phe Asn Leu Ser Glu Arg Arg
    50                  55                  60
Pro Asp Ile Thr Lys Leu His Ala Lys Val Leu Glu Phe Gly Trp Pro
65                  70                  75                  80
Asp Leu His Thr Pro Ala Leu Glu Lys Ile Cys Ser Ile Cys Lys Ala
                85                  90                  95
Met Asp Thr Trp Leu Asn Ala Asp Pro His Asn Val Val Val Leu His
            100                 105                 110
Asn Lys Gly Asn Arg Gly Arg Ile Gly Val Val Ile Ala Ala Tyr Met
        115                 120                 125
His Tyr Ser Asn Ile Ser Ala Ser Ala Asp Gln Ala Leu Asp Arg Phe
    130                 135                 140
Ala Met Lys Arg Phe Tyr Glu Asp Lys Ile Val Pro Ile Gly Gln Pro
145                 150                 155                 160
Ser Gln Arg Arg Tyr Val His Tyr Phe Ser Gly Leu Leu Ser Gly Ser
                165                 170                 175
Ile Lys Ile Asn Asn Lys Pro Leu Phe Leu His His Val Ile Met His
            180                 185                 190
Gly Ile Pro Asn Phe Glu Ser Lys Gly Gly Cys Arg Pro Phe Leu Arg
        195                 200                 205
Ile Tyr Gln Ala Met Gln Pro Val Tyr Thr Ser Gly Ile Tyr Asn Ile
    210                 215                 220
Pro Gly Asp Ser Gln Thr Ser Val Cys Ile Thr Ile Glu Pro Gly Leu
225                 230                 235                 240
Leu Leu Lys Gly Asp Ile Leu Leu Lys Cys Tyr His Lys Lys Phe Arg
                245                 250                 255
Ser Pro Ala Arg Asp Val Ile Phe Arg Val Gln Phe His Thr Cys Ala
            260                 265                 270
Ile His Asp Leu Gly Val Val Phe Gly Lys Glu Asp Leu Asp Asp Ala
        275                 280                 285
Phe Lys Asp Asp Arg Phe Pro Glu Tyr Gly Lys Val Glu Phe Val Phe
    290                 295                 300
Ser Tyr Gly Pro Glu Lys Ile Gln Gly Met Glu His Leu Glu Asn Gly
305                 310                 315                 320
Pro Ser Val Ser Val Asp Tyr Asn Thr Ser Asp Pro Leu Ile Arg Trp
                325                 330                 335
```

Asp Ser Tyr Asp Asn Phe Ser Gly His Arg Asp Asp Gly Met Glu Glu
340 345 350
Val Val Gly His Thr Gln Gly Pro Leu Asp Gly Ser Leu Tyr Ala Lys
355 360 365
Val Lys Lys Lys Asp Ser Leu His Gly Ser Thr Gly Ala Val Asn Ala
370 375 380
Thr Arg Pro Thr Leu Ser Ala Thr Pro Asn His Val Glu His Thr Leu
385 390 395 400
Ser Val Ser Ser Asp Ser Gly Asn Ser Thr Ala Ser Thr Lys Thr Asp
405 410 415
Lys Thr Asp Glu Pro Val Pro Gly Ala Ser Ser Ala Thr Ala Ala Leu
420 425 430
Ser Pro Gln Glu Lys Arg Glu Leu Asp Arg Leu Leu Ser Gly Phe Gly
435 440 445
Leu Glu Arg Glu Lys Gln Gly Ala Met Tyr His Thr Gln His Leu Arg
450 455 460
Ser Arg Pro Ala Gly Gly Ser Ala Val Pro Ser Ser Gly Arg His Val
465 470 475 480
Val Pro Ala Gln Val His Val Asn Gly Gly Ala Leu Ala Ser Glu Arg
485 490 495
Glu Thr Asp Ile Leu Asp Asp Glu Leu Pro Asn Gln Asp Gly His Ser
500 505 510
Ala Gly Ser Met Gly Thr Leu Ser Ser Leu Asp Gly Val Thr Asn Thr
515 520 525
Ser Glu Gly Gly Tyr Pro Glu Ala Leu Ser Pro Leu Thr Asn Gly Leu
530 535 540
Asp Lys Ser Tyr Pro Met Glu Pro Met Val Asn Gly Gly Gly Tyr Pro
545 550 555 560
Tyr Glu Ser Ala Ser Arg Ala Gly Pro Ala His Ala Gly His Thr Ala
565 570 575
Pro Met Arg Pro Ser Tyr Ser Ala Gln Glu Gly Leu Ala Gly Tyr Gln
580 585 590
Arg Glu Gly Pro His Pro Ala Trp Pro Gln Pro Val Thr Thr Ser His
595 600 605
Tyr Ala His Asp Pro Ser Gly Met Phe Arg Ser Gln Ser Phe Ser Glu
610 615 620
Ala Glu Pro Gln Leu Pro Pro Ala Pro Val Arg Gly Gly Ser Ser Arg
625 630 635 640
Glu Ala Val Gln Arg Gly Leu Asn Ser Trp Gln Gln Gln Gln Gln Gln
645 650 655
Gln Gln Gln Pro Arg Pro Pro Pro Arg Gln Gln Glu Arg Ala His Leu
660 665 670
Glu Ser Leu Val Ala Ser Arg Pro Ser Pro Gln Pro Leu Ala Glu Thr
675 680 685
Pro Ile Pro Ser Leu Pro Glu Phe Pro Arg Ala Ala Ser Gln Gln Glu
690 695 700
Ile Glu Gln Ser Ile Glu Thr Leu Asn Met Leu Met Leu Asp Leu Glu
705 710 715 720
Pro Ala Ser Ala Ala Ala Pro Leu His Lys Ser Gln Ser Val Pro Gly
725 730 735
Ala Trp Pro Gly Ala Ser Pro Leu Ser Ser Gln Pro Leu Ser Gly Ser
740 745 750
Ser Arg Gln Ser His Pro Leu Thr Gln Ser Arg Ser Gly Tyr Ile Pro
755 760 765
Ser Gly His Ser Leu Gly Thr Pro Glu Pro Ala Pro Arg Ala Ser Leu
770 775 780
Glu Ser Val Pro Pro Gly Arg Ser Tyr Ser Pro Tyr Asp Tyr Gln Pro
785 790 795 800
Cys Leu Ala Gly Pro Asn Gln Asp Phe His Ser Lys Ser Pro Ala Ser
805 810 815
Ser Ser Leu Pro Ala Phe Leu Pro Thr Thr His Ser Pro Pro Gly Pro

820 825 830
Gln Gln Pro Pro Ala Ser Leu Pro Gly Leu Thr Ala Gln Pro Leu Leu
835 840 845
Ser Pro Lys Glu Ala Thr Ser Asp Pro Ser Arg Thr Pro Glu Glu Glu
850 855 860
Pro Leu Asn Leu Glu Gly Leu Val Ala His Arg Val Ala Gly Val Gln
865 870 875 880
Ala Arg Glu Lys Gln Pro Ala Glu Pro Pro Ala Pro Leu Arg Arg Arg
885 890 895
Ala Ala Ser Asp Gly Gln Tyr Glu Asn Gln Ser Pro Glu Ala Thr Ser
900 905 910
Pro Arg Ser Pro Gly Val Arg Ser Pro Val Gln Cys Val Ser Pro Glu
915 920 925
Leu Ala Leu Thr Ile Ala Leu Asn Pro Gly Gly Arg Pro Lys Glu Pro
930 935 940
His Leu His Ser Tyr Lys Glu Ala Phe Glu Glu Met Glu Gly Thr Ser
945 950 955 960
Pro Ser Ser Pro Pro Pro Ser Gly Val Arg Ser Pro Pro Gly Leu Ala
965 970 975
Lys Thr Pro Leu Ser Ala Leu Gly Leu Lys Pro His Asn Pro Ala Asp
980 985 990
Ile Leu Leu His Pro Thr Gly Val Thr Arg Arg Arg Ile Gln Pro Glu
995 1000 1005
Glu Asp Glu Gly Lys Val Val Val Arg Leu Ser Glu Glu Pro Arg Ser
1010 1015 1020
Tyr Val Glu Ser Val Ala Arg Thr Ala Val Ala Gly Pro Arg Ala Gln
1025 1030 1035 1040
Asp Ser Glu Pro Lys Ser Phe Ser Ala Pro Ala Thr Gln Ala Tyr Gly
1045 1050 1055
His Glu Ile Pro Leu Arg Asn Gly Thr Leu Gly Gly Ser Phe Val Ser
1060 1065 1070
Pro Ser Pro Leu Ser Thr Ser Ser Pro Ile Leu Ser Ala Asp Ser Thr
1075 1080 1085
Ser Val Gly Ser Phe Pro Ser Gly Glu Ser Ser Asp Gln Gly Pro Arg
1090 1095 1100
Thr Pro Thr Gln Pro Leu Leu Glu Ser Gly Phe Arg Ser Gly Ser Leu
1105 1110 1115 1120
Gly Gln Pro Ser Pro Ser Ala Gln Arg Asn Tyr Gln Ser Ser Ser Pro
1125 1130 1135
Leu Pro Thr Val Gly Ser Ser Tyr Ser Ser Pro Asp Tyr Ser Leu Gln
1140 1145 1150
His Phe Ser Ser Ser Pro Glu Ser Gln Ala Arg Ala Gln Phe Ser Val
1155 1160 1165
Ala Gly Val His Thr Val Pro Gly Ser Pro Gln Ala Arg His Arg Thr
1170 1175 1180
Val Gly Thr Asn Thr Pro Pro Ser Pro Gly Phe Gly Arg Arg Ala Ile
1185 1190 1195 1200
Asn Pro Ser Met Ala Ala Pro Ser Ser Pro Ser Leu Ser His His Gln
1205 1210 1215
Met Met Gly Pro Pro Gly Thr Gly Phe His Gly Ser Thr Val Ser Ser
1220 1225 1230
Pro Gln Ser Ser Ala Ala Thr Thr Pro Gly Ser Pro Ser Leu Cys Arg
1235 1240 1245
His Pro Ala Gly Val Tyr Gln Val Ser Gly Leu His Asn Lys Val Ala
1250 1255 1260
Thr Thr Pro Gly Ser Pro Ser Leu Gly Arg His Pro Gly Ala His Gln
1265 1270 1275 1280
Gly Asn Leu Ala Ser Gly Leu His Ser Asn Ala Ile Ala Ser Pro Gly
1285 1290 1295
Ser Pro Ser Leu Gly Arg His Leu Gly Gly Ser Gly Ser Val Val Pro
1300 1305 1310

Gly Ser Pro Cys Leu Asp Arg His Val Ala Tyr Gly Gly Tyr Ser Thr
1315 1320 1325
Pro Glu Asp Arg Arg Pro Thr Leu Ser Arg Gln Ser Ser Ala Ser Gly
1330 1335 1340
Tyr Gln Ala Pro Ser Thr Pro Ser Phe Pro Val Ser Pro Ala Tyr Tyr
1345 1350 1355 1360
Pro Gly Leu Ser Ser Pro Ala Thr Ser Pro Ser Pro Asp Ser Ala Ala
1365 1370 1375
Phe Arg Gln Gly Ser Pro Thr Pro Ala Leu Pro Glu Lys Arg Arg Met
1380 1385 1390
Ser Val Gly Asp Arg Ala Gly Ser Leu Pro Asn Tyr Ala Thr Ile Asn
1395 1400 1405
Gly Lys Val Ala Ser Pro Val Pro Ser Gly Met Ser Ser Pro Ser Gly
1410 1415 1420
Gly Ser Thr Val Ser Phe Ser His Thr Leu Pro Asp Phe Ser Lys Tyr
1425 1430 1435 1440
Ser Met Pro Asp Asn Ser Pro Glu Thr Arg Ala Lys Val Lys Phe Val
1445 1450 1455
Gln Asp Thr Ser Lys Tyr Trp Tyr Lys Pro Glu Ile Ser Arg Glu Gln
1460 1465 1470
Ala Ile Ala Leu Leu Lys Asp Gln Glu Pro Gly Ala Phe Ile Ile Arg
1475 1480 1485
Asp Ser His Ser Phe Arg Gly Ala Tyr Gly Leu Ala Met Lys Val Ser
1490 1495 1500
Ser Pro Pro Pro Thr Ile Met Gln Gln Asn Lys Lys Gly Asp Met Thr
1505 1510 1515 1520
His Glu Leu Val Arg His Phe Leu Ile Glu Thr Gly Pro Arg Gly Val
1525 1530 1535
Lys Leu Lys Gly Cys Pro Asn Glu Pro Asn Phe Gly Ser Leu Ser Ala
1540 1545 1550
Leu Val Tyr Gln His Ser Ile Ile Pro Leu Ala Leu Pro Cys Lys Leu
1555 1560 1565
Val Ile Pro Asn Arg Asp Pro Thr Asp Glu Ser Lys Asp Ser Ser Gly
1570 1575 1580
Pro Ala Asn Ser Thr Ala Asp Leu Leu Lys Gln Gly Ala Ala Cys Asn
1585 1590 1595 1600
Val Leu Phe Ile Asn Ser Val Asp Met Glu Ser Leu Thr Gly Pro Gln
1605 1610 1615
Ala Ile Ser Lys Ala Thr Ser Glu Thr Leu Ala Ala Asp Pro Thr Pro
1620 1625 1630
Ala Ala Thr Ile Val His Phe Lys Val Ser Ala Gln Gly Ile Thr Leu
1635 1640 1645
Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His Tyr Pro Leu Asn
1650 1655 1660
Thr Val Thr Phe Cys Asp Leu Asp Pro Gln Glu Arg Lys Trp Met Lys
1665 1670 1675 1680
Thr Glu Gly Gly Ala Pro Ala Lys Leu Phe Gly Phe Val Ala Arg Lys
1685 1690 1695
Gln Gly Ser Thr Thr Cys His Leu Phe Ala Glu Leu Asp Pro Asn Gln
1700 1705 1710
Pro Ala Ser Ala Ile Val Asn Phe Val Ser Lys Val Met Leu Asn Ala
1715 1720 1725
Gly Gln Lys Arg
1730

<210> 241
<211> 3557
<212> DNA
<213> Homo sapiens

<400> 241

```
atgcccggcg tggcccgcct gccgctgctg ctcgggctgc tgctgctccc gcgtcccggc     60
cggccgctgg acttggccga ctacacctat gacctggcgg aggaggacga ctcggagccc    120
ctcaactaca aagacccctg caaggcggct gcctttcttg ggacattgc cctggacgaa    180
gaggacctga gggccttcca ggtacagcag gctgtggatc tcagacggca cacagctcgt    240
aagtcctcca tcaaagctgc agttccagga aacacttcta cccccagctg ccagagcacc    300
aacgggcagc ctcagagggg agcctgtggg agatggagag gtagatcccg tagccggcgg    360
gcggcgacgt cccgaccaga gcgtgtgtgg cccgatgggg tcatcccctt tgtcattggg    420
ggaaacttca ctggtagcca gagggcagtc ttccggcagg ccatgaggca ctgggagaag    480
cacacctgtg tcaccttcct ggagcgcact gacgaggaca gctatattgt gttcacctat    540
cgaccttgcg ggtgctgctc ctacgtgggt cgccgcggcg ggggccccca ggccatctcc    600
atcggcaaga actgtgacaa gttcggcatt gtggtccacg agctgggcca cgtcgtcggc    660
ttctggcacg aacacactcg gccagaccgg gaccgccacg tttccatcgt tcgtgagaac    720
atccagccag ggcaggagta taacttcctg aagatggagc ctcaggaggt ggagtccctg    780
ggggagacct atgacttcga cagcatcatg cattacgctc ggaacacatt ctccaggggc    840
atcttcctgg ataccattgt ccccaagtat gaggtgaacg gggtgaaacc tcccattggc    900
caaaggacac ggctcagcaa gggggacatt gcccaagccc gcaagcttta caagtgccca    960
gcctgtggag agaccctgca agacagcaca ggcaacttct cctcccctga ataccccaat   1020
ggctactctg ctcacatgca ctgcgtgtgg cgcatctctg tcacacccgg ggagaagatc   1080
atcctgaact tcacgtccct ggacctgtac cgcagccgcc tgtgctggta cgactatgtg   1140
gaggtccgag atggcttctg gaggaaggcg cccctccgag gccgcttctg cgggtccaaa   1200
ctccctgagc ctatcgtctc cactgacagc cgcctctggg ttgaattccg cagcagcagc   1260
aattgggttg gaaagggctt ctttgcagtc tacgaagcca tctgcggggg tgatgtgaaa   1320
aaggactatg gccacattca atcgcccaac tacccagacg attaccggcc cagcaaagtc   1380
tgcatctggc ggatccaggt gtctgagggc ttccacgtgg gcctcacatt ccagtccttt   1440
gagattgagc gccacgacag ctgtgcctac gactatctgg aggtgcgcga cgggcacagt   1500
gagagcagca ccctcatcgg gcgctactgt ggctatgaga agcctgatga catcaagagc   1560
acgtccagcc gcctctggct caagttcgtc tctgacgggt ccattaacaa agcgggcttt   1620
gccgtcaact tttcaaaga ggtggacgag tgctctcggc ccaaccgcgg gggctgtgag    1680
cagcggtgcc tcaacaccct gggcagctac aagtgcagct gtgaccccgg gtacgagctg   1740
gccccagaca agcgccgctg tgaggctgct tgtggcggat tcctcaccaa gctcaacggc   1800
tccatcacca gcccgggctg gcccaaggag taccccccca acaagaactg catctggcag   1860
ctggtggccc ccacccagta ccgcatctcc ctgcagtttg acttctttga gacagagggc   1920
aatgatgtgt gcaagtacga cttcgtggag gtgcgcagtg gactcacagc tgactccaag   1980
ctgcatggca agttctgtgg ttctgagaag cccgaggtca tcacctccca gtacaacaac   2040
atgcgcgtgg agttcaagtc cgacaacacc gtgtccaaaa agggcttcaa ggcccacttc   2100
ttctcagaca aggacgagtg ctccaaggat aacggcggct gccagcagga ctgcgtcaac   2160
acgttcggca gttatgagtg ccaatgccgc agtggcttcg tcctccatga caacaagcac   2220
gactgcaaag aagccggctg tgaccacaag gtgacatcca ccagtggtac catcaccagc   2280
cccaactggc ctgacaagta tcccagcaag aaggagtgca cgtgggccat ctccagcacc   2340
cccgggcacc gggtcaagct gaccttcatg gagatggaca tcgagtccca gcctgagtgt   2400
gcctacgacc acctagaggt gttcgacggg cgagacgcca aggcccccgt cctcggccgc   2460
ttctgtggga gcaagaagcc cgagcccgtc ctggccacag gcagccgcat gttcctgcgc   2520
ttctactcag ataactcggt ccagcgaaag ggcttccagg cctcccacgc cacagagtgc   2580
gggggccagg tacgggcaga cgtgaagacc aaggaccttt actcccacgc ccagtttggc   2640
gacaacaact accctggggg tgtggactgt gagtgggtca ttgtggccga ggaaggctac   2700
ggcgtggagc tcgtgttcca gacctttgag gtggaggagg agaccgactg cggctatgac   2760
tacatggagc tcttcgacgg ctacgacagc acagccccca ggctggggcg ctactgtggc   2820
tcagggcctc ctgaggaggt gtactcggcg ggagattctg tcctggtgaa gttccactcg   2880
gatgacacca tcaccaaaaa aggtttccac ctgcgataca ccagcaccaa gttccaggac   2940
acactccaca gcaggaagtg accactgcct gagcaggggc ggggactgga gcctgctgcc   3000
cttggtcgcc tagactggat agtgggggtg ggcggaaggc aacgcaccat ccctctcccc   3060
caggccccag gacctgcagg gccaatggcc tggtgagact gtccatagga ggtgggggaa   3120
ctggactccg gcataagcca cttccccaca aacccccacc agcaaggggc tggggccagg   3180
gagcagagct tccacaagac atttcgaagt catcattcct ctcttagggg gccctgcctg   3240
gtggcaagag ggaatgtcag caggacccca tcgccatccc tgtgtctcta cacgctgtat   3300
tgtgtatcac cgggggcatt atttcattg taatgttcat ttcccacccc tgctccagcc    3360
tcgatttggt tttattttga gcccccattc caccacccca gtttcctggg gcacaagtgt   3420
ctgtgcatgt cccccaggag ccaccgtggg gagccgatgg ggaggggatg gagaaacaag   3480
acagggcttc tctcaggccc agtggccggt cagccacacc agggcaccgc agccaataaa   3540
ccgaaagtgt tacagcc                                                   3557
```

<210> 242
<211> 986
<212> PRT
<213> Homo sapiens

<400> 242

Met Pro Gly Val Ala Arg Leu Pro Leu Leu Leu Gly Leu Leu Leu Leu
1 5 10 15
Pro Arg Pro Gly Arg Pro Leu Asp Leu Ala Asp Tyr Thr Tyr Asp Leu
20 25 30
Ala Glu Glu Asp Asp Ser Glu Pro Leu Asn Tyr Lys Asp Pro Cys Lys
35 40 45
Ala Ala Ala Phe Leu Gly Asp Ile Ala Leu Asp Glu Glu Asp Leu Arg
50 55 60
Ala Phe Gln Val Gln Gln Ala Val Asp Leu Arg Arg His Thr Ala Arg
65 70 75 80
Lys Ser Ser Ile Lys Ala Ala Val Pro Gly Asn Thr Ser Thr Pro Ser
85 90 95
Cys Gln Ser Thr Asn Gly Gln Pro Gln Arg Gly Ala Cys Gly Arg Trp
100 105 110
Arg Gly Arg Ser Arg Ser Arg Arg Ala Ala Thr Ser Arg Pro Glu Arg
115 120 125
Val Trp Pro Asp Gly Val Ile Pro Phe Val Ile Gly Gly Asn Phe Thr
130 135 140
Gly Ser Gln Arg Ala Val Phe Arg Gln Ala Met Arg His Trp Glu Lys
145 150 155 160
His Thr Cys Val Thr Phe Leu Glu Arg Thr Asp Glu Asp Ser Tyr Ile
165 170 175
Val Phe Thr Tyr Arg Pro Cys Gly Cys Cys Ser Tyr Val Gly Arg Arg
180 185 190
Gly Gly Gly Pro Gln Ala Ile Ser Ile Gly Lys Asn Cys Asp Lys Phe
195 200 205
Gly Ile Val Val His Glu Leu Gly His Val Val Gly Phe Trp His Glu
210 215 220
His Thr Arg Pro Asp Arg Asp Arg His Val Ser Ile Val Arg Glu Asn
225 230 235 240
Ile Gln Pro Gly Gln Glu Tyr Asn Phe Leu Lys Met Glu Pro Gln Glu
245 250 255
Val Glu Ser Leu Gly Glu Thr Tyr Asp Phe Asp Ser Ile Met His Tyr
260 265 270
Ala Arg Asn Thr Phe Ser Arg Gly Ile Phe Leu Asp Thr Ile Val Pro
275 280 285
Lys Tyr Glu Val Asn Gly Val Lys Pro Pro Ile Gly Gln Arg Thr Arg
290 295 300
Leu Ser Lys Gly Asp Ile Ala Gln Ala Arg Lys Leu Tyr Lys Cys Pro
305 310 315 320
Ala Cys Gly Glu Thr Leu Gln Asp Ser Thr Gly Asn Phe Ser Ser Pro
325 330 335
Glu Tyr Pro Asn Gly Tyr Ser Ala His Met His Cys Val Trp Arg Ile
340 345 350
Ser Val Thr Pro Gly Glu Lys Ile Ile Leu Asn Phe Thr Ser Leu Asp
355 360 365
Leu Tyr Arg Ser Arg Leu Cys Trp Tyr Asp Tyr Val Glu Val Arg Asp
370 375 380
Gly Phe Trp Arg Lys Ala Pro Leu Arg Gly Arg Phe Cys Gly Ser Lys
385 390 395 400
Leu Pro Glu Pro Ile Val Ser Thr Asp Ser Arg Leu Trp Val Glu Phe
405 410 415
Arg Ser Ser Ser Asn Trp Val Gly Lys Gly Phe Phe Ala Val Tyr Glu
420 425 430
Ala Ile Cys Gly Gly Asp Val Lys Lys Asp Tyr Gly His Ile Gln Ser

```
                435                 440                 445
Pro Asn Tyr Pro Asp Asp Tyr Arg Pro Ser Lys Val Cys Ile Trp Arg
    450                 455                 460
Ile Gln Val Ser Glu Gly Phe His Val Gly Leu Thr Phe Gln Ser Phe
465                 470                 475                 480
Glu Ile Glu Arg His Asp Ser Cys Ala Tyr Asp Tyr Leu Glu Val Arg
                485                 490                 495
Asp Gly His Ser Glu Ser Ser Thr Leu Ile Gly Arg Tyr Cys Gly Tyr
            500                 505                 510
Glu Lys Pro Asp Asp Ile Lys Ser Thr Ser Ser Arg Leu Trp Leu Lys
        515                 520                 525
Phe Val Ser Asp Gly Ser Ile Asn Lys Ala Gly Phe Ala Val Asn Phe
    530                 535                 540
Phe Lys Glu Val Asp Glu Cys Ser Arg Pro Asn Arg Gly Gly Cys Glu
545                 550                 555                 560
Gln Arg Cys Leu Asn Thr Leu Gly Ser Tyr Lys Cys Ser Cys Asp Pro
                565                 570                 575
Gly Tyr Glu Leu Ala Pro Asp Lys Arg Arg Cys Glu Ala Ala Cys Gly
            580                 585                 590
Gly Phe Leu Thr Lys Leu Asn Gly Ser Ile Thr Ser Pro Gly Trp Pro
        595                 600                 605
Lys Glu Tyr Pro Pro Asn Lys Asn Cys Ile Trp Gln Leu Val Ala Pro
    610                 615                 620
Thr Gln Tyr Arg Ile Ser Leu Gln Phe Asp Phe Phe Glu Thr Glu Gly
625                 630                 635                 640
Asn Asp Val Cys Lys Tyr Asp Phe Val Glu Val Arg Ser Gly Leu Thr
                645                 650                 655
Ala Asp Ser Lys Leu His Gly Lys Phe Cys Gly Ser Glu Lys Pro Glu
            660                 665                 670
Val Ile Thr Ser Gln Tyr Asn Asn Met Arg Val Glu Phe Lys Ser Asp
        675                 680                 685
Asn Thr Val Ser Lys Lys Gly Phe Lys Ala His Phe Phe Ser Asp Lys
    690                 695                 700
Asp Glu Cys Ser Lys Asp Asn Gly Gly Cys Gln Gln Asp Cys Val Asn
705                 710                 715                 720
Thr Phe Gly Ser Tyr Glu Cys Gln Cys Arg Ser Gly Phe Val Leu His
                725                 730                 735
Asp Asn Lys His Asp Cys Lys Glu Ala Gly Cys Asp His Lys Val Thr
            740                 745                 750
Ser Thr Ser Gly Thr Ile Thr Ser Pro Asn Trp Pro Asp Lys Tyr Pro
        755                 760                 765
Ser Lys Lys Glu Cys Thr Trp Ala Ile Ser Ser Thr Pro Gly His Arg
    770                 775                 780
Val Lys Leu Thr Phe Met Glu Met Asp Ile Glu Ser Gln Pro Glu Cys
785                 790                 795                 800
Ala Tyr Asp His Leu Glu Val Phe Asp Gly Arg Asp Ala Lys Ala Pro
                805                 810                 815
Val Leu Gly Arg Phe Cys Gly Ser Lys Lys Pro Glu Pro Val Leu Ala
            820                 825                 830
Thr Gly Ser Arg Met Phe Leu Arg Phe Tyr Ser Asp Asn Ser Val Gln
        835                 840                 845
Arg Lys Gly Phe Gln Ala Ser His Ala Thr Glu Cys Gly Gly Gln Val
    850                 855                 860
Arg Ala Asp Val Lys Thr Lys Asp Leu Tyr Ser His Ala Gln Phe Gly
865                 870                 875                 880
Asp Asn Asn Tyr Pro Gly Gly Val Asp Cys Glu Trp Val Ile Val Ala
                885                 890                 895
Glu Glu Gly Tyr Gly Val Glu Leu Val Phe Gln Thr Phe Glu Val Glu
            900                 905                 910
Glu Glu Thr Asp Cys Gly Tyr Asp Tyr Met Glu Leu Phe Asp Gly Tyr
        915                 920                 925
```

Asp Ser Thr Ala Pro Arg Leu Gly Arg Tyr Cys Gly Ser Gly Pro Pro
    930   935   940
Glu Glu Val Tyr Ser Ala Gly Asp Ser Val Leu Val Lys Phe His Ser
945   950   955   960
Asp Asp Thr Ile Thr Lys Lys Gly Phe His Leu Arg Tyr Thr Ser Thr
                965   970   975
Lys Phe Gln Asp Thr Leu His Ser Arg Lys
            980   985

<210> 243
<211> 5015
<212> DNA
<213> Homo sapiens

<400> 243
gcgctccgca cctgggcact cccagcgatg cgcagcgggg cagcgccggc cccgccgatg 60
gagctgctgt tgctgccgcc gccgccgccc ggagcgcccc gctccgcccg cgccccgtgc 120
gcctgagcac cgagctcgcc cctcctccgc gctaactccg ccgcccgctc cccaggccgc 180
ccgcgctccc cgcgcgcctc ctcgggctcc acgcgtcttg ccccgcagag gcagcctcct 240
ccaggagcgg ggccctgcac accatggccc ccgggtgggc aggggtcggc gccgccgtgc 300
gcgcccgcct ggcgctggcc ttggcgctgg cgagcgtcct gagtgggcct ccagccgtcg 360
cctgccccac caagtgtacc tgctccgctg ccagcgtgga ctgccacggg ctgggcctcc 420
gcgcggttcc tcggggcatc ccccgcaacg ctgagcgcct tgacctggac agaaataata 480
tcaccaggat caccaagatg gacttcgctg ggctcaagaa cctccgagtc ttgcatctgg 540
aagacaacca ggtcagcgtc atcgagagag gcgccttcca ggacctgaag cagctagagc 600
gactgcgcct gaacaagaat aagctgcaag tccttccaga attgcttttc cagagcacgc 660
cgaagctcac cagactagat ttgagtgaaa accagatcca ggggatcccg aggaaggcgt 720
tccgcggcat caccgatgtg aagaacctgc aactggacaa caaccacatc agctgcattg 780
aagatggagc cttccgagcg ctgcgcgatt tggagatcct taccctcaac aacaacaaca 840
tcagtcgcat cctggtcacc agcttcaacc acatgccgaa gatccgaact ctgcgcctcc 900
actccaacca cctgtactgc gactgccacc tggcctggct ctcggattgg ctgcgacagc 960
gacggacagt tggccagttc acactctgca tggctcctgt gcatttgagg ggcttcaacg 1020
tggcggatgt gcagaagaag gagtacgtgt gcccagcccc ccactcggag ccccccatcct 1080
gcaatgccaa ctccatctcc tgcccttcgc cctgcacgtg cagcaataac atcgtggact 1140
gtcgaggaaa gggcttgatg gagattcctg ccaacttgcc ggagggcatc gtcgaaatac 1200
gcctagaaca gaactccatc aaagccatcc ctgcaggagc cttcacccag tacaagaaac 1260
tgaagcgaat agacatcagc aagaatcaga tatcggatat tgctccagat gccttccagg 1320
gcctgaaatc actcacatcg ctggtcctgt atgggaacaa gatcaccgag attgccaagg 1380
gactgtttga tgggctggtg tccctacagc tgctcctcct caatgccaac aagatcaact 1440
gcctgcgggt gaacacgttt caggacctgc agaacctcaa cttgctctcc ctgtatgaca 1500
acaagctgca gaccatcagc aaggggctct tcgcccctct gcagtccatc cagacactcc 1560
acttagccca aaacccattt gtgtgcgact gccacttgaa gtggctggcc gactacctcc 1620
aggacaaccc catcgagaca agcggggccc gctgcagcag cccgcgccga ctcgccaaca 1680
agcgcatcag ccagatcaag agcaagaagt tccgctgctc aggctccgag gattaccgca 1740
gcaggttcag cagcgagtgc ttcatggacc tcgtgtgccc cgagaagtgt cgctgtgagg 1800
gcacgattgt ggactgctcc aaccagaagc tggtccgcat cccaagccac ctccctgaat 1860
atgtcaccga cctgcgactg aatgacaatg aggtatctgt tctggaggcc actggcatct 1920
tcaagaagtt gcccaacctg cggaaaataa atctgagtaa caataagatc aaggaggtgc 1980
gagagggagc tttcgatgga gcagccagcg tgcaggagct gatgctgaca gggaaccagc 2040
tggagaccgt gcacgggcgc gtgttccgtg gcctcagtgg cctcaaaacc ttgatgctga 2100
ggagtaactt gatcggctgt gtgagtaatg acacctttgc cggcctgagt tcggtgagac 2160
tgctgtccct ctatgacaat cggatcacca ccatcacccc tggggccttc accacgcttg 2220
tctccctgtc caccataaac ctcctgtcca acccctccaa ctgcaactgc cacctggcct 2280
ggctcggcaa gtggttgagg aagaggcgga tcgtcagtgg gaaccctagg tgccagaagc 2340
catttttcct caaggagatt cccatccagg atgtggccat ccaggacttc acctgtgatg 2400
gcaacgagga gagtagctgc cagctgagcc cgcgctgccc ggagcagtgc acctgtatgg 2460
agacagtggt gcgatgcagc aacaaggggc tccgcgccct ccccagaggc atgcccaagg 2520
atgtgaccga gctgtacctg gaaggaaacc acctaacagc cgtgcccaga gagctgtccg 2580
ccctccgaca cctgacgctt attgacctga gcaacaacag catcagcatg ctgaccaatt 2640
acaccttcag taacatgtct cacctctcca ctctgatcct gagctacaac cggctgaggt 2700
gcatccccgt ccacgccttc aacgggctgc ggtccctgcg agtgctaacc ctccatggca 2760

atgacatttc cagcgttcct gaaggctcct tcaacgacct cacatctctt tcccatctgg 2820
cgctgggaac caacccactc cactgtgact gcagtcttcg gtggctgtcg gagtgggtga 2880
aggcggggta caaggagcct ggcatcgccc gctgcagtag ccctgagccc atggctgaca 2940
ggctcctgct caccacccca acccaccgct tccagtgcaa agggccagtg gacatcaaca 3000
ttgtggccaa atgcaatgcc tgcctctcca gcccgtgcaa gaataacggg acatgcaccc 3060
aggaccctgt ggagctgtac cgctgtgcct gccctacag ctacaagggc aaggactgca 3120
ctgtgcccat caacacctgc atccagaacc cctgtcagca tggaggcacc tgccacctga 3180
gtgacagcca caaggatggg ttcagctgct cctgccctct gggctttgag gggcagcggt 3240
gtgagatcaa cccagatgac tgtgaggaca acgactgcga aaacaatgcc acctgcgtgg 3300
acgggatcaa caactacgtg tgtatctgtc cgcctaacta cacaggtgag ctatgcgacg 3360
aggtgattga ccactgtgtg cctgagctga acctctgtca gcatgaggcc aagtgcatcc 3420
ccctggacaa aggattcagc tgcgagtgtg tccctggcta cagcgggaag ctctgtgaga 3480
cagacaatga tgactgtgtg gcccacaagt gccgccacgg ggcccagtgc gtggacacaa 3540
tcaatggcta cacatgcacc tgcccccagg gcttcagtgg acccttctgt gaacaccccc 3600
cacccatggt cctactgcag accagcccat gcgaccagta cgagtgccag aacggggccc 3660
agtgcatcgt ggtgcagcag gagcccacct gccgctgccc accaggtttc gccggcccca 3720
gatgcgagaa gctcatcact gtcaacttcg tgggcaaaga ctcctacgtg gaactggcct 3780
ccgccaaggt ccgaccccag gccaacatct ccctgcaggt ggccactgac aaggacaacg 3840
gcatccttct ctacaaagga gacaatgacc ccctggcact ggagctgtac cagggccacg 3900
tgcggctggt ctatgacagc ctgagttccc ctccaaccac agtgtacagt gtggagacag 3960
tgaatgatgg gcagtttcac agtgtggagc tggtgacgct aaaccagacc ctgaacctag 4020
tagtggacaa aggaactcca aagagcctgg ggaagctcca gaagcagcca gcagtgggca 4080
tcaacagccc cctctacctt ggaggcatcc ccacctccac cggcctctcc gccttgcgcc 4140
agggcacgga ccggcctcta ggcggcttcc acggatgcat ccatgaggtg cgcatcaaca 4200
acgagctgca ggacttcaag gccctcccac cacagtccct gggggtgtca ccaggctgca 4260
agtcctgcac cgtgtgcaag cacggcctgt gccgctccgt ggagaaggac agcgtggtgt 4320
gcgagtgccg cccaggctgg accggcccac tctgcgatca ggaggcccgg gacccctgcc 4380
tcggccacag atgccaccat ggaaaatgtg tggcaactgg gacctcatac atgtgcaagt 4440
gtgccgaggg ctatggaggg gacttgtgtg acaacaagaa tgactctgcc aatgcctgct 4500
cagccttcaa gtgtcaccat gggcagtgcc acatctcaga ccaaggggag ccctactgcc 4560
tgtgccagcc cggctttagc ggcgagcact gccaacaaga gaatccgtgc ctgggacaag 4620
tagtccgaga ggtgatccgc cgccagaaag gttatgcatc atgtgccaca gcctccaagg 4680
tgcccatcat ggaatgtcgt gggggctgtg ggccccagtg ctgccagccc acccgcagca 4740
agcggcggaa atacgtcttc cagtgcacgg acggctcctc gtttgtagaa gaggtggaga 4800
gacacttaga gtgcggctgc ctcgcgtgtt cctaagcccc tgcccgcctg cctgccacct 4860
ctcggactcc agcttgatgg agttgggaca gccatgtggg accccctggt gattcagcat 4920
gaaggaaatg aagctggaga ggaaggtaaa gaagaagaga atattaagta tattgtaaaa 4980
taaacaaaaa atagaactta tttttattat ggaaa 5015

<210> 244
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 244
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg Leu
1 5 10 15
Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro Ala Val
20 25 30
Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val Asp Cys His
35 40 45
Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro Arg Asn Ala Glu
50 55 60
Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg Ile Thr Lys Met Asp
65 70 75 80
Phe Ala Gly Leu Lys Asn Leu Arg Val Leu His Leu Glu Asp Asn Gln
85 90 95
Val Ser Val Ile Glu Arg Gly Ala Phe Gln Asp Leu Lys Gln Leu Glu
100 105 110

Arg Leu Arg Leu Asn Lys Asn Lys Leu Gln Val Leu Pro Glu Leu Leu
115 120 125
Phe Gln Ser Thr Pro Lys Leu Thr Arg Leu Asp Leu Ser Glu Asn Gln
130 135 140
Ile Gln Gly Ile Pro Arg Lys Ala Phe Arg Gly Ile Thr Asp Val Lys
145 150 155 160
Asn Leu Gln Leu Asp Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala
165 170 175
Phe Arg Ala Leu Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn
180 185 190
Ile Ser Arg Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg
195 200 205
Thr Leu Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala
210 215 220
Trp Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
225 230 235 240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp Val
245 250 255
Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro Pro Ser
260 265 270
Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr Cys Ser Asn
275 280 285
Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu Ile Pro Ala Asn
290 295 300
Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu Gln Asn Ser Ile Lys
305 310 315 320
Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr Lys Lys Leu Lys Arg Ile
325 330 335
Asp Ile Ser Lys Asn Gln Ile Ser Asp Ile Ala Pro Asp Ala Phe Gln
340 345 350
Gly Leu Lys Ser Leu Thr Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr
355 360 365
Glu Ile Ala Lys Gly Leu Phe Asp Gly Leu Val Ser Leu Gln Leu Leu
370 375 380
Leu Leu Asn Ala Asn Lys Ile Asn Cys Leu Arg Val Asn Thr Phe Gln
385 390 395 400
Asp Leu Gln Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln
405 410 415
Thr Ile Ser Lys Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu
420 425 430
His Leu Ala Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu
435 440 445
Ala Asp Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys
450 455 460
Ser Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser
465 470 475 480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe Ser
485 490 495
Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg Cys Glu
500 505 510
Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg Ile Pro Ser
515 520 525
His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn Asp Asn Glu Val
530 535 540
Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Asn Leu Arg
545 550 555 560
Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys Glu Val Arg Glu Gly Ala
565 570 575
Phe Asp Gly Ala Ala Ser Val Gln Glu Leu Met Leu Thr Gly Asn Gln
580 585 590
Leu Glu Thr Val His Gly Arg Val Phe Arg Gly Leu Ser Gly Leu Lys

595 600 605
Thr Leu Met Leu Arg Ser Asn Leu Ile Gly Cys Val Ser Asn Asp Thr
610 615 620
Phe Ala Gly Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg
625 630 635 640
Ile Thr Thr Ile Thr Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser
645 650 655
Thr Ile Asn Leu Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala
660 665 670
Trp Leu Gly Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro
675 680 685
Arg Cys Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val
690 695 700
Ala Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln
705 710 715 720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val Val
725 730 735
Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met Pro Lys
740 745 750
Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr Ala Val Pro
755 760 765
Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile Asp Leu Ser Asn
770 775 780
Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe Ser Asn Met Ser His
785 790 795 800
Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Val
805 810 815
His Ala Phe Asn Gly Leu Arg Ser Leu Arg Val Leu Thr Leu His Gly
820 825 830
Asn Asp Ile Ser Ser Val Pro Glu Gly Ser Phe Asn Asp Leu Thr Ser
835 840 845
Leu Ser His Leu Ala Leu Gly Thr Asn Pro Leu His Cys Asp Cys Ser
850 855 860
Leu Arg Trp Leu Ser Glu Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly
865 870 875 880
Ile Ala Arg Cys Ser Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu
885 890 895
Thr Thr Pro Thr His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn
900 905 910
Ile Val Ala Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn
915 920 925
Gly Thr Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro
930 935 940
Tyr Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
945 950 955 960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser His
965 970 975
Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly Gln Arg
980 985 990
Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn
995 1000 1005
Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys Ile Cys Pro Pro
1010 1015 1020
Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile Asp His Cys Val Pro
1025 1030 1035 1040
Glu Leu Asn Leu Cys Gln His Glu Ala Lys Cys Ile Pro Leu Asp Lys
1045 1050 1055
Gly Phe Ser Cys Glu Cys Val Pro Gly Tyr Ser Gly Lys Leu Cys Glu
1060 1065 1070
Thr Asp Asn Asp Asp Cys Val Ala His Lys Cys Arg His Gly Ala Gln
1075 1080 1085

Cys Val Asp Thr Ile Asn Gly Tyr Thr Cys Thr Cys Pro Gln Gly Phe
1090 1095 1100
Ser Gly Pro Phe Cys Glu His Pro Pro Pro Met Val Leu Leu Gln Thr
1105 1110 1115 1120
Ser Pro Cys Asp Gln Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val
1125 1130 1135
Val Gln Gln Glu Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro
1140 1145 1150
Arg Cys Glu Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr
1155 1160 1165
Val Glu Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu
1170 1175 1180
Gln Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp
1185 1190 1195 1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu Val
1205 1210 1215
Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val Glu Thr
1220 1225 1230
Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr Leu Asn Gln
1235 1240 1245
Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys Ser Leu Gly Lys
1250 1255 1260
Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser Pro Leu Tyr Leu Gly
1265 1270 1275 1280
Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala Leu Arg Gln Gly Thr Asp
1285 1290 1295
Arg Pro Leu Gly Gly Phe His Gly Cys Ile His Glu Val Arg Ile Asn
1300 1305 1310
Asn Glu Leu Gln Asp Phe Lys Ala Leu Pro Pro Gln Ser Leu Gly Val
1315 1320 1325
Ser Pro Gly Cys Lys Ser Cys Thr Val Cys Lys His Gly Leu Cys Arg
1330 1335 1340
Ser Val Glu Lys Asp Ser Val Val Cys Glu Cys Arg Pro Gly Trp Thr
1345 1350 1355 1360
Gly Pro Leu Cys Asp Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg
1365 1370 1375
Cys His His Gly Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys
1380 1385 1390
Cys Ala Glu Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser
1395 1400 1405
Ala Asn Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile
1410 1415 1420
Ser Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1425 1430 1435 1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg Glu
1445 1450 1455
Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala Ser Lys
1460 1465 1470
Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln Cys Cys Gln
1475 1480 1485
Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln Cys Thr Asp Gly
1490 1495 1500
Ser Ser Phe Val Glu Glu Val Glu Arg His Leu Glu Cys Gly Cys Leu
1505 1510 1515 1520
Ala Cys Ser

<210> 245
<211> 4227
<212> DNA
<213> Homo sapiens

(

<400> 245
gactgggagc aggcagcccg ggcggagcgg gccggtgccg aggacggccc caggcattgc 60
tctgccccgg gcattgcgcg gcgcgcgtga gggggatgcg gcaggaggcg gcgcggcggg 120
aggagtaggc ggcggcgccc tcgggaggga gctgcgcgcg ggccagacgg cgcccggagg 180
ctccgcagtg ccgccgccgt cgcccgggag gctccgcgcg ggagccatgt aaccctgcgg 240
cgggctccgg gctgctccgt ccttccccag ctcccgggct agcgcggcag cggggccacg 300
atgaagaagc agttcaatcg catgcgccag ctggccaacc agacggtggg cagggctgaa 360
aagacagaag ttttgagtga agaccttctt caggtggaga agcgtctgga gctggtgaaa 420
caggtgtccc acagcacgca caagaagctc accgcatgtc tgcagggcca gcaaggggca 480
gaggctgaca agcgctccaa aaagttgcct ttgacaacac tggctcagtg tctgatggag 540
gggtcagcta tcctgggaga tgacacactt cttgggaaga tgctgaaact ctgtggagag 600
acggaggaca agctggctca ggagctgata catttgagt tgcaagtaga gagagacgtg 660
attgagcccc tgtttttgct ggcggaggtg gaaatcccaa atattcaaaa gcagaggaaa 720
cacttagcca agttggtgct ggacatggat tcctcacgaa ccaggtggca gcagacttcc 780
aagtcttcag gtttgtccag cagcttacag cctgcgggtg ccaaggctga tgccctcagg 840
gaagaaatgg aagaggctgc caacagagtg gagatttgca gggaccagct ctcagctgat 900
atgtacagtt ttgtggccaa agaaattgac tatgcaaact actttcaaac gctaatagaa 960
gtgcaagctg aataccacag gaagtccctg acactattgc aggctgtatt gcctcagatc 1020
aaagcacaac aggaggcctg ggtagagaag ccttccttcg ggaagccgct ggaggagcac 1080
ctcaccatca gcggccggga gatcgccttc cccatcgagg cgtgtgtgac catgctgctt 1140
gagtgtggga tgcaggagga gggactcttc cgagtagccc cctctgcctc caaactgaag 1200
aagctgaaag cggccctgga ctgctgcgtg gtggatgtgc aggagtactc ggcagacccc 1260
cacgcaattg caggagcttt gaaatcttac ctccgagagt tgccagaacc tcttatgacc 1320
tttgaactct atgatgagtg gatccaggct tccaatgtcc aggagcaaga caagaagctt 1380
caggctctat ggaatgcttg tgaaaagttg cccaaggcca atcacaacaa catccgatac 1440
ttgataaaat ttttatccaa gctgtcagaa tatcaagatg taaacaagat gactcccagt 1500
aatatggcaa ttgttttagg acccaacctc ctatggccac aagcagaagg gaacattaca 1560
gagatgatga ccacagtgtc gctgcaaatt gttgggatca ttgaacctat catccagcat 1620
gcagactggt tcttccctgg ggagatagag ttcaacatta ctggcaatta tgggagtcca 1680
gtacacgtga accataatgc caactacagc tcaatgccct ccccagacat ggaccctgct 1740
gaccggcgcc agcccgagca ggcccgccgg cccctcagcg tcgccacgga taatatgatg 1800
ctggagtttt acaaaaagga tggccttagg aaaatccaaa gcatgggtgt gagggtcatg 1860
gacacaaact gggtggctcg aagaggctcc tcggccggtc ggaaagtgtc ctgcgccccg 1920
ccctccatgc agcctcccgc cccgcccgcc gagctggctg cgcccctgcc ttcgccgctg 1980
ccggagcagc cctggacag ccccgcggcc cccgcgctct ctccatccgg cctgggcctc 2040
cagcctgggc ccgagcgcac cagcacaaca aaaagcaagg aactttctcc aggctctgca 2100
cagaaaggaa gtccaggctc cagccagggc acagcctgtg cagggactca accaggggct 2160
caacctggag ctcagccggg cgccagcccc agccccagcc agccgcctgc agaccagagt 2220
cctcacaccc tccggaaagt ttcaaagaag ctggcaccga ttccacccaa ggtccccttt 2280
ggccagccgg gggctatggc agaccagtcc gctggccagc tgtccccagt cagcctgtcc 2340
cccaccccgc ccagcacccc gtcaccctat ggactgagct accctcaggg gtactccttg 2400
gcctcggcc agctctcccc agctgcagct cctcccctgg cctctccttc tgtctttaca 2460
agcactttga gcaaatcgcg gcccactcct aagccgcgac agagacctac tctgccgcct 2520
cctcagcctc ccacagtaaa cctctcggcc tctagtccac agtccacgga ggcccccatg 2580
ctagatggca tgtcccctgg ggaaagcatg tctacagatc ttgtccactt tgatattccc 2640
tcgatccaca tagagctcgg gtcgacgctc cgcctgagtc ccctggagca catgcggcga 2700
cactcagtaa ctgacaagag ggactcggag gaggagtctg agagcaccgc cctctgacat 2760
gacaccgccc atcctgcctc gcgtgtacat acatcacggg ccctaggaac gccgccagga 2820
gcagcgtcca tgagcttgcc aagtgttctc tgctggctct ttcctgccac tgccaacacg 2880
aggttggaat ttggcagaaa attgtgatct ccagtccgtg tggtgatgct ggtggtgcag 2940
gttttgtttg ttcctttcgg gtggtgactt cggccttttg tttgaccttt gccttttgac 3000
tttgtgcctc ttttgatcca ctttcagcct ccatgccaga aaacacccac ctctccatcc 3060
aaggctggtc aggaacgtcc tttgcagggt cggggtggtg cgggagaggc tcactttgcc 3120
tggttagacc caagggctgc taccttttcc ttggacggct catgtcaggt cttgcaggat 3180
cagtttaatg gccacagaaa ggaagcagga cagcagggcc cctctcaccc acaactggac 3240
caggtccagg attctagcag tcctggggca ctgacctttg ccagctacct gggggagggc 3300
ttgccactgg aaaacctttc aggccgcccc catcagtggg ctccaaagta aatggctgaa 3360
aacaaaaatg tttcacttcc taacagtttt cctttttcca ctgtgtgact gaaagctcct 3420
atatcatttt atatttctga atctataaaa caaaacaaac aagcctgaaa gtgtctggag 3480
gagccaaagg tggcctccct gtccccaaat atattggcta tatgagagta atttacccc 3540

```
tctacgtacc taaaggcacc cagttcacta gtctgtgggg tcctggagcc tgtctcttct 3600
ttctggaggt tcaaactgaa tagcaataat tacgttaccc aaagcatgtg gaggaaaagt 3660
gaaaccagcc acggagacgc tggcccacgg ctcggcctgc ggtgtggcct gctttgctca 3720
ccagcgtcag ccgctcattt ccttctcatg aagtcccatc tggtcatggg gacgagggcc 3780
gggagggcac cgggtagcct tttcacactt ggggattagg ggagtgagaa aagatttggg 3840
ccatgcatgc aaagtcaaag tttaaaattt tatccttttc aaatagatga tataatatac 3900
ctatacatga tataatattt gtatatatga aatctctcta tatttgttta atttgagcca 3960
ttcaatctaa accaatgtac aggtgtacaa tgaaaaattt aaatgcttag ttatttttcc 4020
caacacagtg taaagtcacc ctcctctgag agtgggatgt gcagagtttt gatgttgcag 4080
ctttgctcac ttcctggcaa gggcaggtca tgcctcaatt tgtaatggga gtctggggta 4140
agggtggggg ttgaaagttg ttatctttaa atacatgtac aaatcgttgt caaaagtaac 4200
gttattaaaa tagatttatt atccctg                                     4227
```

<210> 246
<211> 818
<212> PRT
<213> Homo sapiens

<400> 246

```
Met Lys Lys Gln Phe Asn Arg Met Arg Gln Leu Ala Asn Gln Thr Val
1               5                   10                  15
Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Val
            20                  25                  30
Glu Lys Arg Leu Glu Leu Val Lys Gln Val Ser His Ser Thr His Lys
        35                  40                  45
Lys Leu Thr Ala Cys Leu Gln Gly Gln Gln Gly Ala Glu Ala Asp Lys
    50                  55                  60
Arg Ser Lys Lys Leu Pro Leu Thr Thr Leu Ala Gln Cys Leu Met Glu
65                  70                  75                  80
Gly Ser Ala Ile Leu Gly Asp Asp Thr Leu Leu Gly Lys Met Leu Lys
                85                  90                  95
Leu Cys Gly Glu Thr Glu Asp Lys Leu Ala Gln Glu Leu Ile His Phe
            100                 105                 110
Glu Leu Gln Val Glu Arg Asp Val Ile Glu Pro Leu Phe Leu Leu Ala
        115                 120                 125
Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys His Leu Ala Lys
    130                 135                 140
Leu Val Leu Asp Met Asp Ser Ser Arg Thr Arg Trp Gln Gln Thr Ser
145                 150                 155                 160
Lys Ser Ser Gly Leu Ser Ser Ser Leu Gln Pro Ala Gly Ala Lys Ala
                165                 170                 175
Asp Ala Leu Arg Glu Glu Met Glu Glu Ala Ala Asn Arg Val Glu Ile
            180                 185                 190
Cys Arg Asp Gln Leu Ser Ala Asp Met Tyr Ser Phe Val Ala Lys Glu
        195                 200                 205
Ile Asp Tyr Ala Asn Tyr Phe Gln Thr Leu Ile Glu Val Gln Ala Glu
    210                 215                 220
Tyr His Arg Lys Ser Leu Thr Leu Leu Gln Ala Val Leu Pro Gln Ile
225                 230                 235                 240
Lys Ala Gln Gln Glu Ala Trp Val Glu Lys Pro Ser Phe Gly Lys Pro
                245                 250                 255
Leu Glu Glu His Leu Thr Ile Ser Gly Arg Glu Ile Ala Phe Pro Ile
            260                 265                 270
Glu Ala Cys Val Thr Met Leu Leu Glu Cys Gly Met Gln Glu Glu Gly
        275                 280                 285
Leu Phe Arg Val Ala Pro Ser Ala Ser Lys Leu Lys Lys Leu Lys Ala
    290                 295                 300
Ala Leu Asp Cys Cys Val Val Asp Val Gln Glu Tyr Ser Ala Asp Pro
305                 310                 315                 320
His Ala Ile Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu
                325                 330                 335
```

Pro Leu Met Thr Phe Glu Leu Tyr Asp Glu Trp Ile Gln Ala Ser Asn
340 345 350
Val Gln Glu Gln Asp Lys Lys Leu Gln Ala Leu Trp Asn Ala Cys Glu
355 360 365
Lys Leu Pro Lys Ala Asn His Asn Asn Ile Arg Tyr Leu Ile Lys Phe
370 375 380
Leu Ser Lys Leu Ser Glu Tyr Gln Asp Val Asn Lys Met Thr Pro Ser
385 390 395 400
Asn Met Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Pro Gln Ala Glu
405 410 415
Gly Asn Ile Thr Glu Met Met Thr Thr Val Ser Leu Gln Ile Val Gly
420 425 430
Ile Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Gly Glu
435 440 445
Ile Glu Phe Asn Ile Thr Gly Asn Tyr Gly Ser Pro Val His Val Asn
450 455 460
His Asn Ala Asn Tyr Ser Ser Met Pro Ser Pro Asp Met Asp Pro Ala
465 470 475 480
Asp Arg Arg Gln Pro Glu Gln Ala Arg Arg Pro Leu Ser Val Ala Thr
485 490 495
Asp Asn Met Met Leu Glu Phe Tyr Lys Lys Asp Gly Leu Arg Lys Ile
500 505 510
Gln Ser Met Gly Val Arg Val Met Asp Thr Asn Trp Val Ala Arg Arg
515 520 525
Gly Ser Ser Ala Gly Arg Lys Val Ser Cys Ala Pro Pro Ser Met Gln
530 535 540
Pro Pro Ala Pro Pro Ala Glu Leu Ala Ala Pro Leu Pro Ser Pro Leu
545 550 555 560
Pro Glu Gln Pro Leu Asp Ser Pro Ala Ala Pro Ala Leu Ser Pro Ser
565 570 575
Gly Leu Gly Leu Gln Pro Gly Pro Glu Arg Thr Ser Thr Thr Lys Ser
580 585 590
Lys Glu Leu Ser Pro Gly Ser Ala Gln Lys Gly Ser Pro Gly Ser Ser
595 600 605
Gln Gly Thr Ala Cys Ala Gly Thr Gln Pro Gly Ala Gln Pro Gly Ala
610 615 620
Gln Pro Gly Ala Ser Pro Ser Pro Ser Gln Pro Pro Ala Asp Gln Ser
625 630 635 640
Pro His Thr Leu Arg Lys Val Ser Lys Lys Leu Ala Pro Ile Pro Pro
645 650 655
Lys Val Pro Phe Gly Gln Pro Gly Ala Met Ala Asp Gln Ser Ala Gly
660 665 670
Gln Leu Ser Pro Val Ser Leu Ser Pro Thr Pro Pro Ser Thr Pro Ser
675 680 685
Pro Tyr Gly Leu Ser Tyr Pro Gln Gly Tyr Ser Leu Ala Ser Gly Gln
690 695 700
Leu Ser Pro Ala Ala Ala Pro Pro Leu Ala Ser Pro Ser Val Phe Thr
705 710 715 720
Ser Thr Leu Ser Lys Ser Arg Pro Thr Pro Lys Pro Arg Gln Arg Pro
725 730 735
Thr Leu Pro Pro Gln Pro Pro Thr Val Asn Leu Ser Ala Ser Ser
740 745 750
Pro Gln Ser Thr Glu Ala Pro Met Leu Asp Gly Met Ser Pro Gly Glu
755 760 765
Ser Met Ser Thr Asp Leu Val His Phe Asp Ile Pro Ser Ile His Ile
770 775 780
Glu Leu Gly Ser Thr Leu Arg Leu Ser Pro Leu Glu His Met Arg Arg
785 790 795 800
His Ser Val Thr Asp Lys Arg Asp Ser Glu Glu Glu Ser Glu Ser Thr
805 810 815
Ala Leu

<210> 247
<211> 2850
<212> DNA
<213> Homo sapiens

<400> 247
tcccgagccc tccacccgtc gtgccggcgc cgcccggacc gccagatgct gtgtgctgtg 60
gacccacctg ggttcatgg agtgggccac ggggcccagc cctaagcact gctgcgccca 120
gggtcgccgc gcctcctgct gaggggtccc cgtgccactg gctctcacca ttgccctcgc 180
ctgccgatgg cctctgctgc ccagcctggg gccagctcta ccgcctgagc cccctgcccc 240
actccaggac tcaccgtacc ccgatggggt aacgtgacac aggccccaca cgtcagaggc 300
cgctgtcccc acggccactg cccgtgaccc ctggcccaag gcagctggag ttggttcagt 360
tcaagttcat tcttcctctg gcccttgggg gcttggggcc cacctctgag tgaagggggc 420
tgtctgccca tccaccaatg tggagagggc gcccccggtg tggggtccag ctctggacac 480
tgcttggcgg ccgggttcac tttgagtttt taagtttttct ttgctgagct tttttggttg 540
ttctttttat tttttgcctc tttatgacta tccagctctg agagacggga gtttggagtt 600
gcccgcttta ctttggttgg gttggggggg gcggcgggct gttttgttcc ttttcttttt 660
taagagttgg gtttttctttt ttaattatcc aaacagtggg cagcttcctc ccccacaccc 720
aagtatttgc acaatatttg tgcggggtat gggggtgggt ttttaaatct cgtttctctt 780
ggacaagcac agggatctcg ttctcctcat tttttggggg tgtgtgggga cttctcaggt 840
cgtgtcccca gccttctctg cagtcccttc tgccctgccg ggcccgtcgg gaggcgccat 900
ggctcggatg aaccgcccgg ccccggtgga ggtgagctac aaacacatgc gcttcctcat 960
cacccacaac cccaccaacg ccacgctcag caccttcatt gaggacctga agaagtacgg 1020
ggctaccact gtggtgcgtg tgtgtgaagt gacctatgac aaaacgccgc tggagaagga 1080
tggcatcacc gttgtggact ggccgtttga cgatggggcg cccccgcccg gcaaggtagt 1140
ggaagactgg ctgagcctgg tgaaggccaa gttctgtgag gcccccggca gctgcgtggc 1200
tgtgcactgc gtggcgggcc tgggccgggc tccagtcctt gtggcgctgg cccttattga 1260
gagcgggatg aagtacgagg acgccatcca gttcatccgc cagaagcgcc gcggagccat 1320
caacagcaag cagctcacct acctggagaa ataccggccc aaacagaggc tgcggttcaa 1380
agacccacac acgcacaaga cccggtgctg cgttatgtag ctcaggacct tggctgggcc 1440
tggtcgtcat gtaggtcagg accttggctg gacctggagg ccctgcccag ccctgctctg 1500
cccagcccag caggggctcc aggccttggc tggccccaca tcgccttttc ctccccgaca 1560
cctccgtgca cttgtgtccg aggagcgagg agcccctcgg gccctgggtg gcctctgggc 1620
cctttctcct gtctccgcca ctccctctgg cggcgctggc cgtggctctg tctctctgag 1680
gtgggtcggg cgccctctgc ccgccccctc ccacaccagc caggctggtc tcctctagcc 1740
tgtttgttgt ggggtggggg tatattttgt aaccactggg cccccagccc ctcttttgcg 1800
acccctgtc ctgacctgtt ctcggcacct taaattatta gaccccgggg cagtcaggtg 1860
ctccggacac ccgaaggcaa taaaacagga gccgtggccg tgtgtgtgga gtgggctgca 1920
gcgtcaggcg gggcgggctg gtggcctggg ggccccagag gctgctgtct ggatcctggg 1980
ctgctgccca ggatggggct cccgcgtgct cttgcgctgc cctctggtgg ccgctctggg 2040
tccttgcacc ccgacccagg ggccagcctg ccctgtcctg tcctgatacc gaggtgggag 2100
ccctgccttg gccagggtgg ccgtgttgac ggttcttggg actgtgacat tggaaggcga 2160
ggcaggtcac cagcactgtc ctctgcagga tgggctggga ttcatttggc agcttctcag 2220
ggcctgtgtc cggctggttg gtccctgtgc tgcccaaacc aggtgtccac atttccggct 2280
ccgaggcgca gagaaggggg caggtggtgg cttgggtgga ggaagtcacc atccatcagc 2340
ccagggaggg agggtaccac ctgggcacct ggggctggat gtgagaggcc tggaccaggg 2400
cccgccggag ggcgtggacc agatgctcat gtgttcctgg gtgcagtgtc tgtgttgggg 2460
gctggcccca ccctgggcca gggtgcatgg agggcatggc cccagcgggg aggaaggtgg 2520
gcctagggct ggctccaggg tgtggagagc ctgggagtgg tctccgtcct ggggccccag 2580
gaggttcccg caaggagcga ctggggcagg tgctggagga ggtcagtgga caagatgggg 2640
agatgtggaa accccaaaag cccctttca ggcagccctg cctccaagac cgacagatgg 2700
ctaagggggc cgcagacctg gctcccccag ctcctgtgtg gagaaagggc aacagctgtc 2760
ccggatggtt attctctcct ttcctcaaac acatttggaa ctcaagtaaa tccgatgcat 2820
gttgggtgaa aaaaaaaaaa aaaaaaaaaa 2850

<210> 248
<211> 173
<212> PRT
<213> Homo sapiens

<400> 248
Met Ala Arg Met Asn Arg Pro Ala Pro Val Glu Val Ser Tyr Lys His
1 5 10 15
Met Arg Phe Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Ser Thr
20 25 30
Phe Ile Glu Asp Leu Lys Lys Tyr Gly Ala Thr Thr Val Val Arg Val
35 40 45
Cys Glu Val Thr Tyr Asp Lys Thr Pro Leu Glu Lys Asp Gly Ile Thr
50 55 60
Val Val Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Gly Lys Val
65 70 75 80
Val Glu Asp Trp Leu Ser Leu Val Lys Ala Lys Phe Cys Glu Ala Pro
85 90 95
Gly Ser Cys Val Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro
100 105 110
Val Leu Val Ala Leu Ala Leu Ile Glu Ser Gly Met Lys Tyr Glu Asp
115 120 125
Ala Ile Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Ile Asn Ser Lys
130 135 140
Gln Leu Thr Tyr Leu Glu Lys Tyr Arg Pro Lys Gln Arg Leu Arg Phe
145 150 155 160
Lys Asp Pro His Thr His Lys Thr Arg Cys Cys Val Met
165 170

<210> 249
<211> 3853
<212> DNA
<213> Homo sapiens

<400> 249
gaagctggct ttatttgtcc atgtctcgga cagagcctgg gaagctgcca gtgagatttc 60
agagaccaag agcgcgaagg ggcgggcgat gtggcaatcc gtctgggatg tgaaaagcgt 120
ggagcgcatt tagaggcatt cgacgaaaac acaggaaatc actcctctcc cgctcctggg 180
cgccgctgcc actggggcag aggactggga accgcggcag cgggataagt ggcccagcca 240
gagagcgcag ctcccgcgcc cggtcctgcc ctgcgaacca gcgcggcccc ctggcgctga 300
ggctgctccg gccatggccc ctcggccccg cgcccgccca ggggtcgctg tcgcctgctg 360
ctggctcctc actgttgttc tacgctgctg cgtatcattc aatgttgatg tgaaaaactc 420
aatgactttc agcggcccgg tggaagacat gtttggatat actgttcaac aatatgaaaa 480
tgaagaagga aaatgggtgc ttattggttc tccgttagtt ggccaaccca aaaacagaac 540
tggagatgtc tataagtgtc cagttgggag aggtgaatca ttaccttgcg taaagttgga 600
tctaccagtt aatacatcaa ttcccaatgt cacagaagta aaggagaaca tgacatttgg 660
atcaacttta gtcaccaacc caaatggagg atttctggct tgtgggccct tatatgccta 720
tagatgtgga catttgcatt acacaactgg aatctgttct gacgtcagcc ccacatttca 780
agtcgtgaat tccattgccc ctgtacaaga atgcagcact caactggaca tagtcatagt 840
gctggatggt tccaacagta tttacccatg ggacagtgtt acagcttttt taaatgacct 900
cttgaaaaga atggatattg gtcctaaaca gacacaggtt ggaattgtac agtatggaga 960
aaacgtgacc catgagttca acctcaataa gtattcttcc accgaagagg tacttgttgc 1020
agcaaagaaa atagtccaga gaggtggccg ccagactatg acagctcttg gaacagacac 1080
agcaagaaag gaggcattca cggaagcccg gggtgcccga agaggagtta aaaaagtcat 1140
ggttattgtg acagatggag agtctcatga caatcatcga ctgaagaagg tcatccaaga 1200
ctgtgaagat gaaaacattc aacggttttc catagctatt cttggcagct ataaccgagg 1260
aaatttaagc actgaaaaat ttgtggagga aataaaatca attgcaagtg aacccactga 1320
aaagcatttc ttcaatgtct ctgatgaatt ggctctagtc accattgtta aaactctggg 1380
agaaagaata tttgccctgg aagccacagc tgaccagtca gcagcttcat ttgaaatgga 1440
aatgtctcag actggcttca gtgctcatta ttcacaggac tgggtcatgc ttggagcagt 1500
aggagcctat gattggaatg gaacagttgt catgcagaag gctagtcaaa tcataatccc 1560
tcgaaacaca acctttaatg ttgagtctac caaaaagaat gaaccgcttg cttcttattt 1620
aggttacact gtaaactctg ctactgcttc ttctggagat gtgctctata ttgctggaca 1680
gcctcggtac aatcatacag gccaggtcat tatctacagg atggaagatg gaaacatcaa 1740
aattctccag acgctcagtg gagaacagat tggttcctac tttggcagta ttttaacaac 1800

aactgacatt gacaaggatt ctaatactga cattcttcta gtcggagccc ctatgtacat 1860
gggaacagag aaggaggagc aaggaaaagt gtatgtgtat gctctcaatc agacaaggtt 1920
tgaatatcaa atgagcctgg aacctattaa gcagacgtgc tgttcatctc ggcagcacaa 1980
ttcatgcaca acagaaaaca aaaatgagcc atgcggggct cgttttggaa ctgcaattgc 2040
tgctgtaaaa gacctcaatc ttgatggatt taatgacatc gtgataggag ctccgctgga 2100
agatgatcac ggggggagctg tgtacattta tcatggaagt ggcaagacta taaggaaaga 2160
gtatgcacaa cgtattccat caggtgggga tggtaagaca ctgaaatttt ttggccagtc 2220
tatccacgga gaaatggatt taaatggtga cggtctgaca gatgtgacta ttgggggcct 2280
tggtggtgct gccctcttct ggtcccgaga tgtggccgta gttaaagtga ccatgaattt 2340
tgagccaaat aaagtgaata ttcaaaagaa aaactgccat atggagggaa aggaaacagt 2400
atgcataaat gctacagtgt gttttgaggt taaattaaag tctaaagaag acacgattta 2460
tgaagctgat ttgcagtacc gtgtcaccct agattcacta agacaaatat cacgaagttt 2520
tttctctgga actcaagaga gaaaggttca aaggaacatc acagttcgaa aatcagaatg 2580
cactaagcac tccttctaca tgttggacaa gcatgacttt caggactctg tgagaataac 2640
gttggacttt aatcttaccg atccagaaaa tgggcctgtt cttgatgatt ctctaccaaa 2700
ctcagtacat gaatatattc cctttgccaa agattgtgga aataaggaaa aatgtatctc 2760
agacctcagc ctgcatgtcg ccaccactga aaaggacctg ctgattgtcc gatcccagaa 2820
tgataagttc aacgttagcc tcacagtcaa aaatacaaag gacagtgcct ataacaccag 2880
gacaatagtg cattattctc caaatctagt tttttcagga attgaggcta tccaaaaaga 2940
cagttgtgaa tctaatcata atatcacatg taaagttgga tatcccttcc tgagaagagg 3000
agagatggta actttcaaaa tattgtttca gtttaacaca tcctatctca tggaaaatgt 3060
gaccatttat ttaagtgcaa caagtgacag cgaagaacct cctgaaaccc tttctgataa 3120
tgtagtaaac atttctatcc cggtaaaata tgaagttgga ctacagtttt acagctctgc 3180
aagtgaatac cacatttcaa ttgctgccaa tgagacagtc cctgaagtta ttaattctac 3240
tgaggacatt ggaaatgaaa ttaatatctt ctacttgatt agaaaaagtg gatcttttcc 3300
aatgccagag cttaagctgt caatttcatt ccccaatatg acatcaaatg gttaccctgt 3360
gctgtaccca actggattgt catcttctga gaatgcaaac tgcagacccc atatctttga 3420
ggatcctttc agtatcaact ctggaaagaa aatgactaca tcaactgacc atctcaaacg 3480
aggcacaatt ctggactgca atacatgtaa atttgctacc atcacatgta atctcacttc 3540
ttctgacatc agccaagtca atgtttcgct tatcttgtgg aaaccaactt ttataaaatc 3600
atatttttcc agcttaaatc ttactataag gggagaactt cggagtgaaa atgcatctct 3660
ggttttaagt agcagcaatc aaaaaagaga gcttgctatt caaatatcca aagatgggct 3720
accgggcaga gtgccattat gggtcatcct gctgagtgct tttgccggat tgttgctgtt 3780
aatgctgctc attttagcac tgtggaagat tggattcttc aaaagaccac tgaaaaagaa 3840
aatggagaaa tga 3853

<210> 250
<211> 1179
<212> PRT
<213> Homo sapiens

<400> 250
Met Ala Pro Arg Pro Arg Ala Arg Pro Gly Val Ala Val Ala Cys Cys
1   5   10   15
Trp Leu Leu Thr Val Val Leu Arg Cys Cys Val Ser Phe Asn Val Asp
            20   25   30
Val Lys Asn Ser Met Thr Phe Ser Gly Pro Val Glu Asp Met Phe Gly
        35   40   45
Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
    50   55   60
Gly Ser Pro Leu Val Gly Gln Pro Lys Asn Arg Thr Gly Asp Val Tyr
65   70   75   80
Lys Cys Pro Val Gly Arg Gly Glu Ser Leu Pro Cys Val Lys Leu Asp
                85   90   95
Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Val Lys Glu Asn
            100   105   110
Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
        115   120   125
Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
    130   135   140
Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser

145 150 155 160
Ile Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val
165 170 175
Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Asp Ser Val Thr Ala Phe
180 185 190
Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln
195 200 205
Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
210 215 220
Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Lys Lys Ile
225 230 235 240
Val Gln Arg Gly Gly Arg Gln Thr Met Thr Ala Leu Gly Thr Asp Thr
245 250 255
Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val
260 265 270
Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn His
275 280 285
Arg Leu Lys Lys Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg
290 295 300
Phe Ser Ile Ala Ile Leu Gly Ser Tyr Asn Arg Gly Asn Leu Ser Thr
305 310 315 320
Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu
325 330 335
Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val
340 345 350
Lys Thr Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln
355 360 365
Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala
370 375 380
His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp
385 390 395 400
Trp Asn Gly Thr Val Val Met Gln Lys Ala Ser Gln Ile Ile Ile Pro
405 410 415
Arg Asn Thr Thr Phe Asn Val Glu Ser Thr Lys Lys Asn Glu Pro Leu
420 425 430
Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ala Ser Ser Gly
435 440 445
Asp Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln
450 455 460
Val Ile Ile Tyr Arg Met Glu Asp Gly Asn Ile Lys Ile Leu Gln Thr
465 470 475 480
Leu Ser Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Ile Leu Thr Thr
485 490 495
Thr Asp Ile Asp Lys Asp Ser Asn Thr Asp Ile Leu Leu Val Gly Ala
500 505 510
Pro Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val
515 520 525
Tyr Ala Leu Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro
530 535 540
Ile Lys Gln Thr Cys Cys Ser Ser Arg Gln His Asn Ser Cys Thr Thr
545 550 555 560
Glu Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala
565 570 575
Ala Val Lys Asp Leu Asn Leu Asp Gly Phe Asn Asp Ile Val Ile Gly
580 585 590
Ala Pro Leu Glu Asp Asp His Gly Gly Ala Val Tyr Ile Tyr His Gly
595 600 605
Ser Gly Lys Thr Ile Arg Lys Glu Tyr Ala Gln Arg Ile Pro Ser Gly
610 615 620
Gly Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu
625 630 635 640

Met Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu
645 650 655
Gly Gly Ala Ala Leu Phe Trp Ser Arg Asp Val Ala Val Val Lys Val
660 665 670
Thr Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys
675 680 685
His Met Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Val Cys Phe
690 695 700
Glu Val Lys Leu Lys Ser Lys Glu Asp Thr Ile Tyr Glu Ala Asp Leu
705 710 715 720
Gln Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe
725 730 735
Phe Ser Gly Thr Gln Glu Arg Lys Val Gln Arg Asn Ile Thr Val Arg
740 745 750
Lys Ser Glu Cys Thr Lys His Ser Phe Tyr Met Leu Asp Lys His Asp
755 760 765
Phe Gln Asp Ser Val Arg Ile Thr Leu Asp Phe Asn Leu Thr Asp Pro
770 775 780
Glu Asn Gly Pro Val Leu Asp Asp Ser Leu Pro Asn Ser Val His Glu
785 790 795 800
Tyr Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Lys Cys Ile Ser
805 810 815
Asp Leu Ser Leu His Val Ala Thr Thr Glu Lys Asp Leu Leu Ile Val
820 825 830
Arg Ser Gln Asn Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Thr
835 840 845
Lys Asp Ser Ala Tyr Asn Thr Arg Thr Ile Val His Tyr Ser Pro Asn
850 855 860
Leu Val Phe Ser Gly Ile Glu Ala Ile Gln Lys Asp Ser Cys Glu Ser
865 870 875 880
Asn His Asn Ile Thr Cys Lys Val Gly Tyr Pro Phe Leu Arg Arg Gly
885 890 895
Glu Met Val Thr Phe Lys Ile Leu Phe Gln Phe Asn Thr Ser Tyr Leu
900 905 910
Met Glu Asn Val Thr Ile Tyr Leu Ser Ala Thr Ser Asp Ser Glu Glu
915 920 925
Pro Pro Glu Thr Leu Ser Asp Asn Val Val Asn Ile Ser Ile Pro Val
930 935 940
Lys Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu Tyr His
945 950 955 960
Ile Ser Ile Ala Ala Asn Glu Thr Val Pro Glu Val Ile Asn Ser Thr
965 970 975
Glu Asp Ile Gly Asn Glu Ile Asn Ile Phe Tyr Leu Ile Arg Lys Ser
980 985 990
Gly Ser Phe Pro Met Pro Glu Leu Lys Leu Ser Ile Ser Phe Pro Asn
995 1000 1005
Met Thr Ser Asn Gly Tyr Pro Val Leu Tyr Pro Thr Gly Leu Ser Ser
1010 1015 1020
Ser Glu Asn Ala Asn Cys Arg Pro His Ile Phe Glu Asp Pro Phe Ser
1025 1030 1035 1040
Ile Asn Ser Gly Lys Lys Met Thr Thr Ser Thr Asp His Leu Lys Arg
1045 1050 1055
Gly Thr Ile Leu Asp Cys Asn Thr Cys Lys Phe Ala Thr Ile Thr Cys
1060 1065 1070
Asn Leu Thr Ser Ser Asp Ile Ser Gln Val Asn Val Ser Leu Ile Leu
1075 1080 1085
Trp Lys Pro Thr Phe Ile Lys Ser Tyr Phe Ser Ser Leu Asn Leu Thr
1090 1095 1100
Ile Arg Gly Glu Leu Arg Ser Glu Asn Ala Ser Leu Val Leu Ser Ser
1105 1110 1115 1120
Ser Asn Gln Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly Leu

```
                1125                1130                1135
Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala Gly
            1140                1145                1150
Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly Phe
        1155                1160                1165
Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys
    1170                1175

      <210> 251
      <211> 5010
      <212> DNA
      <213> Homo sapiens

      <400> 251
atggggcccc ggctcagcgt ctggctgctg ctgctgcccg ccgcccttct gctccacgag      60
gagcacagcc gggccgctgc gaagggtggc tgtgctggct ctggctgtgg caaatgtgac     120
tgccatggag tgaagggaca aaagggtgaa agaggcctcc cggggttaca aggtgtcatt     180
gggtttcctg gaatgcaagg acctgagggg ccacagggac caccaggaca aaagggtgat     240
actggagaac caggactacc tggaacaaaa gggacaagag gacctccggg agcatctggc     300
taccctggaa acccaggact tcccggaatt cctggccaag acggcccgcc aggcccccca     360
ggtattccag gatgcaatgg cacaaagggg gagagagggc cgctcgggcc tcctggcttg     420
cctggtttcg caggaaatcc cggaccacca ggcttaccag ggatgaaggg tgatccaggt     480
gagatacttg gccatgtgcc cgggatgctg ttgaaaggtg aaagaggatt tcccggaatc     540
ccagggactc caggcccacc aggactgcca gggcttcaag gtcctgttgg gcctccagga     600
tttaccggac caccaggtcc cccaggccct cccggccctc caggtgaaaa gggacaaatg     660
ggcttaagtt ttcaaggacc aaaaggtgac aagggtgacc aaggggtcag tgggcctcca     720
ggagtaccag gacaagctca agttcaagaa aaaggagact tcgccaccaa gggagaaaag     780
ggccaaaaag gtgaacctgg atttcagggg atgccagggg tcggagagaa aggtgaaccc     840
ggaaaaccag gacccagagg caaacccgga aaagatggtg acaaagggga aaaagggagt     900
cccggtttc ctggtgaacc cgggtaccca ggactcatag gccgccaggg cccgcaggga      960
gaaaagggtg aagcaggtcc tcctggccca cctggaattg ttataggcac aggacctttg    1020
ggagaaaaag gagagagggg ctaccctgga actccggggc caagaggaga gccaggccca    1080
aaaggtttcc caggactacc aggccaaccc ggacctccag gcctccctgt acctgggcag    1140
gctggtgccc ctggcttccc tggtgaaaga ggagaaaaag gtgaccgagg atttcctggt    1200
acatctctgc caggaccaag tggaagagat gggctcccgg gtcctcctgg ttccccccggg   1260
cccccctgggc agcctggcta cacaaatgga attgtggaat gtcagcccgg acctccaggt   1320
gaccagggtc ctcctggaat tccagggcag ccaggattta taggcgaaat tggagagaaa    1380
ggtcaaaaag gagagagttg cctcatctgt gatatagacg gatatcgggg gcctcccggg    1440
ccacagggac ccccgggaga aataggtttc ccagggcagc caggggccaa gggcgacaga    1500
ggtttgcctg gcagagatgg tgttgcagga gtgccaggcc ctcaaggtac accagggctg    1560
ataggccagc caggagccaa gggggagcct ggtgagtttt atttcgactt gcggctcaaa    1620
ggtgacaaag gagacccagg ctttccagga cagcccggca tgccagggag agcgggttct    1680
cctggaagag atggccatcc gggtcttcct ggccccaagg gctcgccggg ttctgtagga    1740
ttgaaaggag agcgtggccc ccctggagga gttggattcc caggcagtcg tggtgacacc    1800
ggcccccctg ggcctccagg atatggtcct gctggtccca ttggtgacaa aggacaagca    1860
ggctttcctg gaggccctgg atccccaggc ctgccaggtc caaagggtga accaggaaaa    1920
attgttcctt taccaggccc ccctggagca gaaggactgc cggggtcccc aggcttccca    1980
ggtccccaag gagaccgagg ctttcccgga accccaggaa ggccaggcct gccaggagag    2040
aagggcgctg tgggccagcc aggcattgga tttccagggc cccccggccc caaaggtgtt    2100
gacggcttac ctggagacat ggggccaccg gggactccag gtcgcccggg atttaatggc    2160
ttacctggga acccaggtgt gcagggccag aagggagagc ctggagttgg tctaccggga    2220
ctcaaaggtt tgccaggtct tcccggcatt cctggcacac ccggggagaa ggggagcatt    2280
ggggtaccag gcgttcctgg agaacatgga gcgatcggac cccctgggct tcaggggatc    2340
agaggtgaac cgggacctcc tggattgcca ggctccgtgg ggtctccagg agttccagga    2400
ataggccccc ctggagctag ggtccccct ggaggacagg gaccaccggg gttgtcaggc     2460
cctcctggaa taaaaggaga gaagggtttc cccggattcc ctggactgga catgccgggc    2520
cctaaaggag ataaaggggc tcaaggactc cctggcataa cgggacagtc ggggctccct    2580
ggccttcctg gacagcaggg ggctcctggg attcctgggt ttccaggttc caagggagaa    2640
atgggcgtca tggggacccc cgggcagccg ggctcaccag gaccagtggg tgctcctgga    2700
ttaccgggtg aaaaagggga ccatggcttt ccgggctcct caggacccag gggagaccct    2760
ggcttgaaag gtgataaggg ggatgtcggt ctccctggca agcctggctc catggataag    2820
```

```
gtggacatgg gcagcatgaa gggccagaaa ggagaccaag gagagaaagg acaaattgga   2880
ccaattggtg agaagggatc ccgaggagac cctgggaccc caggagtgcc tggaaaggac   2940
gggcaggcag gacagcctgg gcagccagga cctaaaggtg atccaggtat aagtggaacc   3000
ccaggtgctc caggacttcc gggaccaaaa ggatctgttg gtggaatggg cttgccagga   3060
acacctggag agaaaggtgt gcctggcatc cctggcccac aaggttcacc tggcttacct   3120
ggagacaaag gtgcaaaagg agagaaaggg caggcaggcc cacctggcat aggcatccca   3180
ggactgcgtg gtgaaaaggg agatcaaggg atagcgggtt tcccaggaag ccctggagag   3240
aagggagaaa aaggaagcat tgggatccca ggaatgccag ggtccccagg ccttaaaggg   3300
tctcccggga gtgttggcta tccaggaagt cctgggctac ctggagaaaa aggtgacaaa   3360
ggcctcccag gattggatgg catccctggt gtcaaaggag aagcaggtct tcctgggact   3420
cctggcccca caggcccagc tggccagaaa ggggagccag gcagtgatgg aatcccgggg   3480
tcagcaggag agaagggtga accaggtcta ccaggaagag gattcccagg gtttccaggg   3540
gccaaaggag acaaaggttc aaagggtgag gtgggtttcc caggattagc cgggagccca   3600
ggaattcctg gatccaaagg agagcaagga ttcatgggtc ctccggggcc ccagggacag   3660
ccggggttac cgggatcccc aggccatgcc acggaggggc ccaaaggaga ccgcggacct   3720
cagggccagc ctggcctgcc aggacttccg ggacccatgg ggcctccagg gcttcctggg   3780
attgatggag ttaaaggtga caaaggaaat ccaggctggc caggagcacc cggtgtccca   3840
gggcccaagg gagaccctgg attccagggc atgcctggta ttggtggctc tccaggaatc   3900
acaggctcta agggtgatat ggggcctcca ggagttccag gatttcaagg tccaaaaggt   3960
cttcctggcc tccagggaat taaaggtgat caaggcgatc aaggcgtccc gggagctaaa   4020
ggtctcccgg gtcctcctgg ccccccaggt ccttacgaca tcatcaaagg ggagcccggg   4080
ctccctggtc ctgagggccc cccagggctg aaagggcttc agggactgcc aggcccgaaa   4140
ggccagcaag gtgttacagg attggtgggt atacctggac ctccaggtat tcctgggttt   4200
gacggtgccc ctggccagaa aggagagatg ggacctgccg ggcctactgg tccaagagga   4260
tttccaggtc caccaggccc cgatgggttg ccaggatcca tggggccccc aggcaccccа   4320
tctgttgatc acggcttcct tgtgaccagg catagtcaaa caatagatga cccacagtgt   4380
ccttctggga ccaaaattct ttaccacggg tactctttgc tctacgtgca aggcaatgaa   4440
cgggcccatg gacaggactt gggcacggcc ggcagctgcc tgcgcaagtt cagcacaatg   4500
ccсttcctgt tctgcaatat taacaacgtg tgcaactttg catcacgaaa tgactactcg   4560
tactggctgt ccacccctga gcccatgccc atgtcaatgg cacccatcac ggggaaaaac   4620
ataagaccat ttattagtag gtgtgctgtg tgtgaggcgc ctgccatggt gatggccgtg   4680
cacagccaga ccattcagat cccaccgtgc cccagcgggt ggtcctcgct gtggatcggc   4740
tactcttttg tgatgcacac cagcgctggt gcagaaggct ctggccaagc cctggcgtcc   4800
cccggctcct gcctggagga gtttagaagt gcgccattca tcgagtgtca cggccgtggg   4860
acctgcaatt actacgcaaa cgcttacagc ttttggctcg ccaccataga gaggagcgag   4920
atgttcaaga agcctacgcc gtccaccttg aaggcagggg agctgcgcac gcacgtcagc   4980
cgctgccaag tctgtatgag aagaacataa                                    5010
```

<210> 252
<211> 1669
<212> PRT
<213> Homo sapiens

<400> 252

```
Met Gly Pro Arg Leu Ser Val Trp Leu Leu Leu Leu Pro Ala Ala Leu
1               5                   10                  15
Leu Leu His Glu Glu His Ser Arg Ala Ala Ala Lys Gly Gly Cys Ala
            20                  25                  30
Gly Ser Gly Cys Gly Lys Cys Asp Cys His Gly Val Lys Gly Gln Lys
        35                  40                  45
Gly Glu Arg Gly Leu Pro Gly Leu Gln Gly Val Ile Gly Phe Pro Gly
    50                  55                  60
Met Gln Gly Pro Glu Gly Pro Gln Gly Pro Pro Gly Gln Lys Gly Asp
65                  70                  75                  80
Thr Gly Glu Pro Gly Leu Pro Gly Thr Lys Gly Thr Arg Gly Pro Pro
                85                  90                  95
Gly Ala Ser Gly Tyr Pro Gly Asn Pro Gly Leu Pro Gly Ile Pro Gly
            100                 105                 110
Gln Asp Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Cys Asn Gly Thr
```

115 120 125
Lys Gly Glu Arg Gly Pro Leu Gly Pro Pro Gly Leu Pro Gly Phe Ala
130 135 140
Gly Asn Pro Gly Pro Pro Gly Leu Pro Gly Met Lys Gly Asp Pro Gly
145 150 155 160
Glu Ile Leu Gly His Val Pro Gly Met Leu Leu Lys Gly Glu Arg Gly
165 170 175
Phe Pro Gly Ile Pro Gly Thr Pro Gly Pro Pro Gly Leu Pro Gly Leu
180 185 190
Gln Gly Pro Val Gly Pro Pro Gly Phe Thr Gly Pro Pro Gly Pro Pro
195 200 205
Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Gln Met Gly Leu Ser Phe
210 215 220
Gln Gly Pro Lys Gly Asp Lys Gly Asp Gln Gly Val Ser Gly Pro Pro
225 230 235 240
Gly Val Pro Gly Gln Ala Gln Val Gln Glu Lys Gly Asp Phe Ala Thr
245 250 255
Lys Gly Glu Lys Gly Gln Lys Gly Glu Pro Gly Phe Gln Gly Met Pro
260 265 270
Gly Val Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Arg Gly Lys
275 280 285
Pro Gly Lys Asp Gly Asp Lys Gly Glu Lys Gly Ser Pro Gly Phe Pro
290 295 300
Gly Glu Pro Gly Tyr Pro Gly Leu Ile Gly Arg Gln Gly Pro Gln Gly
305 310 315 320
Glu Lys Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Ile Val Ile Gly
325 330 335
Thr Gly Pro Leu Gly Glu Lys Gly Glu Arg Gly Tyr Pro Gly Thr Pro
340 345 350
Gly Pro Arg Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Leu Pro Gly
355 360 365
Gln Pro Gly Pro Pro Gly Leu Pro Val Pro Gly Gln Ala Gly Ala Pro
370 375 380
Gly Phe Pro Gly Glu Arg Gly Glu Lys Gly Asp Arg Gly Phe Pro Gly
385 390 395 400
Thr Ser Leu Pro Gly Pro Ser Gly Arg Asp Gly Leu Pro Gly Pro Pro
405 410 415
Gly Ser Pro Gly Pro Pro Gly Gln Pro Gly Tyr Thr Asn Gly Ile Val
420 425 430
Glu Cys Gln Pro Gly Pro Pro Gly Asp Gln Gly Pro Pro Gly Ile Pro
435 440 445
Gly Gln Pro Gly Phe Ile Gly Glu Ile Gly Glu Lys Gly Gln Lys Gly
450 455 460
Glu Ser Cys Leu Ile Cys Asp Ile Asp Gly Tyr Arg Gly Pro Pro Gly
465 470 475 480
Pro Gln Gly Pro Pro Gly Glu Ile Gly Phe Pro Gly Gln Pro Gly Ala
485 490 495
Lys Gly Asp Arg Gly Leu Pro Gly Arg Asp Gly Val Ala Gly Val Pro
500 505 510
Gly Pro Gln Gly Thr Pro Gly Leu Ile Gly Gln Pro Gly Ala Lys Gly
515 520 525
Glu Pro Gly Glu Phe Tyr Phe Asp Leu Arg Leu Lys Gly Asp Lys Gly
530 535 540
Asp Pro Gly Phe Pro Gly Gln Pro Gly Met Pro Gly Arg Ala Gly Ser
545 550 555 560
Pro Gly Arg Asp Gly His Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro
565 570 575
Gly Ser Val Gly Leu Lys Gly Glu Arg Gly Pro Pro Gly Gly Val Gly
580 585 590
Phe Pro Gly Ser Arg Gly Asp Thr Gly Pro Pro Gly Pro Pro Gly Tyr
595 600 605

Gly Pro Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly
610 615 620
Gly Pro Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Lys
625 630 635 640
Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly Ser
645 650 655
Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr Pro
660 665 670
Gly Arg Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro Gly
675 680 685
Ile Gly Phe Pro Gly Pro Pro Gly Pro Lys Gly Val Asp Gly Leu Pro
690 695 700
Gly Asp Met Gly Pro Pro Gly Thr Pro Gly Arg Pro Gly Phe Asn Gly
705 710 715 720
Leu Pro Gly Asn Pro Gly Val Gln Gly Gln Lys Gly Glu Pro Gly Val
725 730 735
Gly Leu Pro Gly Leu Lys Gly Leu Pro Gly Leu Pro Gly Ile Pro Gly
740 745 750
Thr Pro Gly Glu Lys Gly Ser Ile Gly Val Pro Gly Val Pro Gly Glu
755 760 765
His Gly Ala Ile Gly Pro Pro Gly Leu Gln Gly Ile Arg Gly Glu Pro
770 775 780
Gly Pro Pro Gly Leu Pro Gly Ser Val Gly Ser Pro Gly Val Pro Gly
785 790 795 800
Ile Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Gly Gln Gly Pro Pro
805 810 815
Gly Leu Ser Gly Pro Pro Gly Ile Lys Gly Glu Lys Gly Phe Pro Gly
820 825 830
Phe Pro Gly Leu Asp Met Pro Gly Pro Lys Gly Asp Lys Gly Ala Gln
835 840 845
Gly Leu Pro Gly Ile Thr Gly Gln Ser Gly Leu Pro Gly Leu Pro Gly
850 855 860
Gln Gln Gly Ala Pro Gly Ile Pro Gly Phe Pro Gly Ser Lys Gly Glu
865 870 875 880
Met Gly Val Met Gly Thr Pro Gly Gln Pro Gly Ser Pro Gly Pro Val
885 890 895
Gly Ala Pro Gly Leu Pro Gly Glu Lys Gly Asp His Gly Phe Pro Gly
900 905 910
Ser Ser Gly Pro Arg Gly Asp Pro Gly Leu Lys Gly Asp Lys Gly Asp
915 920 925
Val Gly Leu Pro Gly Lys Pro Gly Ser Met Asp Lys Val Asp Met Gly
930 935 940
Ser Met Lys Gly Gln Lys Gly Asp Gln Gly Glu Lys Gly Gln Ile Gly
945 950 955 960
Pro Ile Gly Glu Lys Gly Ser Arg Gly Asp Pro Gly Thr Pro Gly Val
965 970 975
Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro Lys
980 985 990
Gly Asp Pro Gly Ile Ser Gly Thr Pro Gly Ala Pro Gly Leu Pro Gly
995 1000 1005
Pro Lys Gly Ser Val Gly Gly Met Gly Leu Pro Gly Thr Pro Gly Glu
1010 1015 1020
Lys Gly Val Pro Gly Ile Pro Gly Pro Gln Gly Ser Pro Gly Leu Pro
1025 1030 1035 1040
Gly Asp Lys Gly Ala Lys Gly Glu Lys Gly Gln Ala Gly Pro Pro Gly
1045 1050 1055
Ile Gly Ile Pro Gly Leu Arg Gly Glu Lys Gly Asp Gln Gly Ile Ala
1060 1065 1070
Gly Phe Pro Gly Ser Pro Gly Glu Lys Gly Glu Lys Gly Ser Ile Gly
1075 1080 1085
Ile Pro Gly Met Pro Gly Ser Pro Gly Leu Lys Gly Ser Pro Gly Ser

1090 1095 1100
Val Gly Tyr Pro Gly Ser Pro Gly Leu Pro Gly Glu Lys Gly Asp Lys
1105 1110 1115 1120
Gly Leu Pro Gly Leu Asp Gly Ile Pro Gly Val Lys Gly Glu Ala Gly
1125 1130 1135
Leu Pro Gly Thr Pro Gly Pro Thr Gly Pro Ala Gly Gln Lys Gly Glu
1140 1145 1150
Pro Gly Ser Asp Gly Ile Pro Gly Ser Ala Gly Glu Lys Gly Glu Pro
1155 1160 1165
Gly Leu Pro Gly Arg Gly Phe Pro Gly Phe Pro Gly Ala Lys Gly Asp
1170 1175 1180
Lys Gly Ser Lys Gly Glu Val Gly Phe Pro Gly Leu Ala Gly Ser Pro
1185 1190 1195 1200
Gly Ile Pro Gly Ser Lys Gly Glu Gln Gly Phe Met Gly Pro Pro Gly
1205 1210 1215
Pro Gln Gly Gln Pro Gly Leu Pro Gly Ser Pro Gly His Ala Thr Glu
1220 1225 1230
Gly Pro Lys Gly Asp Arg Gly Pro Gln Gly Gln Pro Gly Leu Pro Gly
1235 1240 1245
Leu Pro Gly Pro Met Gly Pro Pro Gly Leu Pro Gly Ile Asp Gly Val
1250 1255 1260
Lys Gly Asp Lys Gly Asn Pro Gly Trp Pro Gly Ala Pro Gly Val Pro
1265 1270 1275 1280
Gly Pro Lys Gly Asp Pro Gly Phe Gln Gly Met Pro Gly Ile Gly Gly
1285 1290 1295
Ser Pro Gly Ile Thr Gly Ser Lys Gly Asp Met Gly Pro Pro Gly Val
1300 1305 1310
Pro Gly Phe Gln Gly Pro Lys Gly Leu Pro Gly Leu Gln Gly Ile Lys
1315 1320 1325
Gly Asp Gln Gly Asp Gln Gly Val Pro Gly Ala Lys Gly Leu Pro Gly
1330 1335 1340
Pro Pro Gly Pro Pro Gly Pro Tyr Asp Ile Ile Lys Gly Glu Pro Gly
1345 1350 1355 1360
Leu Pro Gly Pro Glu Gly Pro Pro Gly Leu Lys Gly Leu Gln Gly Leu
1365 1370 1375
Pro Gly Pro Lys Gly Gln Gln Gly Val Thr Gly Leu Val Gly Ile Pro
1380 1385 1390
Gly Pro Pro Gly Ile Pro Gly Phe Asp Gly Ala Pro Gly Gln Lys Gly
1395 1400 1405
Glu Met Gly Pro Ala Gly Pro Thr Gly Pro Arg Gly Phe Pro Gly Pro
1410 1415 1420
Pro Gly Pro Asp Gly Leu Pro Gly Ser Met Gly Pro Pro Gly Thr Pro
1425 1430 1435 1440
Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp
1445 1450 1455
Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser
1460 1465 1470
Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly
1475 1480 1485
Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe
1490 1495 1500
Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser
1505 1510 1515 1520
Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile
1525 1530 1535
Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu
1540 1545 1550
Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile Pro
1555 1560 1565
Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe Val
1570 1575 1580

Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala Ser
1585 1590 1595 1600
Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
1605 1610 1615
His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
1620 1625 1630
Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
1635 1640 1645
Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
1650 1655 1660
Cys Met Arg Arg Thr
1665

<210> 253
<211> 2798
<212> DNA
<213> Homo sapiens

<400> 253
gccctctccc acagcggagt ccaaaacagg cctaccagtc agttcttatt tctattgggt 60
gtttccatgc tccaccatgt taagagctaa gaatcagctt tttttacttt cacctcatta 120
cctgaggcag gtaaaagaat catcaggctc caggctcata cagcaacgac ttctacacca 180
gcaacagccc cttcacccag aatgggctgc cctggctaaa aagcagctga aaggcaaaaa 240
cccagaagac ctaatatggc acaccccgga agggatctct ataaaaccct tgtattccaa 300
gagagatact atggacttac ctgaagaact tccaggagtg aagccattca cacgtggacc 360
atatcctacc atgtatacct ttaggccctg gaccatccgc cagtatgctg gttttagtac 420
tgtggaagaa agcaataagt tctataagga caacattaag gctggtcagc agggattatc 480
agttgccttt gatctggcga cacatcgtgg ctatgattca gacaaccctc gagttcgtgg 540
tgatgttgga atggctggag ttgctattga cactgtggaa gataccaaaa ttctttttga 600
tggaattcct ttagaaaaaa tgtcagtttc catgactatg aatggagcag ttattccagt 660
tcttgcaaat tttatagtaa ctggagaaga acaaggtgta cctaaagaga aacttactgg 720
taccatccaa aatgatatac taaaggaatt tatggttcga aatacataca tttttcctcc 780
agaaccatcc atgaaaatta ttgctgacat atttgaatat acagcaaagc acatgccaaa 840
atttaattca atttcaatta gtggatacca tatgcaggaa gcaggggctg atgccattct 900
ggagctggcc tatactttag cagatggatt ggagtactct agaactggac tccaggctgg 960
cctgacaatt gatgaatttg caccaaggtt gtctttcttc tggggaattg gaatgaattt 1020
ctatatggaa atagcaaaga tgagagctgg tagaagactc tgggctcact taatagagaa 1080
aatgtttcag cctaaaaact caaaatctct tcttctaaga gcacactgtc agacatctgg 1140
atggtcactt actgagcagg atccctacaa taatattgtc cgtactgcaa tagaagcaat 1200
ggcagcagta tttggaggga ctcagtcttt gcacacaaat tcttttgatg aagctttggg 1260
tttgccaact gtgaaaagtg ctcgaattgc caggaacaca caaatcatca ttcaagaaga 1320
atctgggatt cccaaagtgg ctgatccttg gggaggttct tacatgatgg aatgtctcac 1380
aaatgatgtt tatgatgctg ctttaaagct cattaatgaa attgaagaaa tgggtggaat 1440
ggccaaagct gtagctgagg gaatacctaa acttcgaatt gaagaatgtg ctgcccgaag 1500
acaagctaga atagattctg gttctgaagt aattgttgga gtaaataagt accagttgga 1560
aaaagaagac gctgtagaag ttctggcaat tgataatact tcagtgcgaa acaggcagat 1620
tgaaaaactt aagaagatca aatccagcag ggatcaagct ttggctgaac attgtcttgc 1680
tgcactaacc gaatgtgctg ctagcggaga tggaaatatc ctggctcttg cagtggatgc 1740
atctcgggca agatgtacag tgggagaaat cacagatgcc ctgaaaaagg tatttggtga 1800
acataaagcg aatgatcgaa tggtgagtgg agcatatcgc caggaatttg gagaaagtaa 1860
agagataaca tctgctatca agagggttca taaattcatg gaacgtgaag gtcgcagacc 1920
tcgtcttctt gtagcaaaaa tgggacaaga tggccatgac agaggagcaa aagttattgc 1980
tacaggattt gctgatcttg gttttgatgt ggacataggc cctcttttcc agactcctcg 2040
tgaagtggcc cagcaggctg tggatgcgga tgtgcatgct gtgggcgtaa gcaccctcgc 2100
tgctggtcat aaaaccctag ttcctgaact catcaaagaa cttaactccc ttggacggcc 2160
agatattctt gtcatgtgtg gaggggtgat accacctcag gattatgaat ttctgtttga 2220
agttggtgtt tccaatgtat ttggtcctgg gactcgaatt ccaaaggctg ccgttcaggt 2280
gcttgatgat attgagaagt gtttggaaaa gaagcagcaa tctgtataat atcctctttt 2340
tgttttagct tttgtctaaa atattatttt agttatgatc aaagaagaga gtaaagctat 2400
gtcttcaatt taatttcaat acctgatttg tactttcctt gaaagcttta ctttaaaata 2460
ccttacttat aggcctggtg tcatgctata agtatgtaca tacagtttca cttcaaaaat 2520

aaaaaaaaat ccctaaaaac tctctatact ctctataaca atactttatc aagaactctg 2580
gacaatggta ttatttttaa aaatcatggt gatgtattta ttagaatgtt tcttataaat 2640
ctctttcatt tttatattaa gaattaaact gtacctaaaa aaactctgac tattcccatt 2700
tctcagttta gcattacatt gtcttgagca ccagaaaata aaatccatat attaattaaa 2760
acctatcttg aaaaaaaaaa aaaaaaaaaa aaaaaaa 2798

<210> 254
<211> 750
<212> PRT
<213> Homo sapiens

<400> 254
Met Leu Arg Ala Lys Asn Gln Leu Phe Leu Leu Ser Pro His Tyr Leu
1 5 10 15
Arg Gln Val Lys Glu Ser Ser Gly Ser Arg Leu Ile Gln Gln Arg Leu
20 25 30
Leu His Gln Gln Gln Pro Leu His Pro Glu Trp Ala Ala Leu Ala Lys
35 40 45
Lys Gln Leu Lys Gly Lys Asn Pro Glu Asp Leu Ile Trp His Thr Pro
50 55 60
Glu Gly Ile Ser Ile Lys Pro Leu Tyr Ser Lys Arg Asp Thr Met Asp
65 70 75 80
Leu Pro Glu Glu Leu Pro Gly Val Lys Pro Phe Thr Arg Gly Pro Tyr
85 90 95
Pro Thr Met Tyr Thr Phe Arg Pro Trp Thr Ile Arg Gln Tyr Ala Gly
100 105 110
Phe Ser Thr Val Glu Glu Ser Asn Lys Phe Tyr Lys Asp Asn Ile Lys
115 120 125
Ala Gly Gln Gln Gly Leu Ser Val Ala Phe Asp Leu Ala Thr His Arg
130 135 140
Gly Tyr Asp Ser Asp Asn Pro Arg Val Arg Gly Asp Val Gly Met Ala
145 150 155 160
Gly Val Ala Ile Asp Thr Val Glu Asp Thr Lys Ile Leu Phe Asp Gly
165 170 175
Ile Pro Leu Glu Lys Met Ser Val Ser Met Thr Met Asn Gly Ala Val
180 185 190
Ile Pro Val Leu Ala Asn Phe Ile Val Thr Gly Glu Glu Gln Gly Val
195 200 205
Pro Lys Glu Lys Leu Thr Gly Thr Ile Gln Asn Asp Ile Leu Lys Glu
210 215 220
Phe Met Val Arg Asn Thr Tyr Ile Phe Pro Pro Glu Pro Ser Met Lys
225 230 235 240
Ile Ile Ala Asp Ile Phe Glu Tyr Thr Ala Lys His Met Pro Lys Phe
245 250 255
Asn Ser Ile Ser Ile Ser Gly Tyr His Met Gln Glu Ala Gly Ala Asp
260 265 270
Ala Ile Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Leu Glu Tyr Ser
275 280 285
Arg Thr Gly Leu Gln Ala Gly Leu Thr Ile Asp Glu Phe Ala Pro Arg
290 295 300
Leu Ser Phe Phe Trp Gly Ile Gly Met Asn Phe Tyr Met Glu Ile Ala
305 310 315 320
Lys Met Arg Ala Gly Arg Arg Leu Trp Ala His Leu Ile Glu Lys Met
325 330 335
Phe Gln Pro Lys Asn Ser Lys Ser Leu Leu Leu Arg Ala His Cys Gln
340 345 350
Thr Ser Gly Trp Ser Leu Thr Glu Gln Asp Pro Tyr Asn Asn Ile Val
355 360 365
Arg Thr Ala Ile Glu Ala Met Ala Ala Val Phe Gly Gly Thr Gln Ser
370 375 380
Leu His Thr Asn Ser Phe Asp Glu Ala Leu Gly Leu Pro Thr Val Lys

```
385                 390                 395                 400
Ser Ala Arg Ile Ala Arg Asn Thr Gln Ile Ile Ile Gln Glu Glu Ser
                405                 410                 415
Gly Ile Pro Lys Val Ala Asp Pro Trp Gly Gly Ser Tyr Met Met Glu
            420                 425                 430
Cys Leu Thr Asn Asp Val Tyr Asp Ala Ala Leu Lys Leu Ile Asn Glu
        435                 440                 445
Ile Glu Glu Met Gly Gly Met Ala Lys Ala Val Ala Glu Gly Ile Pro
    450                 455                 460
Lys Leu Arg Ile Glu Glu Cys Ala Ala Arg Arg Gln Ala Arg Ile Asp
465                 470                 475                 480
Ser Gly Ser Glu Val Ile Val Gly Val Asn Lys Tyr Gln Leu Glu Lys
                485                 490                 495
Glu Asp Ala Val Glu Val Leu Ala Ile Asp Asn Thr Ser Val Arg Asn
            500                 505                 510
Arg Gln Ile Glu Lys Leu Lys Lys Ile Lys Ser Ser Arg Asp Gln Ala
        515                 520                 525
Leu Ala Glu His Cys Leu Ala Ala Leu Thr Glu Cys Ala Ala Ser Gly
    530                 535                 540
Asp Gly Asn Ile Leu Ala Leu Ala Val Asp Ala Ser Arg Ala Arg Cys
545                 550                 555                 560
Thr Val Gly Glu Ile Thr Asp Ala Leu Lys Lys Val Phe Gly Glu His
                565                 570                 575
Lys Ala Asn Asp Arg Met Val Ser Gly Ala Tyr Arg Gln Glu Phe Gly
            580                 585                 590
Glu Ser Lys Glu Ile Thr Ser Ala Ile Lys Arg Val His Lys Phe Met
        595                 600                 605
Glu Arg Glu Gly Arg Arg Pro Arg Leu Leu Val Ala Lys Met Gly Gln
    610                 615                 620
Asp Gly His Asp Arg Gly Ala Lys Val Ile Ala Thr Gly Phe Ala Asp
625                 630                 635                 640
Leu Gly Phe Asp Val Asp Ile Gly Pro Leu Phe Gln Thr Pro Arg Glu
                645                 650                 655
Val Ala Gln Gln Ala Val Asp Ala Asp Val His Ala Val Gly Val Ser
            660                 665                 670
Thr Leu Ala Ala Gly His Lys Thr Leu Val Pro Glu Leu Ile Lys Glu
        675                 680                 685
Leu Asn Ser Leu Gly Arg Pro Asp Ile Leu Val Met Cys Gly Gly Val
    690                 695                 700
Ile Pro Pro Gln Asp Tyr Glu Phe Leu Phe Glu Val Gly Val Ser Asn
705                 710                 715                 720
Val Phe Gly Pro Gly Thr Arg Ile Pro Lys Ala Ala Val Gln Val Leu
                725                 730                 735
Asp Asp Ile Glu Lys Cys Leu Glu Lys Lys Gln Gln Ser Val
            740                 745                 750
```

<210> 255
<211> 806
<212> DNA
<213> Homo sapiens

<400> 255

```
agcctgggtg acagagtaag actgtcgcca aaaaagagga aaaaagttat ccagtgcagt      60
ttctacagag ataaaagaag taatagttct ggctgggtgt ggtggcttat gcctgtaatc     120
ccaacacttt gggaggccaa ggcaggtgga tcacatgagg tcaggagttc gagaccagcc     180
tggccaacat ggcaaaactg tctctactaa aaatataaaa attaggtatg gtggcacgtg     240
cctgtactta cagctacttg ggaggctgag gcatgagatg acaatctctt gaacccagga     300
ggcggaggtt gcagtgagct gagattgcac cactgcactc cagcttgggt gatggagtga     360
gactcaaata aaaaaggtac tagttctgca tttcagagtt ggcttgttga accaggctat     420
atgcttccaa gatttaaatg tttttctgta ttatactctc aattgtgttt taaaaaaatc     480
tcttacagaa atctctacct caggcactaa gtgttatgac atgggtagca tattgatatt     540
```

gaaaacttag ctaggacttc cagcctttta agataattta aatgtaaaat taaatggtta 600
accagcaatc taatgtcatg tggtgtgcag tttggatatt gcatgaacag ctaaggaatc 660
acctgttcta gtgccaaaga tcactcattg ctaattttgt tctgtacagc ttatgtaata 720
ttttcatggt ggagacggac tctgtgtgct cagggccttg tctctaggaa gattttgtca 780
attccaaata cagttttgaa gattca 806

<210> 256
<211> 9192
<212> DNA
<213> Homo sapiens

<400> 256
atgcggagta ggcttccccc agcgcttgcc gccctgggcg cggccctact cctgtcttcc 60
attgaggcag aagttgaccc accttcagac ttgaatttta aaattataga tgaaaatact 120
gttcatatgt catgggcaga accagttgat ccaattgtgg gttacagaat aacggtggac 180
cctacaacgg atgggcctac taaagaattt acccttttcag ctagtaccac tgaaacttta 240
ttgtcagaac ttgtacctga aacagagtat gtggtgacaa taacttcata tgatgaagta 300
gaagaaagtg taccagttat aggacaacta acaattcaaa caggtagttc gacaaagcca 360
gtggagaaga aacctggaaa aaccgagata caaaaatgct ctgtcagtgc ctggactgat 420
ttggttttcc tcgtggatgg ctcttggagt gtgggaagaa ataatttcaa gtacatttta 480
gacttcattg ctgctcttgt gtctgctttt gacattgggg aagagaagac aagagttgga 540
gttgttcaat acagctctga caccaggact gaatttaact taaatcagta ctaccaaagg 600
gatgaacttc ttgctgcaat aaaaaaaatt ccatataaag gtggcaacac aatgacaggg 660
gatgccattg attatttagt taaaaatact ttcacggaat ctgctggggc aagagttggc 720
tttcctaaag tggcaattat tattacggat ggaaaatccc aggatgaagt ggaaattcca 780
gcaagagagc ttcgtaatgt tggagttgaa gttttctcct tgggcattaa agctgcagat 840
gcaaaagaac tcaaacaaat tgcctccaca ccttcactga accatgtttt caatgtggcc 900
aactttgatg caattgtgga tattcagaat gagatcatct cccaggtgtg ctcaggagtt 960
gatgagcagc ttggtgaatt ggttagtgga gaagaagttg ttgagcctcc ttcaaatttg 1020
attgccatgg aagtctcttc aaaatatgtt aagctaaatt ggaatccatc tcctagtcca 1080
gtgactggct acaaagtcat cctcacacca atgactgcag gaagccgaca gcacgctctg 1140
agtgtggggc ctcagacaac cacgctcagt gttcgcgacc tctcagcaga cacggagtac 1200
cagatcagtg tttccgccat gaagggaatg acatccagtg aacccatttc aataatggag 1260
aagactcagc caatgaaagt tcaagtggaa tgttcacgtg gtgtggatat aaagccgat 1320
attgtgtttt tggttgatgg ctcctatagc attgggattg caaactttgt taaagttaga 1380
gcctttttgg aagttcttgt aaaaagtttt gaaatttcac caaatagggt ccagattagt 1440
cttgtgcaat acagccggga tcctcatact gagttcactt tgaaaaaatt caccaaagtt 1500
gaagatataa ttgaagcaat aaacaccttc ccttacagag gaggatctac aaatactggc 1560
aaagcaatga cttatgtcag agagaaaata tttgtgccta gcaagggatc aagaagcaat 1620
gtgccaaagg tcatgattct tatcacggat gggaaatcat cagatgcttt cagagatcct 1680
gcgataaaac tgaggaattc agatgttgaa atctttgcag ttggtgtgaa ggatgccgtt 1740
cgctcagaat tggaagctat tgcctctcct cctgcagaga cccatgtgtt cacagtggaa 1800
gattttgatg cttttcagag gatatctttt gaactcacac agtctatctg tcttagaatt 1860
gagcaagaat tggcagctat aaagaagaaa gcttacgtcc ctccaaagga tcttagtttt 1920
tcagaagtga cttcttatgg tttcaaaacc aactggtctc cagctggaga aaatgttttt 1980
tcatatcaca tcacctacaa ggaagcggct ggggatgatg aggtcactgt ggtggagcca 2040
gcatcgagca ccagtgttgt tctcagcagc ctgaagccag agaccttgta tttggtcaat 2100
gtgactgcgg agtatgagga tggcttcagc attcccttag ctggagagga gaccaccgaa 2160
gaagtaaaag gagcacctcg aaacctaaag gtgacagatg agactacaga tagtttcaaa 2220
attacttgga ctcaagctcc agggagagtt ttaagatgtc gaattatata tagaccagtt 2280
gctggtggag agagcagaga agttaccacc ccacccaatc agaggaggag aacactggag 2340
aacttgattc cagacacgaa atatgaagta tctgtaattc ctgaatactt ctcaggacct 2400
ggtactccat taactggaaa tgcagccact gaagaagtta gagggaatcc aagagactta 2460
agagtttctg accctacgac gtctactatg aaattatctt ggagtggggc accaggaaaa 2520
gtgaaacagt atctcgtcac atataccccca gtggcagggg gtgaaactca agaggtcact 2580
gtgaggggag atacaaccaa tacggtgctg cagggattga aggaagggac acaatacgcc 2640
ttatctgtga cagcactgta tgcgtctggg gctggcgacg ccctctttgg tgaaggaaca 2700
acacttgaag aacgtggttc tcctcaagat ttagttacta aagacatcac tgacacatca 2760
attggggctt attggacatc tgctccagga atggttcgcg gttacagggt ctcatggaaa 2820
tcactttatg atgatgttga cactggagag aaaaatctgc ctgaagatgc aattcatacg 2880
atgatagaaa atctgcagcc agagaccaaa tacagaattt cagtatttgc cacttacagc 2940

agtggagaag gagaaccttt gactggagat gccacaactg aattatctca agattccaaa 3000
accctgaaag tagatgaaga aacagaaaac acaatgagag ttacatggaa accagcacca 3060
gggaaagtcg tcaactaccg tgttgtctat cgccctcatg ggagagggaa gcaaatggtt 3120
gctaaggtgc cccccacagt cacttcgaca gtgttaaagc gacttcagcc acagaccaca 3180
tatgacatca cagttcttcc tatttacaag atgggagaag gaaagcttag gcaaggatca 3240
ggaacaacag cttctcggtt taagtctcct agaaacctca aaacatctga cccaaccatg 3300
tcaagcttcc gagtgacttg ggagcctgcc cctggggaag tgaagggtta taaagtcaca 3360
ttccacccta cgggggatga cagaagactg gggagttag tggttggacc ctatgacaac 3420
acagttgttt tggaggaact tagggctggt accacctata aagtaaatgt ttttggaatg 3480
tttgatggag gagaaagctc accacttgtt ggacaagaaa tgacaaccct ttccgacaca 3540
actgttatgc caattttatc ttctgggatg gagtgtctca ccagagctga ggcagacatt 3600
gtgttgctgg tggatggatc atggagcatc ggccgggcaa attttagaac cgtgaggagt 3660
ttcatttctc gtattgtgga agtctttgac attggcccca aaagagtaca aattgctctt 3720
gctcagtata gtggggatcc cagaacagag tggcagttaa atgcacacag agacaagaag 3780
agcttgttgc aagctgtggc aaacttgccg tacaaaggag gcaatactct cacaggcatg 3840
gctttgaatt tcattcgcca acagaacttc aggacccaag ctggcatgag acctcgagct 3900
cgaaaaattg gtgtgctcat tactgatgga aaatcacaag acgatgttga agcaccttca 3960
aagaaactca aggatgaggg agtggagctg tttgctattg gtattaaaaa tgctgatgaa 4020
gtcgaattaa agatgattgc aactgatcct gatgataccc atgactacaa tgtggcagat 4080
tttgagtcac tctccaggat agtggatgat ctcaccatta atttgtgtaa cagtgtcaaa 4140
ggtccaggtg atttggaagc accttctaac ttagttattt ctgagcgaac ccatcgttct 4200
tttagagtga gctggacacc accttctgac agtgtggatc gatataaggt ggaatactat 4260
ccagtttctg gagggaaacg tcaagaattt tatgtgagtc gaatggaaac tagcacagtg 4320
ctgaaagatc tgaaacctga aactgaatat gttgtcaatg tgtattctgt ggtagaagat 4380
gaatatagtg agcctctgaa ggggacagaa aaaaccttgc cagtgcctgt agtcagcctg 4440
aatatttatg atgttggccc taccaccatg catgtgcagt ggcagcctgt gggaggagct 4500
actggctaca tcttgtcata caaacctgtt aaggacacag agccaacaag acccaaagag 4560
gtgcgtttgg ggccaacagt gaatgacatg cagctgactg accttgttcc caacacggag 4620
tatgcagtca cagtccaggc tgtcctgcac gacctcacta gtgaacctgt cactgttcgg 4680
gaagtcacct tgcctttacc cagacctcag gatctgaaac tcagagatgt gactcacagc 4740
actatgaatg tcttttggga acctgtgcct ggaaaagtgc gtaaatatat tgttcgatac 4800
aaaacaccag aagaggatgt caaagaggta gaggtggaca gatcagagac cagcacttcc 4860
ctcaaagacc tcttctcaca gaccttgtac acagtcagcg tttctgcagt acatgacgag 4920
ggggagtctc ctccagtgac tgctcaagaa actacccgac ccgtgccagc cccaacaaac 4980
ttaaagatta ctgaagtaac atcagagggt ttcagaggga cttgggatca tggagcttca 5040
gatgtgtctc tctacagaat aacttgggga ccttttggaa gctcagataa gatggagacc 5100
atcttaaatg gagatgaaaa cactttggtg ttcgaaaacc tgaaccccaa caccatctat 5160
gaagtttcca ttactgccat ctatgctgat gagtcagaaa gtgatgacct gattggcagt 5220
gagcgcactc tgcctatctt aacaacacaa gctcccaaaa gtgggccacg aaaccttcaa 5280
gtgtacaatg caacatctaa cagcctgact gttaagtggg atcctgctag tggtcgtgtg 5340
cagaaatata ggatcactta tcagcccttcc acaggggaag gcaatgagca aacgaccaca 5400
ataggaggac ggcagaacag tgtggtcctg cagaaactga agccagacac tccttacact 5460
atcaccgtat cctctctgta tcctgatggt gaaggaggtc ggatgacggg aagaggcaag 5520
accaaacctc taaacactgt aaggaacctg agagtgtatg acccttctac cagcactctg 5580
aatgtccgct gggaccatgc agagggaaat cctcgtcagt acaagctctt ctatgcacca 5640
gcagcaggtg gtccagagga actggtacca atccccggga ataccaatta tgccattctt 5700
aggaatctgc agccagatac ctcatacact gtgactgtag ttcccgttta tactgaaggt 5760
gatgggggac gcacatcaga tactggaagg acattgatga gaggactggc aagaaatgtc 5820
caagtataca atcctacacc taacaggctc ggtgttcgct gggaccctgc accaggacct 5880
gtgctgcaat atcgcgttgt gtattctcct gtggatggca caagaccctc agaatctata 5940
gtagtgccag gaaacacgcg catggtgcat ctggagcggc tgattccgga cacactctat 6000
tccgtgaacc ttgtggctct gtactcggat ggagagggaa atcccagccc tgcccagggc 6060
cgaacgctac cacgcagtgg accaaggaac ctgagagtct ttggtgaaac aaccaatagc 6120
ctctcggtag cctgggatca tgctgatggg ccagttcagc agtacaggat catctattct 6180
cccactgttg gtgatccaat tgatgaatat accacagtcc caggcagaag aaacaatgta 6240
atactgcagc ccctgcaacc tgacactcca tataaaatta ctgttattgc tgtttatgaa 6300
gatggagatg gtggccatct aacaggaaat ggaagaactg tgggactcct tcctcctcag 6360
aacatacaca tctctgacga atggtataca agattcaggg tgtcctggga tccttcacct 6420
tctccagttc ttggatataa aatagtatat aagccagtgg gttccaatga gcccatggaa 6480
gcctttgttg gagaaatgac atcatatacc ttacacaatc tcaatcccag caccacctac 6540
gatgtgaatg tttatgctca atatgattct ggactcagtg tcccccttgac agatcaaggc 6600

actacattat atttaaatgt aacagatctg aaaacttacc agattgggtg ggatacattc 6660
tgtgtcaaat ggtcacctca ccgggcagcc acctcctaca ggctaaaact aagccctgca 6720
gatggaacca ggggacaaga aattacagtg cgtggatcag aaaccagtca ctgcttcact 6780
ggcctttcac cagacactga ttatggtgtc actgttttg tgcagacacc aaatctcgag 6840
ggaccaggag tctctgttaa agaacatacc actgtgaaac caacagaagc ccctacagag 6900
ccacccacac ctcctccccc tcccaccatt ccaccagccc gggatgtatg caaaggggcc 6960
aaggcagata ttgtgttctt gactgatgcc tcctggagca ttggggacga taattttaac 7020
aaagttgtaa aattcatctt caatactgtg ggaggctttg atgaaatcag tcctgctggg 7080
attcaggttt catttgtgca atacagcgat gaggtcaagt ctgagttcaa gctgaacacg 7140
tacaatgaca aggccctagc ccttggggcc ctccagaata ttaggtacag aggaggaaac 7200
acaagaacag gcaaggccct cacgtttatc aaggagaaag tcttgacttg ggagagcggc 7260
atgaggaaga atgtccctaa ggtgttggtt gtggtcacgg acggtcggtc ccaggatgag 7320
gtcaagaagg cggctttggt catccagcag tcagggttca gtgtctttgt agttggtgtg 7380
gctgatgtcg actacaatga gcttgccaac attgccagca aaccaagtga acggcacgtg 7440
ttcattgtgg acgactttga atcttttgag aagatcgaag acaatcttat tacatttgtt 7500
tgtgaaactg ccacttcaag ttgtcctctc atttatttgg atggctacac ctcaccaggt 7560
tttaaaatgc ttgaagcata caacctgaca gaaaagaatt ttgcttctgt acaaggagta 7620
tctttggagt cagggtcttt ccccagctac tcagcataca ggattcagaa gaatgcgttt 7680
gtgaatcagc ctacagcaga cctacaccca aatggactcc ctccttcata cacgattata 7740
ttattattca gacttctccc agaaactccc agtgacccctt ttgcaatttg gcaaatcaca 7800
gacagagact acaaaccaca agttggagtg attgcagatc cttctagcaa gacgttatca 7860
ttctttaaca aggatacaag aggcgaggtg caaactgtta catttgacac agaagaagta 7920
aagacattat tttatggaag ttttcacaag gttcatattg tagtgacctc aaaaagtgtt 7980
aagatttaca ttgactgcta tgaaattata gaaaaagaca tcaaggaagc tggaaatata 8040
acaactgatg gttatgaaat tcttggaaaa ctccttaaag gggaaaggaa atcagccgca 8100
ttccaaatcc agagttttga cattgtctgc agtccagtgt ggaccagtag agacagatgc 8160
tgtgatattc cctctaggag agatgaggga aaatgccctg cttttccaaa ttcttgcaca 8220
tgtacacagg acagcgttgg acctccagga cctccaggcc ctgcaggagg acctggtgct 8280
aaaggtccca gaggtgaaag aggtatcagt ggggcaattg ggccccctgg tcctcgtgga 8340
gacataggtc ctccaggccc ccagggtcct ccaggccctc agggacccaa tggactctct 8400
attccgggag agcaaggtcg ccaagggatg aaaggtgatg ctggagagcc aggacttcca 8460
ggccgaacag gaaccccagg attacctggc ccaccaggac caatgggacc tccaggagac 8520
agaggcttca ctggaaaaga cagtgcaatg ggacccaggg gcccaccagg gcggccggga 8580
agcccaggct ccccaggagt cacaggacca agtgggaagc caggaaaacc tggagatcat 8640
ggcagaccag gtccatctgg gttgaaagga gaaaaaggtg atagggggaga cattgcttcc 8700
cagaacatga tgcgagcagt tgcaagacaa gtctgtgaac aattgataag tggtcagatg 8760
aacagattca atcagatgct gaatcagatt ccaaatgatt accagtccag tcgcaaccag 8820
ccaggcccgc cgggtccacc gggacctcct ggtagcgcag gagccagagg agaacctggg 8880
cctgggggc ggccaggctt cccgggcaca ccagggatgc agggaccccc tggggaacga 8940
ggtttgccag gagagaaagg tgaaaggggt actggatctt caggacctcg ggggctgcct 9000
gggcccccag gtccacaagg agaatccaga acaggtccac cagggtccac aggttcaaga 9060
ggtccccctg gcccccctgg ccgtcctgga aactcaggta tccagggccc cccaggtcct 9120
cctggatact gtgattcttc tcagtgtgcc agcatcccat acaacgggca aagctatcca 9180
ggttccggct aa 9192

<210> 257
<211> 3063
<212> PRT
<213> Homo sapiens

<400> 257
Met Arg Ser Arg Leu Pro Pro Ala Leu Ala Ala Leu Gly Ala Ala Leu
1 5 10 15
Leu Leu Ser Ser Ile Glu Ala Glu Val Asp Pro Pro Ser Asp Leu Asn
20 25 30
Phe Lys Ile Ile Asp Glu Asn Thr Val His Met Ser Trp Ala Glu Pro
35 40 45
Val Asp Pro Ile Val Gly Tyr Arg Ile Thr Val Asp Pro Thr Thr Asp
50 55 60

Gly Pro Thr Lys Glu Phe Thr Leu Ser Ala Ser Thr Thr Glu Thr Leu
65 70 75 80
Leu Ser Glu Leu Val Pro Glu Thr Glu Tyr Val Val Thr Ile Thr Ser
85 90 95
Tyr Asp Glu Val Glu Glu Ser Val Pro Val Ile Gly Gln Leu Thr Ile
100 105 110
Gln Thr Gly Ser Ser Thr Lys Pro Val Glu Lys Lys Pro Gly Lys Thr
115 120 125
Glu Ile Gln Lys Cys Ser Val Ser Ala Trp Thr Asp Leu Val Phe Leu
130 135 140
Val Asp Gly Ser Trp Ser Val Gly Arg Asn Asn Phe Lys Tyr Ile Leu
145 150 155 160
Asp Phe Ile Ala Ala Leu Val Ser Ala Phe Asp Ile Gly Glu Glu Lys
165 170 175
Thr Arg Val Gly Val Val Gln Tyr Ser Ser Asp Thr Arg Thr Glu Phe
180 185 190
Asn Leu Asn Gln Tyr Tyr Gln Arg Asp Glu Leu Leu Ala Ala Ile Lys
195 200 205
Lys Ile Pro Tyr Lys Gly Gly Asn Thr Met Thr Gly Asp Ala Ile Asp
210 215 220
Tyr Leu Val Lys Asn Thr Phe Thr Glu Ser Ala Gly Ala Arg Val Gly
225 230 235 240
Phe Pro Lys Val Ala Ile Ile Ile Thr Asp Gly Lys Ser Gln Asp Glu
245 250 255
Val Glu Ile Pro Ala Arg Glu Leu Arg Asn Val Gly Val Glu Val Phe
260 265 270
Ser Leu Gly Ile Lys Ala Ala Asp Ala Lys Glu Leu Lys Gln Ile Ala
275 280 285
Ser Thr Pro Ser Leu Asn His Val Phe Asn Val Ala Asn Phe Asp Ala
290 295 300
Ile Val Asp Ile Gln Asn Glu Ile Ile Ser Gln Val Cys Ser Gly Val
305 310 315 320
Asp Glu Gln Leu Gly Glu Leu Val Ser Gly Glu Glu Val Val Glu Pro
325 330 335
Pro Ser Asn Leu Ile Ala Met Glu Val Ser Ser Lys Tyr Val Lys Leu
340 345 350
Asn Trp Asn Pro Ser Pro Ser Pro Val Thr Gly Tyr Lys Val Ile Leu
355 360 365
Thr Pro Met Thr Ala Gly Ser Arg Gln His Ala Leu Ser Val Gly Pro
370 375 380
Gln Thr Thr Thr Leu Ser Val Arg Asp Leu Ser Ala Asp Thr Glu Tyr
385 390 395 400
Gln Ile Ser Val Ser Ala Met Lys Gly Met Thr Ser Ser Glu Pro Ile
405 410 415
Ser Ile Met Glu Lys Thr Gln Pro Met Lys Val Gln Val Glu Cys Ser
420 425 430
Arg Gly Val Asp Ile Lys Ala Asp Ile Val Phe Leu Val Asp Gly Ser
435 440 445
Tyr Ser Ile Gly Ile Ala Asn Phe Val Lys Val Arg Ala Phe Leu Glu
450 455 460
Val Leu Val Lys Ser Phe Glu Ile Ser Pro Asn Arg Val Gln Ile Ser
465 470 475 480
Leu Val Gln Tyr Ser Arg Asp Pro His Thr Glu Phe Thr Leu Lys Lys
485 490 495
Phe Thr Lys Val Glu Asp Ile Ile Glu Ala Ile Asn Thr Phe Pro Tyr
500 505 510
Arg Gly Gly Ser Thr Asn Thr Gly Lys Ala Met Thr Tyr Val Arg Glu
515 520 525
Lys Ile Phe Val Pro Ser Lys Gly Ser Arg Ser Asn Val Pro Lys Val
530 535 540
Met Ile Leu Ile Thr Asp Gly Lys Ser Ser Asp Ala Phe Arg Asp Pro

```
545                 550                 555                 560
Ala Ile Lys Leu Arg Asn Ser Asp Val Glu Ile Phe Ala Val Gly Val
                565                 570                 575
Lys Asp Ala Val Arg Ser Glu Leu Glu Ala Ile Ala Ser Pro Pro Ala
            580                 585                 590
Glu Thr His Val Phe Thr Val Glu Asp Phe Asp Ala Phe Gln Arg Ile
        595                 600                 605
Ser Phe Glu Leu Thr Gln Ser Ile Cys Leu Arg Ile Glu Gln Glu Leu
    610                 615                 620
Ala Ala Ile Lys Lys Lys Ala Tyr Val Pro Pro Lys Asp Leu Ser Phe
625                 630                 635                 640
Ser Glu Val Thr Ser Tyr Gly Phe Lys Thr Asn Trp Ser Pro Ala Gly
                645                 650                 655
Glu Asn Val Phe Ser Tyr His Ile Thr Tyr Lys Glu Ala Ala Gly Asp
            660                 665                 670
Asp Glu Val Thr Val Val Glu Pro Ala Ser Ser Thr Ser Val Val Leu
        675                 680                 685
Ser Ser Leu Lys Pro Glu Thr Leu Tyr Leu Val Asn Val Thr Ala Glu
    690                 695                 700
Tyr Glu Asp Gly Phe Ser Ile Pro Leu Ala Gly Glu Glu Thr Thr Glu
705                 710                 715                 720
Glu Val Lys Gly Ala Pro Arg Asn Leu Lys Val Thr Asp Glu Thr Thr
                725                 730                 735
Asp Ser Phe Lys Ile Thr Trp Thr Gln Ala Pro Gly Arg Val Leu Arg
            740                 745                 750
Cys Arg Ile Ile Tyr Arg Pro Val Ala Gly Gly Glu Ser Arg Glu Val
        755                 760                 765
Thr Thr Pro Pro Asn Gln Arg Arg Arg Thr Leu Glu Asn Leu Ile Pro
    770                 775                 780
Asp Thr Lys Tyr Glu Val Ser Val Ile Pro Glu Tyr Phe Ser Gly Pro
785                 790                 795                 800
Gly Thr Pro Leu Thr Gly Asn Ala Ala Thr Glu Glu Val Arg Gly Asn
                805                 810                 815
Pro Arg Asp Leu Arg Val Ser Asp Pro Thr Thr Ser Thr Met Lys Leu
            820                 825                 830
Ser Trp Ser Gly Ala Pro Gly Lys Val Lys Gln Tyr Leu Val Thr Tyr
        835                 840                 845
Thr Pro Val Ala Gly Gly Glu Thr Gln Glu Val Thr Val Arg Gly Asp
    850                 855                 860
Thr Thr Asn Thr Val Leu Gln Gly Leu Lys Glu Gly Thr Gln Tyr Ala
865                 870                 875                 880
Leu Ser Val Thr Ala Leu Tyr Ala Ser Gly Ala Gly Asp Ala Leu Phe
                885                 890                 895
Gly Glu Gly Thr Thr Leu Glu Glu Arg Gly Ser Pro Gln Asp Leu Val
            900                 905                 910
Thr Lys Asp Ile Thr Asp Thr Ser Ile Gly Ala Tyr Trp Thr Ser Ala
        915                 920                 925
Pro Gly Met Val Arg Gly Tyr Arg Val Ser Trp Lys Ser Leu Tyr Asp
    930                 935                 940
Asp Val Asp Thr Gly Glu Lys Asn Leu Pro Glu Asp Ala Ile His Thr
945                 950                 955                 960
Met Ile Glu Asn Leu Gln Pro Glu Thr Lys Tyr Arg Ile Ser Val Phe
                965                 970                 975
Ala Thr Tyr Ser Ser Gly Glu Gly Glu Pro Leu Thr Gly Asp Ala Thr
            980                 985                 990
Thr Glu Leu Ser Gln Asp Ser Lys Thr Leu Lys Val Asp Glu Glu Thr
        995                 1000                1005
Glu Asn Thr Met Arg Val Thr Trp Lys Pro Ala Pro Gly Lys Val Val
    1010                1015                1020
Asn Tyr Arg Val Val Tyr Arg Pro His Gly Arg Gly Lys Gln Met Val
1025                1030                1035                1040
```

Ala Lys Val Pro Pro Thr Val Thr Ser Thr Val Leu Lys Arg Leu Gln
1045 1050 1055
Pro Gln Thr Thr Tyr Asp Ile Thr Val Leu Pro Ile Tyr Lys Met Gly
1060 1065 1070
Glu Gly Lys Leu Arg Gln Gly Ser Gly Thr Thr Ala Ser Arg Phe Lys
1075 1080 1085
Ser Pro Arg Asn Leu Lys Thr Ser Asp Pro Thr Met Ser Ser Phe Arg
1090 1095 1100
Val Thr Trp Glu Pro Ala Pro Gly Glu Val Lys Gly Tyr Lys Val Thr
1105 1110 1115 1120
Phe His Pro Thr Gly Asp Asp Arg Arg Leu Gly Glu Leu Val Val Gly
1125 1130 1135
Pro Tyr Asp Asn Thr Val Val Leu Glu Glu Leu Arg Ala Gly Thr Thr
1140 1145 1150
Tyr Lys Val Asn Val Phe Gly Met Phe Asp Gly Gly Glu Ser Ser Pro
1155 1160 1165
Leu Val Gly Gln Glu Met Thr Thr Leu Ser Asp Thr Thr Val Met Pro
1170 1175 1180
Ile Leu Ser Ser Gly Met Glu Cys Leu Thr Arg Ala Glu Ala Asp Ile
1185 1190 1195 1200
Val Leu Leu Val Asp Gly Ser Trp Ser Ile Gly Arg Ala Asn Phe Arg
1205 1210 1215
Thr Val Arg Ser Phe Ile Ser Arg Ile Val Glu Val Phe Asp Ile Gly
1220 1225 1230
Pro Lys Arg Val Gln Ile Ala Leu Ala Gln Tyr Ser Gly Asp Pro Arg
1235 1240 1245
Thr Glu Trp Gln Leu Asn Ala His Arg Asp Lys Lys Ser Leu Leu Gln
1250 1255 1260
Ala Val Ala Asn Leu Pro Tyr Lys Gly Gly Asn Thr Leu Thr Gly Met
1265 1270 1275 1280
Ala Leu Asn Phe Ile Arg Gln Gln Asn Phe Arg Thr Gln Ala Gly Met
1285 1290 1295
Arg Pro Arg Ala Arg Lys Ile Gly Val Leu Ile Thr Asp Gly Lys Ser
1300 1305 1310
Gln Asp Asp Val Glu Ala Pro Ser Lys Lys Leu Lys Asp Glu Gly Val
1315 1320 1325
Glu Leu Phe Ala Ile Gly Ile Lys Asn Ala Asp Glu Val Glu Leu Lys
1330 1335 1340
Met Ile Ala Thr Asp Pro Asp Asp Thr His Asp Tyr Asn Val Ala Asp
1345 1350 1355 1360
Phe Glu Ser Leu Ser Arg Ile Val Asp Asp Leu Thr Ile Asn Leu Cys
1365 1370 1375
Asn Ser Val Lys Gly Pro Gly Asp Leu Glu Ala Pro Ser Asn Leu Val
1380 1385 1390
Ile Ser Glu Arg Thr His Arg Ser Phe Arg Val Ser Trp Thr Pro Pro
1395 1400 1405
Ser Asp Ser Val Asp Arg Tyr Lys Val Glu Tyr Tyr Pro Val Ser Gly
1410 1415 1420
Gly Lys Arg Gln Glu Phe Tyr Val Ser Arg Met Glu Thr Ser Thr Val
1425 1430 1435 1440
Leu Lys Asp Leu Lys Pro Glu Thr Glu Tyr Val Val Asn Val Tyr Ser
1445 1450 1455
Val Val Glu Asp Glu Tyr Ser Glu Pro Leu Lys Gly Thr Glu Lys Thr
1460 1465 1470
Leu Pro Val Pro Val Val Ser Leu Asn Ile Tyr Asp Val Gly Pro Thr
1475 1480 1485
Thr Met His Val Gln Trp Gln Pro Val Gly Gly Ala Thr Gly Tyr Ile
1490 1495 1500
Leu Ser Tyr Lys Pro Val Lys Asp Thr Glu Pro Thr Arg Pro Lys Glu
1505 1510 1515 1520
Val Arg Leu Gly Pro Thr Val Asn Asp Met Gln Leu Thr Asp Leu Val

1525 1530 1535
Pro Asn Thr Glu Tyr Ala Val Thr Val Gln Ala Val Leu His Asp Leu
1540 1545 1550
Thr Ser Glu Pro Val Thr Val Arg Glu Val Thr Leu Pro Leu Pro Arg
1555 1560 1565
Pro Gln Asp Leu Lys Leu Arg Asp Val Thr His Ser Thr Met Asn Val
1570 1575 1580
Phe Trp Glu Pro Val Pro Gly Lys Val Arg Lys Tyr Ile Val Arg Tyr
1585 1590 1595 1600
Lys Thr Pro Glu Glu Asp Val Lys Glu Val Glu Val Asp Arg Ser Glu
1605 1610 1615
Thr Ser Thr Ser Leu Lys Asp Leu Phe Ser Gln Thr Leu Tyr Thr Val
1620 1625 1630
Ser Val Ser Ala Val His Asp Glu Gly Glu Ser Pro Pro Val Thr Ala
1635 1640 1645
Gln Glu Thr Thr Arg Pro Val Pro Ala Pro Thr Asn Leu Lys Ile Thr
1650 1655 1660
Glu Val Thr Ser Glu Gly Phe Arg Gly Thr Trp Asp His Gly Ala Ser
1665 1670 1675 1680
Asp Val Ser Leu Tyr Arg Ile Thr Trp Gly Pro Phe Gly Ser Ser Asp
1685 1690 1695
Lys Met Glu Thr Ile Leu Asn Gly Asp Glu Asn Thr Leu Val Phe Glu
1700 1705 1710
Asn Leu Asn Pro Asn Thr Ile Tyr Glu Val Ser Ile Thr Ala Ile Tyr
1715 1720 1725
Ala Asp Glu Ser Glu Ser Asp Asp Leu Ile Gly Ser Glu Arg Thr Leu
1730 1735 1740
Pro Ile Leu Thr Thr Gln Ala Pro Lys Ser Gly Pro Arg Asn Leu Gln
1745 1750 1755 1760
Val Tyr Asn Ala Thr Ser Asn Ser Leu Thr Val Lys Trp Asp Pro Ala
1765 1770 1775
Ser Gly Arg Val Gln Lys Tyr Arg Ile Thr Tyr Gln Pro Ser Thr Gly
1780 1785 1790
Glu Gly Asn Glu Gln Thr Thr Thr Ile Gly Gly Arg Gln Asn Ser Val
1795 1800 1805
Val Leu Gln Lys Leu Lys Pro Asp Thr Pro Tyr Thr Ile Thr Val Ser
1810 1815 1820
Ser Leu Tyr Pro Asp Gly Glu Gly Gly Arg Met Thr Gly Arg Gly Lys
1825 1830 1835 1840
Thr Lys Pro Leu Asn Thr Val Arg Asn Leu Arg Val Tyr Asp Pro Ser
1845 1850 1855
Thr Ser Thr Leu Asn Val Arg Trp Asp His Ala Glu Gly Asn Pro Arg
1860 1865 1870
Gln Tyr Lys Leu Phe Tyr Ala Pro Ala Ala Gly Gly Pro Glu Glu Leu
1875 1880 1885
Val Pro Ile Pro Gly Asn Thr Asn Tyr Ala Ile Leu Arg Asn Leu Gln
1890 1895 1900
Pro Asp Thr Ser Tyr Thr Val Thr Val Val Pro Val Tyr Thr Glu Gly
1905 1910 1915 1920
Asp Gly Gly Arg Thr Ser Asp Thr Gly Arg Thr Leu Met Arg Gly Leu
1925 1930 1935
Ala Arg Asn Val Gln Val Tyr Asn Pro Thr Pro Asn Arg Leu Gly Val
1940 1945 1950
Arg Trp Asp Pro Ala Pro Gly Pro Val Leu Gln Tyr Arg Val Val Tyr
1955 1960 1965
Ser Pro Val Asp Gly Thr Arg Pro Ser Glu Ser Ile Val Val Pro Gly
1970 1975 1980
Asn Thr Arg Met Val His Leu Glu Arg Leu Ile Pro Asp Thr Leu Tyr
1985 1990 1995 2000
Ser Val Asn Leu Val Ala Leu Tyr Ser Asp Gly Glu Gly Asn Pro Ser
2005 2010 2015

Pro Ala Gln Gly Arg Thr Leu Pro Arg Ser Gly Pro Arg Asn Leu Arg
2020 2025 2030
Val Phe Gly Glu Thr Thr Asn Ser Leu Ser Val Ala Trp Asp His Ala
2035 2040 2045
Asp Gly Pro Val Gln Gln Tyr Arg Ile Ile Tyr Ser Pro Thr Val Gly
2050 2055 2060
Asp Pro Ile Asp Glu Tyr Thr Thr Val Pro Gly Arg Arg Asn Asn Val
2065 2070 2075 2080
Ile Leu Gln Pro Leu Gln Pro Asp Thr Pro Tyr Lys Ile Thr Val Ile
2085 2090 2095
Ala Val Tyr Glu Asp Gly Asp Gly Gly His Leu Thr Gly Asn Gly Arg
2100 2105 2110
Thr Val Gly Leu Leu Pro Pro Gln Asn Ile His Ile Ser Asp Glu Trp
2115 2120 2125
Tyr Thr Arg Phe Arg Val Ser Trp Asp Pro Ser Pro Ser Pro Val Leu
2130 2135 2140
Gly Tyr Lys Ile Val Tyr Lys Pro Val Gly Ser Asn Glu Pro Met Glu
2145 2150 2155 2160
Ala Phe Val Gly Glu Met Thr Ser Tyr Thr Leu His Asn Leu Asn Pro
2165 2170 2175
Ser Thr Thr Tyr Asp Val Asn Val Tyr Ala Gln Tyr Asp Ser Gly Leu
2180 2185 2190
Ser Val Pro Leu Thr Asp Gln Gly Thr Thr Leu Tyr Leu Asn Val Thr
2195 2200 2205
Asp Leu Lys Thr Tyr Gln Ile Gly Trp Asp Thr Phe Cys Val Lys Trp
2210 2215 2220
Ser Pro His Arg Ala Ala Thr Ser Tyr Arg Leu Lys Leu Ser Pro Ala
2225 2230 2235 2240
Asp Gly Thr Arg Gly Gln Glu Ile Thr Val Arg Gly Ser Glu Thr Ser
2245 2250 2255
His Cys Phe Thr Gly Leu Ser Pro Asp Thr Asp Tyr Gly Val Thr Val
2260 2265 2270
Phe Val Gln Thr Pro Asn Leu Glu Gly Pro Gly Val Ser Val Lys Glu
2275 2280 2285
His Thr Thr Val Lys Pro Thr Glu Ala Pro Thr Glu Pro Pro Thr Pro
2290 2295 2300
Pro Pro Pro Pro Thr Ile Pro Pro Ala Arg Asp Val Cys Lys Gly Ala
2305 2310 2315 2320
Lys Ala Asp Ile Val Phe Leu Thr Asp Ala Ser Trp Ser Ile Gly Asp
2325 2330 2335
Asp Asn Phe Asn Lys Val Val Lys Phe Ile Phe Asn Thr Val Gly Gly
2340 2345 2350
Phe Asp Glu Ile Ser Pro Ala Gly Ile Gln Val Ser Phe Val Gln Tyr
2355 2360 2365
Ser Asp Glu Val Lys Ser Glu Phe Lys Leu Asn Thr Tyr Asn Asp Lys
2370 2375 2380
Ala Leu Ala Leu Gly Ala Leu Gln Asn Ile Arg Tyr Arg Gly Gly Asn
2385 2390 2395 2400
Thr Arg Thr Gly Lys Ala Leu Thr Phe Ile Lys Glu Lys Val Leu Thr
2405 2410 2415
Trp Glu Ser Gly Met Arg Lys Asn Val Pro Lys Val Leu Val Val Val
2420 2425 2430
Thr Asp Gly Arg Ser Gln Asp Glu Val Lys Lys Ala Ala Leu Val Ile
2435 2440 2445
Gln Gln Ser Gly Phe Ser Val Phe Val Val Gly Val Ala Asp Val Asp
2450 2455 2460
Tyr Asn Glu Leu Ala Asn Ile Ala Ser Lys Pro Ser Glu Arg His Val
2465 2470 2475 2480
Phe Ile Val Asp Asp Phe Glu Ser Phe Glu Lys Ile Glu Asp Asn Leu
2485 2490 2495
Ile Thr Phe Val Cys Glu Thr Ala Thr Ser Ser Cys Pro Leu Ile Tyr

2500 2505 2510
Leu Asp Gly Tyr Thr Ser Pro Gly Phe Lys Met Leu Glu Ala Tyr Asn
2515 2520 2525
Leu Thr Glu Lys Asn Phe Ala Ser Val Gln Gly Val Ser Leu Glu Ser
2530 2535 2540
Gly Ser Phe Pro Ser Tyr Ser Ala Tyr Arg Ile Gln Lys Asn Ala Phe
2545 2550 2555 2560
Val Asn Gln Pro Thr Ala Asp Leu His Pro Asn Gly Leu Pro Pro Ser
2565 2570 2575
Tyr Thr Ile Ile Leu Leu Phe Arg Leu Leu Pro Glu Thr Pro Ser Asp
2580 2585 2590
Pro Phe Ala Ile Trp Gln Ile Thr Asp Arg Asp Tyr Lys Pro Gln Val
2595 2600 2605
Gly Val Ile Ala Asp Pro Ser Ser Lys Thr Leu Ser Phe Phe Asn Lys
2610 2615 2620
Asp Thr Arg Gly Glu Val Gln Thr Val Thr Phe Asp Thr Glu Glu Val
2625 2630 2635 2640
Lys Thr Leu Phe Tyr Gly Ser Phe His Lys Val His Ile Val Val Thr
2645 2650 2655
Ser Lys Ser Val Lys Ile Tyr Ile Asp Cys Tyr Glu Ile Ile Glu Lys
2660 2665 2670
Asp Ile Lys Glu Ala Gly Asn Ile Thr Thr Asp Gly Tyr Glu Ile Leu
2675 2680 2685
Gly Lys Leu Leu Lys Gly Glu Arg Lys Ser Ala Ala Phe Gln Ile Gln
2690 2695 2700
Ser Phe Asp Ile Val Cys Ser Pro Val Trp Thr Ser Arg Asp Arg Cys
2705 2710 2715 2720
Cys Asp Ile Pro Ser Arg Arg Asp Glu Gly Lys Cys Pro Ala Phe Pro
2725 2730 2735
Asn Ser Cys Thr Cys Thr Gln Asp Ser Val Gly Pro Pro Gly Pro Pro
2740 2745 2750
Gly Pro Ala Gly Gly Pro Gly Ala Lys Gly Pro Arg Gly Glu Arg Gly
2755 2760 2765
Ile Ser Gly Ala Ile Gly Pro Pro Gly Pro Arg Gly Asp Ile Gly Pro
2770 2775 2780
Pro Gly Pro Gln Gly Pro Pro Gly Pro Gln Gly Pro Asn Gly Leu Ser
2785 2790 2795 2800
Ile Pro Gly Glu Gln Gly Arg Gln Gly Met Lys Gly Asp Ala Gly Glu
2805 2810 2815
Pro Gly Leu Pro Gly Arg Thr Gly Thr Pro Gly Leu Pro Gly Pro Pro
2820 2825 2830
Gly Pro Met Gly Pro Pro Gly Asp Arg Gly Phe Thr Gly Lys Asp Ser
2835 2840 2845
Ala Met Gly Pro Arg Gly Pro Pro Gly Arg Pro Gly Ser Pro Gly Ser
2850 2855 2860
Pro Gly Val Thr Gly Pro Ser Gly Lys Pro Gly Lys Pro Gly Asp His
2865 2870 2875 2880
Gly Arg Pro Gly Pro Ser Gly Leu Lys Gly Glu Lys Gly Asp Arg Gly
2885 2890 2895
Asp Ile Ala Ser Gln Asn Met Met Arg Ala Val Ala Arg Gln Val Cys
2900 2905 2910
Glu Gln Leu Ile Ser Gly Gln Met Asn Arg Phe Asn Gln Met Leu Asn
2915 2920 2925
Gln Ile Pro Asn Asp Tyr Gln Ser Ser Arg Asn Gln Pro Gly Pro Pro
2930 2935 2940
Gly Pro Pro Gly Pro Pro Gly Ser Ala Gly Ala Arg Gly Glu Pro Gly
2945 2950 2955 2960
Pro Gly Gly Arg Pro Gly Phe Pro Gly Thr Pro Gly Met Gln Gly Pro
2965 2970 2975
Pro Gly Glu Arg Gly Leu Pro Gly Glu Lys Gly Glu Arg Gly Thr Gly
2980 2985 2990

Ser Ser Gly Pro Arg Gly Leu Pro Gly Pro Pro Gly Pro Gln Gly Glu
2995 3000 3005
Ser Arg Thr Gly Pro Pro Gly Ser Thr Gly Ser Arg Gly Pro Pro Gly
3010 3015 3020
Pro Pro Gly Arg Pro Gly Asn Ser Gly Ile Gln Gly Pro Pro Gly Pro
3025 3030 3035 3040
Pro Gly Tyr Cys Asp Ser Ser Gln Cys Ala Ser Ile Pro Tyr Asn Gly
3045 3050 3055
Gln Ser Tyr Pro Gly Ser Gly
3060

<210> 258
<211> 1717
<212> DNA
<213> Homo sapiens

<400> 258
gtggattctt gtccatagtg catctgcttt aagaattaac gaaagcagtg tcaagacagt 60
aaggattcaa accatttgcc aaaaatgagt ctaagtgcat ttactctctt cctggcattg 120
attggtggta ccagtggcca gtactatgat tatgattttc ccctatcaat ttatgggcaa 180
tcatcaccaa actgtgcacc agaatgtaac tgccctgaaa gctacccaag tgccatgtac 240
tgtgatgagc tgaaattgaa aagtgtacca atggtgcctc ctggaatcaa gtatctttac 300
cttaggaata accagattga ccatattgat gaaaaggcct ttgagaatgt aactgatctg 360
cagtggctca ttctagatca caaccttcta gaaaactcca agataaaagg gagagttttc 420
tctaaattga aacaactgaa gaagctgcat ataaaccaca acaacctgac agagtctgtg 480
ggcccacttc ccaaatctct ggaggatctg cagcttactc ataacaagat cacaaagctg 540
ggctcttttg aaggattggt aaacctgacc ttcatccatc tccagcacaa tcggctgaaa 600
gaggatgctg tttcagctgc ttttaaaggt cttaaatcac tcgaatacct tgacttgagc 660
ttcaatcaga tagccagact gccttctggt ctccctgtct ctcttctaac tctctactta 720
gacaacaata agatcagcaa catccctgat gagtatttca agcgttttaa tgcattgcag 780
tatctgcgtt tatctcacaa cgaactggct gatagtggaa tacctggaaa ttctttcaat 840
gtgtcatccc tggttgagct ggatctgtcc tataacaagc ttaaaaacat accaactgtc 900
aatgaaaacc ttgaaaacta ttacctggag gtcaatcaac ttgagaagtt tgacataaag 960
agcttctgca agatcctggg gccattatcc tactccaaga tcaagcattt gcgtttggat 1020
ggcaatcgca tctcagaaac cagtcttcca ccggatatgt atgaatgtct acgtgttgct 1080
aacgaagtca ctcttaatta atatctgtat cctggaacaa tattttatgg ttatgttttt 1140
ctgtgtgtca gttttcatag tatccatatt ttattactgt ttattacttc catgaatttt 1200
aaaatctgag ggaaatgttt tgtaaacatt tatttttttt aaagaaaaga tgaaaggcag 1260
gcctatttca tcacaagaac acacacatat acacgaatag acatcaaact caatgcttta 1320
tttgtaaatt tagtgttttt ttatttctac tgtcaaatga tgtgcaaaac cttttactgg 1380
ttgcatggaa atcagccaag ttttataatc cttaaatctt aatgttcctc aaagcttgga 1440
ttaaatacat atggatgtta ctctcttgca ccaaattatc ttgatacatt caaatttgtc 1500
tggtaaaaaa ataggtggta gatattgagg ccaagaatat tgcaaaatac atgaagcttc 1560
atgcacttaa agaagtattt ttagaataag aatttgcata cttacctagt gaaacttttc 1620
tagaattatt tttcactcta agtcatgtat gtttctcttt gattatttgc atgttatgtt 1680
taataagcta ctagcaaaat aaaacatagc aaatggc 1717

<210> 259
<211> 338
<212> PRT
<213> Homo sapiens

<400> 259
Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
1 5 10 15
Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
20 25 30
Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro
35 40 45
Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
50 55 60

```
Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His
65                  70                  75                  80
Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
                85                  90                  95
Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
            100                 105                 110
Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
        115                 120                 125
Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
    130                 135                 140
Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
145                 150                 155                 160
Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
                165                 170                 175
Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
            180                 185                 190
Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
        195                 200                 205
Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
    210                 215                 220
Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
225                 230                 235                 240
Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
                245                 250                 255
Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
            260                 265                 270
Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
        275                 280                 285
Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
    290                 295                 300
Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
305                 310                 315                 320
Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
                325                 330                 335
Leu Asn
```

<210> 260
<211> 6728
<212> DNA
<213> Homo sapiens

<400> 260

```
agcagacggg agtttctcct cggggtcgga gcaggaggca cgcggagtgt gaggccacgc      60
atgagcggac gctaaccccc tccccagcca caaagagtct acatgtctag ggtctagaca     120
tgttcagctt tgtggacctc cggctcctgc tcctcttagc ggccaccgcc ctcctgacgc     180
acggccaaga ggaaggccaa gtcgagggcc aagacgaaga catcccacca atcacctgcg     240
tacagaacgg cctcaggtac catgaccgag acgtgtggaa acccgagccc tgccggatct     300
gcgtctgcga caacggcaag gtgttgtgcg atgacgtgat ctgtgacgag accaagaact     360
gccccggcgc cgaagtcccc gagggcgagt gctgtcccgt ctgccccgac ggctcagagt     420
cacccaccga ccaagaaacc accggcgtcg agggacccaa gggagacact ggcccccgag     480
gcccaagggg acccgcaggc ccccctggcc gagatggcat ccctggacag cctggacttc     540
ccggaccccc cggacccccc ggacctcccg gaccccctgg cctcggagga aactttgctc     600
cccagctgtc ttatggctat gatgagaaat caaccggagg aatttccgtg cctggcccca     660
tgggtccctc tggtcctcgt ggtctccctg gccccccctgg tgcacctggt ccccaaggct     720
tccaaggtcc ccctggtgag cctggcgagc ctggagcttc aggtcccatg ggtccccgag     780
gtcccccagg tccccctgga aagaatggag atgatgggga agctggaaaa cctggtcgtc     840
ctggtgagcg tgggcctcct gggcctcagg gtgctcgagg attgcccgga acagctggcc     900
tccctggaat gaagggacac agaggtttca gtggtttgga tggtgccaag ggagatgctg     960
gtcctgctgg tcctaagggt gagcctggca gccctggtga aaatggagct cctggtcaga    1020
tgggcccccg tggcctgcct ggtgagagag gtcgccctgg agcccctggc cctgctggtg    1080
```

ctcgtggaaa tgatggtgct actggtgctg ccgggccccc tggtcccacc ggccccgctg 1140
gtcctcctgg cttccctggt gctgttggtg ctaagggtga agctggtccc caagggcccc 1200
gaggctctga aggtccccag ggtgtgcgtg gtgagcctgg ccccccctggc cctgctggtg 1260
ctgctggccc tgctggaaac cctggtgctg atggacagcc tggtgctaaa ggtgccaatg 1320
gtgctcctgg tattgctggt gctcctggct tccctggtgc ccgaggcccc tctggacccc 1380
agggccccgg cggccctcct ggtcccaagg gtaacagcgg tgaacctggt gctcctggca 1440
gcaaaggaga cactggtgct aagggagagc ctggccctgt tggtgttcaa ggacccccctg 1500
gccctgctgg agaggaagga aagcgaggag ctcgaggtga acccggaccc actggcctgc 1560
ccggaccccc tggcgagcgt ggtggacctg gtagccgtgg tttccctggc gcagatggtg 1620
ttgctggtcc caagggtccc gctggtgaac gtggttctcc tggccccgct ggccccaaag 1680
gatctcctgg tgaagctggt cgtcccggtg aagctggtct gcctggtgcc aagggtctga 1740
ctggaagccc tggcagccct ggtcctgatg gcaaaactgg ccccccctggt cccgccggtc 1800
aagatggtcg ccccggaccc ccaggcccac ctggtgcccg tggtcaggct ggtgtgatgg 1860
gattccctgg acctaaaggt gctgctggag agcccggcaa ggctggagag cgaggtgttc 1920
ccggaccccc tggcgctgtc ggtcctgctg gcaaagatgg agaggctgga gctcagggac 1980
cccctggccc tgctggtccc gctggcgaga gaggtgaaca aggccctgct ggctcccccg 2040
gattccaggg tctccctggt cctgctggtc ctccaggtga agcaggcaaa cctggtgaac 2100
agggtgttcc tggagacctt ggcgcccctg gcccctctgg agcaagaggc gagagaggtt 2160
tccctggcga gcgtggtgtg caaggtcccc ctggtcctgc tggaccccga ggggccaacg 2220
gtgctcccgg caacgatggt gctaagggtg atgctggtgc cctggagct cccggtagcc 2280
agggcgcccc tggccttcag ggaatgcctg gtgaacgtgg tgcagctggt cttccagggc 2340
ctaagggtga cagaggtgat gctggtccca aggtgctga tggctctcct ggcaaagatg 2400
gcgtccgtgg tctgaccggc cccattggtc ctcctggccc tgctggtgcc cctggtgaca 2460
agggtgaaag tggtcccagc ggccctgctg gtcccactgg agctcgtggt gcccccggag 2520
accgtggtga gcctggtccc cccggccctg ctggctttgc tggcccccct ggtgctgacg 2580
gccaacctgg tgctaaaggc gaacctggtg atgctggtgc caaaggcgat gctggtcccc 2640
ctgggcctgc cggacccgct ggaccccctg gccccattgg taatgttggt gctcctggag 2700
ccaaaggtgc tcgcggcagc gctggtcccc ctggtgctac tggtttccct ggtgctgctg 2760
gccgagtcgg tcctcctggc ccctctggaa atgctggacc ccctggccct cctggtcctg 2820
ctggcaaaga aggcggcaaa ggtccccgtg gtgagactgg ccctgctgga cgtcctggtg 2880
aagttggtcc ccctggtccc cctggccctg ctggcgagaa aggatcccct ggtgctgatg 2940
gtcctgctgg tgctcctggt actcccgggc ctcaaggtat tgctggacag cgtggtgtgg 3000
tcggcctgcc tggtcagaga ggagagagag gcttccctgg tcttcctggc ccctctggtg 3060
aacctggcaa acaaggtccc tctggagcaa gtggtgaacg tggtcccccc ggtcccatgg 3120
gcccccctgg attggctgga ccccctggtg aatctggacg tgagggggct cctgctgccg 3180
aaggttcccc tggacgagac ggttctcctg gcgccaaggg tgaccgtggt gagaccggcc 3240
ccgctggacc ccctggtgct cctggtgctc ctggtgcccc tggccccgtt ggccctgctg 3300
gcaagagtgg tgatcgtggt gagactggtc ctgctggtcc cgccggtccc gtcggccccg 3360
tcggcgcccg tggccccgcc ggaccccaag gcccccgtgg tgacaagggt gagacaggcg 3420
aacagggcga cagaggcata aagggtcacc gtggcttctc tggcctccag ggtccccctg 3480
gccctcctgg ctctcctggt gaacaaggtc cctctggagc ctctggtcct gctggtcccc 3540
gaggtccccc tggctctgct ggtgctcctg gcaaagatgg actcaacggt ctccctggcc 3600
ccattgggcc ccctggtcct cgcggtcgca ctggtgatgc tggtcctgtt ggtccccccg 3660
gccctcctgg acctcctggt cccccctggtc ctcccagcgc tggtttcgac ttcagcttcc 3720
tgccccagcc acctcaagag aaggctcacg atggtggccg ctactaccgg gctgatgatg 3780
ccaatgtggt tcgtgaccgt gacctcgagg tggacaccac cctcaagagc ctgagccagc 3840
agatcgagaa catccggagc ccagagggaa gccgcaagaa ccccgcccgc acctgccgtg 3900
acctcaagat gtgccactct gactggaaga gtggagagta ctggattgac ccccaaccaag 3960
gctgcaacct ggatgccatc aaagtcttct gcaacatgga gactggtgag acctgcgtgt 4020
accccactca gcccagtgtg gcccagaaga actggtacat cagcaagaac cccaaggaca 4080
agaggcatgt ctggttcggc gagagcatga ccgatggatt ccagttcgag tatggcggcc 4140
agggctccga ccctgccgat gtggccatcc agctgacctt cctgcgcctg atgtccaccg 4200
aggcctccca gaacatcacc taccactgca agaacagcgt ggcctacatg gaccagcaga 4260
ctggcaacct caagaaggcc ctgctcctca agggctccaa cgagatcgag atccgcgccg 4320
agggcaacag ccgcttcacc tacagcgtca ctgtcgatgg ctgcacgagt cacaccggag 4380
cctggggcaa gacagtgatt gaatacaaaa ccaccaagtc ctcccgcctg cccatcatcg 4440
atgtggcccc cttggacgtt ggtgccccag accaggaatt cggcttcgac gttggccctg 4500
tctgcttcct gtaaactccc tccatcccaa cctggctccc tcccacccaa ccaactttcc 4560
ccccaacccg gaaacagaca agcaacccaa actgaacccc cccaaaagcc aaaaaatggg 4620
agacaatttc acatggactt tggaaaatat ttttttcctt tgcattcatc tctcaaactt 4680
agtttttatc tttgaccaac cgaacatgac caaaaaccaa aagtgcattc aaccttacca 4740

```
aaaaaaaaaa aaaaaaaaaa agaataaata aataagtttt taaaaaagga agcttggtcc    4800
acttgcttga agacccatgc gggggtaagt ccctttctgc ccgttgggtt atgaaacccc    4860
aatgctgccc tttctgctcc tttctccaca cccccccttgg cctcccctcc actccttccc   4920
aaatctgtct ccccagaaga cacaggaaac aatgtattgt ctgcccagca atcaaaggca    4980
atgctcaaac acccaagtgg cccccaccct cagcccgctc ctgcccgccc agcaccccca    5040
ggccctgggg acctggggtt ctcagactgc caaagaagcc ttgccatctg gcgctcccat    5100
ggctcttgca acatctcccc ttcgtttttg aggggtcat gccgggggag ccaccagccc     5160
ctcactgggt tcggaggaga gtcaggaagg gccacgacaa agcagaaaca tcggatttgg    5220
ggaacgcgtg tcatcccttg tgccgcaggc tgggcgggag agactgttct gttctgttcc    5280
ttgtgtaact gtgttgctga aagactacct cgttcttgtc ttgatgtgtc accggggcaa    5340
ctgcctgggg gcggggatgg gggcagggtg gaagcggctc cccattttta taccaaaggt    5400
gctacatcta tgtgatgggt ggggtgggga gggaatcact ggtgctatag aaattgagat    5460
gcccccccag gccagcaaat gttccttttt gttcaaagtc tatttttatt ccttgatatt    5520
ttttctttct tttttttttt ttttgtggat ggggacttgt gaatttttct aaaggtgcta    5580
tttaacatgg gaggagagcg tgtgcgctcc agcccagccc gctgctcact ttccaccctc    5640
tctccacctg cctctggctt ctcaggcctc tgctctccga cctctctcct ctgaaaccct    5700
cctccacagc tgcagcccat cctcccggct ccctcctagt ctgtcctgcg tcctctgtcc    5760
ccgggtttca gagacaactt cccaaagcac aaagcagttt ttccctaggg gtgggaggaa    5820
gcaaaagact ctgtacctat tttgtatgtg tataataatt tgagatgttt ttaattattt    5880
tgattgctgg aataaagcat gtggaaatga cccaaacata atccgcagtg gcctcctaat    5940
ttccttcttt ggagttgggg gaggggtaga catggggaag gggccttggg gtgatgggct    6000
tgccttccat tcctgccctt tccctcccca ctattctctt ctagatccct ccataacccc    6060
actccccttt ctctcaccct tcttataccg caaacctttc tacttcctct ttcatttttct   6120
attcttgcaa tttccttgca cctttttccaa atcctcttct cccctgcaat accatacagg   6180
caatccacgt gcacaacaca cacacacact cttcacatct ggggttgtcc aaacctcata    6240
cccactcccc ttcaagccca tccactctcc accccctgga tgccctgcac ttggtggcgg    6300
tgggatgctc atggatactg ggagggtgag gggagtggaa cccgtgagga ggacctgggg    6360
gcctctcctt gaactgacat gaagggtcat ctggcctctg ctcccttctc acccacgctg    6420
acctcctgcc gaaggagcaa cgcaacagga gaggggtctg ctgagcctgg cgagggtctg    6480
ggagggacca ggaggaaggc gtgctccctg ctcgctgtcc tggccctggg ggagtgaggg    6540
agacagacac ctgggagagc tgtggggaag gcactcgcac cgtgctcttg ggaaggaagg    6600
agacctggcc ctgctcacca cggactgggt gcctcgacct cctgaatccc cagaacacaa    6660
ccccccctggg ctggggtggt ctggggaacc atcgtgcccc cgcctcccgc ctactccttt   6720
ttaagctt                                                             6728
```

<210> 261
<211> 1464
<212> PRT
<213> Homo sapiens

<400> 261

```
Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu Leu Leu Ala Ala Thr
1               5                   10                  15
Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
            20                  25                  30
Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
        35                  40                  45
Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
    50                  55                  60
Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
65                  70                  75                  80
Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
                85                  90                  95
Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
            100                 105                 110
Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro
        115                 120                 125
Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro
    130                 135                 140
```

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala
145 150 155 160
Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser
165 170 175
Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro
180 185 190
Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro
195 200 205
Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly
210 215 220
Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg
225 230 235 240
Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro
245 250 255
Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly
260 265 270
Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu
275 280 285
Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg
290 295 300
Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly
305 310 315 320
Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro
325 330 335
Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys
340 345 350
Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly
355 360 365
Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro
370 375 380
Ala Gly Asn Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Ala Asn
385 390 395 400
Gly Ala Pro Gly Ile Ala Gly Ala Pro Gly Phe Pro Gly Ala Arg Gly
405 410 415
Pro Ser Gly Pro Gln Gly Pro Gly Gly Pro Pro Gly Pro Lys Gly Asn
420 425 430
Ser Gly Glu Pro Gly Ala Pro Gly Ser Lys Gly Asp Thr Gly Ala Lys
435 440 445
Gly Glu Pro Gly Pro Val Gly Val Gln Gly Pro Pro Gly Pro Ala Gly
450 455 460
Glu Glu Gly Lys Arg Gly Ala Arg Gly Glu Pro Gly Pro Thr Gly Leu
465 470 475 480
Pro Gly Pro Pro Gly Glu Arg Gly Gly Pro Gly Ser Arg Gly Phe Pro
485 490 495
Gly Ala Asp Gly Val Ala Gly Pro Lys Gly Pro Ala Gly Glu Arg Gly
500 505 510
Ser Pro Gly Pro Ala Gly Pro Lys Gly Ser Pro Gly Glu Ala Gly Arg
515 520 525
Pro Gly Glu Ala Gly Leu Pro Gly Ala Lys Gly Leu Thr Gly Ser Pro
530 535 540
Gly Ser Pro Gly Pro Asp Gly Lys Thr Gly Pro Pro Gly Pro Ala Gly
545 550 555 560
Gln Asp Gly Arg Pro Gly Pro Pro Gly Pro Pro Gly Ala Arg Gly Gln
565 570 575
Ala Gly Val Met Gly Phe Pro Gly Pro Lys Gly Ala Ala Gly Glu Pro
580 585 590
Gly Lys Ala Gly Glu Arg Gly Val Pro Gly Pro Pro Gly Ala Val Gly
595 600 605
Pro Ala Gly Lys Asp Gly Glu Ala Gly Ala Gln Gly Pro Pro Gly Pro
610 615 620
Ala Gly Pro Ala Gly Glu Arg Gly Glu Gln Gly Pro Ala Gly Ser Pro

625 630 635 640
Gly Phe Gln Gly Leu Pro Gly Pro Ala Gly Pro Pro Gly Glu Ala Gly
645 650 655
Lys Pro Gly Glu Gln Gly Val Pro Gly Asp Leu Gly Ala Pro Gly Pro
660 665 670
Ser Gly Ala Arg Gly Glu Arg Gly Phe Pro Gly Glu Arg Gly Val Gln
675 680 685
Gly Pro Pro Gly Pro Ala Gly Pro Arg Gly Ala Asn Gly Ala Pro Gly
690 695 700
Asn Asp Gly Ala Lys Gly Asp Ala Gly Ala Pro Gly Ala Pro Gly Ser
705 710 715 720
Gln Gly Ala Pro Gly Leu Gln Gly Met Pro Gly Glu Arg Gly Ala Ala
725 730 735
Gly Leu Pro Gly Pro Lys Gly Asp Arg Gly Asp Ala Gly Pro Lys Gly
740 745 750
Ala Asp Gly Ser Pro Gly Lys Asp Gly Val Arg Gly Leu Thr Gly Pro
755 760 765
Ile Gly Pro Pro Gly Pro Ala Gly Ala Pro Gly Asp Lys Gly Glu Ser
770 775 780
Gly Pro Ser Gly Pro Ala Gly Pro Thr Gly Ala Arg Gly Ala Pro Gly
785 790 795 800
Asp Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Phe Ala Gly Pro
805 810 815
Pro Gly Ala Asp Gly Gln Pro Gly Ala Lys Gly Glu Pro Gly Asp Ala
820 825 830
Gly Ala Lys Gly Asp Ala Gly Pro Pro Gly Pro Ala Gly Pro Ala Gly
835 840 845
Pro Pro Gly Pro Ile Gly Asn Val Gly Ala Pro Gly Ala Lys Gly Ala
850 855 860
Arg Gly Ser Ala Gly Pro Pro Gly Ala Thr Gly Phe Pro Gly Ala Ala
865 870 875 880
Gly Arg Val Gly Pro Pro Gly Pro Ser Gly Asn Ala Gly Pro Pro Gly
885 890 895
Pro Pro Gly Pro Ala Gly Lys Glu Gly Gly Lys Gly Pro Arg Gly Glu
900 905 910
Thr Gly Pro Ala Gly Arg Pro Gly Glu Val Gly Pro Pro Gly Pro Pro
915 920 925
Gly Pro Ala Gly Glu Lys Gly Ser Pro Gly Ala Asp Gly Pro Ala Gly
930 935 940
Ala Pro Gly Thr Pro Gly Pro Gln Gly Ile Ala Gly Gln Arg Gly Val
945 950 955 960
Val Gly Leu Pro Gly Gln Arg Gly Glu Arg Gly Phe Pro Gly Leu Pro
965 970 975
Gly Pro Ser Gly Glu Pro Gly Lys Gln Gly Pro Ser Gly Ala Ser Gly
980 985 990
Glu Arg Gly Pro Pro Gly Pro Met Gly Pro Pro Gly Leu Ala Gly Pro
995 1000 1005
Pro Gly Glu Ser Gly Arg Glu Gly Ala Pro Ala Ala Glu Gly Ser Pro
1010 1015 1020
Gly Arg Asp Gly Ser Pro Gly Ala Lys Gly Asp Arg Gly Glu Thr Gly
1025 1030 1035 1040
Pro Ala Gly Pro Pro Gly Ala Pro Gly Ala Pro Gly Ala Pro Gly Pro
1045 1050 1055
Val Gly Pro Ala Gly Lys Ser Gly Asp Arg Gly Glu Thr Gly Pro Ala
1060 1065 1070
Gly Pro Ala Gly Pro Val Gly Pro Val Gly Ala Arg Gly Pro Ala Gly
1075 1080 1085
Pro Gln Gly Pro Arg Gly Asp Lys Gly Glu Thr Gly Glu Gln Gly Asp
1090 1095 1100
Arg Gly Ile Lys Gly His Arg Gly Phe Ser Gly Leu Gln Gly Pro Pro
1105 1110 1115 1120

Gly Pro Pro Gly Ser Pro Gly Glu Gln Gly Pro Ser Gly Ala Ser Gly
1125 1130 1135
Pro Ala Gly Pro Arg Gly Pro Pro Gly Ser Ala Gly Ala Pro Gly Lys
1140 1145 1150
Asp Gly Leu Asn Gly Leu Pro Gly Pro Ile Gly Pro Pro Gly Pro Arg
1155 1160 1165
Gly Arg Thr Gly Asp Ala Gly Pro Val Gly Pro Pro Gly Pro Pro Gly
1170 1175 1180
Pro Pro Gly Pro Pro Gly Pro Pro Ser Ala Gly Phe Asp Phe Ser Phe
1185 1190 1195 1200
Leu Pro Gln Pro Pro Gln Glu Lys Ala His Asp Gly Gly Arg Tyr Tyr
1205 1210 1215
Arg Ala Asp Asp Ala Asn Val Val Arg Asp Arg Asp Leu Glu Val Asp
1220 1225 1230
Thr Thr Leu Lys Ser Leu Ser Gln Gln Ile Glu Asn Ile Arg Ser Pro
1235 1240 1245
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Lys Met
1250 1255 1260
Cys His Ser Asp Trp Lys Ser Gly Glu Tyr Trp Ile Asp Pro Asn Gln
1265 1270 1275 1280
Gly Cys Asn Leu Asp Ala Ile Lys Val Phe Cys Asn Met Glu Thr Gly
1285 1290 1295
Glu Thr Cys Val Tyr Pro Thr Gln Pro Ser Val Ala Gln Lys Asn Trp
1300 1305 1310
Tyr Ile Ser Lys Asn Pro Lys Asp Lys Arg His Val Trp Phe Gly Glu
1315 1320 1325
Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp
1330 1335 1340
Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr
1345 1350 1355 1360
Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr
1365 1370 1375
Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly
1380 1385 1390
Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr
1395 1400 1405
Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys
1410 1415 1420
Thr Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile
1425 1430 1435 1440
Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe
1445 1450 1455
Asp Val Gly Pro Val Cys Phe Leu
1460

<210> 262
<211> 2574
<212> DNA
<213> Homo sapiens

<400> 262
cctgtttaga cacatggaca acaatcccag cgctacaagg cacacagtcc gcttcttcgt 60
cctcagggtt gccagcgctt cctggaagtc ctgaagctct cgcagtgcag tgagttcatg 120
caccttcttg ccaagcctca gtctttggga tctggggagg ccgcctggtt ttcctccctc 180
cttctgcacg tctgctgggg tctcttcctc tccaggcctt gccgtccccc tggcctctct 240
tcccagctca cacatgaaga tgcacttgca aagggctctg gtggtcctgg ccctgctgaa 300
ctttgccacg gtcagcctct ctctgtccac ttgcaccacc ttggacttcg gccacatcaa 360
gaagaagagg gtggaagcca ttaggggaca gatcttgagc aagctcaggc tcaccagccc 420
ccctgagcca acggtgatga cccacgtccc ctatcaggtc ctggcccttt acaacagcac 480
ccgggagctg ctggaggaga tgcatgggga gagggaggaa ggctgcaccc aggaaaacac 540
cgagtcggaa tactatgcca aagaaatcca taaattcgac atgatccagg ggctggcgga 600

gcacaacgaa ctggctgtct gccctaaagg aattacctcc aaggttttcc gcttcaatgt 660
gtcctcagtg gagaaaaata gaaccaacct attccgagca gaattccggg tcttgcgggt 720
gcccaacccc agctctaagc ggaatgagca gaggatcgag ctcttccaga tccttcggcc 780
agatgagcac attgccaaac agcgctatat cggtggcaag aatctgccca cacggggcac 840
tgccgagtgg ctgtcctttg atgtcactga cactgtgcgt gagtggctgt tgagaagaga 900
gtccaactta ggtctagaaa tcagcattca ctgtccatgt cacacctttc agcccaatgg 960
agatatcctg gaaaacattc acgaggtgat ggaaatcaaa ttcaaaggcg tggacaatga 1020
ggatgaccat ggccgtggag atctggggcg cctcaagaag cagaaggatc accacaaccc 1080
tcatctaatc ctcatgatga ttcccccaca ccggctcgac aacccgggcc aggggggtca 1140
gaggaagaag cgggctttgg acaccaatta ctgcttccgc aacttggagg agaactgctg 1200
tgtgcgcccc ctctacattg acttccgaca ggatctgggc tggaagtggg tccatgaacc 1260
taagggctac tatgccaact tctgctcagg cccttgccca tacctccgca gtgcagacac 1320
aacccacagc acggtgctgg gactgtacaa cactctgaac cctgaagcat ctgcctcgcc 1380
ttgctgcgtg ccccaggacc tggagcccct gaccatcctg tactatgttg ggaggacccc 1440
caaagtggag cagctctcca acatggtggt gaagtcttgt aaatgtagct gagaccccac 1500
gtgcgacaga gagaggggag agagaaccac cactgcctga ctgcccgctc ctcgggaaac 1560
acacaagcaa caaacctcac tgagaggcct ggagcccaca accttcggct ccgggcaaat 1620
ggctgagatg gaggtttcct tttggaacat ttctttcttg ctggctctga gaatcacggt 1680
ggtaaagaaa gtgtgggttt ggttagagga aggctgaact cttcagaaca cacagacttt 1740
ctgtgacgca gacagagggg atggggatag aggaaaggga tggtaagttg agatgttgtg 1800
tggcaatggg atttgggcta ccctaaaggg agaaggaagg gcagagaatg gctgggtcag 1860
ggccagactg gaagacactt cagatctgag gttggatttg ctcattgctg taccacatct 1920
gctctaggga atctggatta tgttatacaa ggcaagcatt ttttttttta aagacaggtt 1980
acgaagacaa agtcccagaa ttgtatctca tactgtctgg gattaagggc aaatctatta 2040
cttttgcaaa ctgtcctcta catcaattaa catcgtgggt cactacaggg agaaaatcca 2100
ggtcatgcag ttcctggccc atcaactgta ttgggccttt tggatatgct gaacgcagaa 2160
gaaagggtgg aaatcaaccc tctcctgtct gccctctggg tccctcctct cacctctccc 2220
tcgatcatat ttccccttgg acacttggtt agacgccttc caggtcagga tgcacatttc 2280
tggattgtgg ttccatgcag ccttggggca ttatgggtct tccccacttt cccctccaag 2340
accctgtgtt catttggtgt tcctggaagc aggtgctaca acatgtgagg cattcgggga 2400
agctgcacat gtgccacaca gtgacttggc cccagacgca tagactgagg tataaagaca 2460
agtatgaata ttactctcaa aatctttgta taaataaata tttttggggc atcctggatg 2520
atttcatctt ctggaatatt gtttctagaa cagtaaaagc cttattctaa ggtg 2574

<210> 263
<211> 412
<212> PRT
<213> Homo sapiens

<400> 263
Met Lys Met His Leu Gln Arg Ala Leu Val Val Leu Ala Leu Leu Asn
1 5 10 15
Phe Ala Thr Val Ser Leu Ser Leu Ser Thr Cys Thr Thr Leu Asp Phe
20 25 30
Gly His Ile Lys Lys Lys Arg Val Glu Ala Ile Arg Gly Gln Ile Leu
35 40 45
Ser Lys Leu Arg Leu Thr Ser Pro Pro Glu Pro Thr Val Met Thr His
50 55 60
Val Pro Tyr Gln Val Leu Ala Leu Tyr Asn Ser Thr Arg Glu Leu Leu
65 70 75 80
Glu Glu Met His Gly Glu Arg Glu Glu Gly Cys Thr Gln Glu Asn Thr
85 90 95
Glu Ser Glu Tyr Tyr Ala Lys Glu Ile His Lys Phe Asp Met Ile Gln
100 105 110
Gly Leu Ala Glu His Asn Glu Leu Ala Val Cys Pro Lys Gly Ile Thr
115 120 125
Ser Lys Val Phe Arg Phe Asn Val Ser Ser Val Glu Lys Asn Arg Thr
130 135 140
Asn Leu Phe Arg Ala Glu Phe Arg Val Leu Arg Val Pro Asn Pro Ser
145 150 155 160
Ser Lys Arg Asn Glu Gln Arg Ile Glu Leu Phe Gln Ile Leu Arg Pro

```
                        165                             170                           175
Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro
                180                             185                             190
Thr Arg Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val
        195                             200                             205
Arg Glu Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser
    210                             215                             220
Ile His Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu
225                             230                             235                             240
Asn Ile His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu
                        245                             250                             255
Asp Asp His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp
                260                             265                             270
His His Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu
        275                             280                             285
Asp Asn Pro Gly Gln Gly Gly Gln Arg Lys Lys Arg Ala Leu Asp Thr
    290                             295                             300
Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu
305                             310                             315                             320
Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro
                        325                             330                             335
Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg
                340                             345                             350
Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu
        355                             360                             365
Asn Pro Glú Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu
    370                             375                             380
Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln
385                             390                             395                             400
Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
                        405                             410
```

```
<210> 264
<211> 5086
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(5086)
<223> n = A,T,C or G

<400> 264
agcaccacgg cagcaggagg tttcggncta agttggaggt actggnccac gactgcatgc      60
ccgcgcccgc caggtgatac ctccgccggt gacccagggg ctctgcgaca caaggagtct     120
gcatgtctaa gtgctagaca tgctcagctt tgtggatacg cggactttgt tgctgcttgc     180
agtaacctta tgcctagcaa catgccaatc tttacaagag gaaactgtaa gaaagggccc     240
agccggagat agaggaccac gtggagaaag gggtccacca ggccccccag gcagagatgg     300
tgaagatggt cccacaggcc ctcctggtcc acctggtcct cctggccccc ctggtctcgg     360
tgggaacttt gctgctcagt atgatggaaa aggagttgga cttggccctg gaccaatggg     420
cttaatggga cctagaggcc cacctggtgc agctggagcc ccaggccctc aaggtttcca     480
aggacctgct ggtgagcctg gtgaacctgg tcaaactggt cctgcaggtg ctcgtggtcc     540
agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaacccg gacgacctgg     600
tgagagagga gttgttggac cacagggtgc tcgtggtttc cctggaactc ctggacttcc     660
tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaagggac agcccggtgc     720
tcctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg     780
agcccgtggg cttcctggtg agagaggacg tgttggtgcc cctggcccag ctggtgcccg     840
tggcagtgat ggaagtgtgg gtcccgtggg tcctgctggt cccattgggt ctgctggccc     900
tccaggcttc ccaggtgccc ctggccccaa gggtgaaatt ggagctgttg gtaacgctgg     960
tcctgctggt cccgccggtc cccgtggtga agtgggtctt ccaggcctct ccggccccgt    1020
tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccaagggtg ctgctggcct    1080
```

```
                    165                           170                           175
Asp Glu His Ile Ala Lys Gln Arg Tyr Ile Gly Gly Lys Asn Leu Pro
            180                           185                           190
Thr Arg Gly Thr Ala Glu Trp Leu Ser Phe Asp Val Thr Asp Thr Val
        195                           200                           205
Arg Glu Trp Leu Leu Arg Arg Glu Ser Asn Leu Gly Leu Glu Ile Ser
    210                           215                           220
Ile His Cys Pro Cys His Thr Phe Gln Pro Asn Gly Asp Ile Leu Glu
225                           230                           235                           240
Asn Ile His Glu Val Met Glu Ile Lys Phe Lys Gly Val Asp Asn Glu
                    245                           250                           255
Asp Asp His Gly Arg Gly Asp Leu Gly Arg Leu Lys Lys Gln Lys Asp
            260                           265                           270
His His Asn Pro His Leu Ile Leu Met Met Ile Pro Pro His Arg Leu
        275                           280                           285
Asp Asn Pro Gly Gln Gly Gly Gln Arg Lys Lys Arg Ala Leu Asp Thr
    290                           295                           300
Asn Tyr Cys Phe Arg Asn Leu Glu Glu Asn Cys Cys Val Arg Pro Leu
305                           310                           315                           320
Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp Lys Trp Val His Glu Pro
                    325                           330                           335
Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly Pro Cys Pro Tyr Leu Arg
            340                           345                           350
Ser Ala Asp Thr Thr His Ser Thr Val Leu Gly Leu Tyr Asn Thr Leu
        355                           360                           365
Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys Val Pro Gln Asp Leu Glu
    370                           375                           380
Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg Thr Pro Lys Val Glu Gln
385                           390                           395                           400
Leu Ser Asn Met Val Val Lys Ser Cys Lys Cys Ser
                    405                           410
```

<210> 264
<211> 5086
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(5086)
<223> n = A,T,C or G

<400> 264

```
agcaccacgg cagcaggagg tttcggncta agttggaggt actggnccac gactgcatgc     60
ccgcgcccgc caggtgatac ctccgccggt gacccagggg ctctgcgaca caaggagtct    120
gcatgtctaa gtgctagaca tgctcagctt tgtggatacg cggactttgt tgctgcttgc    180
agtaacctta tgcctagcaa catgccaatc tttacaagag gaaactgtaa gaaagggccc    240
agccggagat agaggaccac gtggagaaag gggtccacca ggccccccag gcagagatgg    300
tgaagatggt cccacaggcc ctcctggtcc acctggtcct cctggccccc ctggtctcgg    360
tgggaacttt gctgctcagt atgatggaaa aggagttgga cttggccctg gaccaatggg    420
cttaatggga cctagaggcc cacctggtgc agctggagcc ccaggccctc aaggtttcca    480
aggacctgct ggtgagcctg gtgaacctgg tcaaactggt cctgcaggtg ctcgtggtcc    540
agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaacccg gacgacctgg    600
tgagagagga gttgttggac cacagggtgc tcgtggtttc cctggaactc ctggacttcc    660
tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaagggac agcccggtgc    720
tcctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg    780
agcccgtggg cttcctggtg agagaggacg tgttggtgcc cctggcccag ctggtgcccg    840
tggcagtgat ggaagtgtgg gtcccgtggg tcctgctggt cccattgggt ctgctggccc    900
tccaggcttc ccaggtgccc ctggccccaa gggtgaaatt ggagctgttg gtaacgctgg    960
tcctgctggt cccgccggtc cccgtggtga agtgggtctt ccaggcctct ccggccccgt   1020
tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccaagggtg ctgctggcct   1080
```

tcccggcgtt gctggggctc ccggcctccc tggaccccgc ggtattcctg gccctgttgg 1140
tgctgccggt gctactggtg ccagaggact tgttggtgag cctggtccag ctggctccaa 1200
aggagagagc ggtaacaagg gtgagcccgg ctctgctggg ccccaaggtc ctcctggtcc 1260
cagtggtgaa gaaggaaaga gaggccctaa tggggaagct ggatctgccg gccctccagg 1320
acctcctggg ctgagaggta gtcctggttc tcgtggtctt cctggagctg atggcagagc 1380
tggcgtcatg ggccctcctg gtagtcgtgg tgcaagtggc cctgctggag tccgaggacc 1440
taatggagat gctggtcgcc ctggggagcc tggtctcatg ggacccagag gtcttcctgg 1500
ttcccctgga aatatcggcc ccgctggaaa agaaggtcct gtcggcctcc ctggcatcga 1560
cggcaggcct ggcccaattg gcccagctgg agcaagagga gagcctggca acattggatt 1620
ccctggaccc aaaggcccca ctggtgatcc tggcaaaaac ggtgataaag gtcatgctgg 1680
tcttgctggt gctcggggtg ctccaggtcc tgatggaaac aatggtgctc agggacctcc 1740
tggaccacag ggtgttcaag gtggaaaagg tgaacagggt cccgctggtc ctccaggctt 1800
ccagggtctg cctggcccct caggtcccgc tggtgaagtt ggcaaaccag gagaaagggg 1860
tctccatggt gagtttggtc tccctggtcc tgctggtcca agaggggaac gcggtccccc 1920
aggtgagagt ggtgctgccg gtcctactgg tcctattgga agccgaggtc cttctggacc 1980
cccagggcct gatggaaaca agggtgaacc tggtgtggtt ggtgctgtgg gcactgctgg 2040
tccatctggt cctagtggac tcccaggaga gaggggtgct gctggcatac ctggaggcaa 2100
gggagaaaag ggtgaacctg gtctcagagg tgaaattggt aaccctggca gagatggtgc 2160
tcgtggtgct catggtgctg taggtgcccc tggtcctgct ggagccacag gtgaccgggg 2220
cgaagctggg gctgctggtc ctgctggtcc tgctggtcct cggggaagcc ctggtgaacg 2280
tggcgaggtc ggtcctgctg gccccaacgg atttgctggt ccggctggtg ctgctggtca 2340
accgggtgct aaaggagaaa gaggagccaa agggcctaag ggtgaaaacg gtgttgttgg 2400
tcccacaggc cccgttggag ctgctggccc agctggtcca aatggtcccc ccggtcctgc 2460
tggaagtcgt ggtgatggag gccccccTgg tatgactggt ttccctggtg ctgctggacg 2520
gactggtccc ccaggaccct ctggtatttc tggccctcct ggtccccctg gtcctgctgg 2580
gaaagaaggg cttcgtggtc ctcgtggtga ccaaggtcca gttggccgaa ctggagaagt 2640
aggtgcagtt ggtccccctg gcttcgctgg tgagaagggt ccctctggag aggctggtac 2700
tgctggacct cctggcactc caggtcctca gggtcttctt ggtgctcctg gtattctggg 2760
tctccctggc tcgagaggtg aacgtggtct acctggtgtt gctggtgctg tgggtgaacc 2820
tggtcctctt ggcattgccg gccctcctgg ggcccgtggt cctcctggtg ctgtgggtag 2880
tcctggagtc aacggtgctc ctggtgaagc tggtcgtgat ggcaaccctg ggaacgatgg 2940
tcccccaggt cgcgatggtc aacccggaca caagggagag cgcggttacc ctggcaatat 3000
tggtcccgtt ggtgctgcag gtgcacctgg tcctcatggc cccgtgggtc ctgctggcaa 3060
acatggaaac cgtggtgaaa ctggtccttc tggtcctgtt ggtcctgctg gtgctgttgg 3120
cccaagaggt cctagtggcc cacaaggcat tcgtggcgat aagggagagc ccggtgaaaa 3180
ggggcccaga ggtcttcctg gcttaaaggg acacaatgga ttgcaaggtc tgcctggtat 3240
cgctggtcac catggtgatc aaggtgctcc tggctccgtg ggtcctgctg gtcctagggg 3300
ccctgctggt ccttctggcc ctgctggaaa agatggtcgc actggacatc ctggtacggt 3360
tggacctgct ggcattcgag gccctcaggg tcaccaaggc cctgctggcc cccctggtcc 3420
ccctggccct cctggacctc caggtgtaag cggtggtggt tatgactttg gttacgatgg 3480
agacttctac agggctgacc agcctcgctc agcaccttct ctcagaccca aggactatga 3540
agttgatgct actctgaagt ctctcaacaa ccagattgag acccttctta ctcctgaagg 3600
ctctagaaag aacccagctc gcacatgccg tgacttgaga ctcagccacc cagagtggag 3660
cagtggttac tactggattg accctaacca aggatgcact atggatgcta tcaaagtata 3720
ctgtgatttc tctactggcg aaacctgtat ccgggcccaa cctgaaaaca tcccagccaa 3780
gaactggtat aggagctcca aggacaagaa acacgtctgg ctaggagaaa ctatcaatgc 3840
tggcagccag tttgaatata atgtagaagg agtgacttcc aaggaaatgg ctacccaact 3900
tgccttcatg cgcctgctgg ccaactatgc ctctcagaac atcacctacc actgcaagaa 3960
cagcattgca tacatggatg aggagactgg caacctgaaa aaggctgtca ttctacaggg 4020
ctctaatgat gttgaacttg ttgctgaggg caacagcagg ttcacttaca ctgttcttgt 4080
agatggctgc tctaaaaaga caaatgaatg ggaaagaca atcattgaat acaaaacaaa 4140
taagccatca cgcctgccct tccttgatat tgcacctttg gacatcggtg gtgctgacca 4200
tgaattcttt gtggacattg gcccagtctg tttcaaataa atgaactcaa tctaaattaa 4260
aaaagaaaga aatttgaaaa aactttctct ttgccatttc ttcttcttct tttttaactg 4320
aaagctgaat ccttccattt cttctgcaca tctacttgct taaattgtgg gcaaaagaga 4380
aaaagaagga ttgatcagag cattgtgcaa tacagtttca ttaactcctt cccccgctcc 4440
cccaaaaatt tgaatttttt tttcaacact cttacacctg ttatggaaaa tgtcaacctt 4500
tgtaagaaaa ccaaaataaa aattgaaaaa taaaaaccat aaacatttgc accacttgtg 4560
gcttttgaat atcttccaca gagggaagtt taaaacccaa acttccaaag gtttaaacta 4620
cctcaaaaca ctttcccatg agtgtgatcc acattgttag gtgctgacct agacagagat 4680
gaactgaggt ccttgttttg ttttgttcat aatacaaagg tgctaattaa tagtatttca 4740

gatacttgaa gaatgttgat ggtgctagaa gaatttgaga agaaatactc ctgtattgag 4800
ttgtatcgtg tggtgtattt tttaaaaaat ttgatttagc attcatattt tccatcttat 4860
tcccaattaa aagtatgcag attatttgcc caaagttgtc ctcttcttca gattcagcat 4920
ttgttctttg ccagtctcat tttcatcttc ttccatggtt ccacagaagc tttgtttctt 4980
gggcaagcag aaaaattaaa ttgtacctat tttgtatatg tgagatgttt aaataaattg 5040
tgaaaaaaat gaaataaagc atgtttggtt ttccaaaaga acatat 5086

<210> 265
<211> 1366
<212> PRT
<213> Homo sapiens

<400> 265
Met Leu Ser Phe Val Asp Thr Arg Thr Leu Leu Leu Leu Ala Val Thr
1 5 10 15
Leu Cys Leu Ala Thr Cys Gln Ser Leu Gln Glu Glu Thr Val Arg Lys
20 25 30
Gly Pro Ala Gly Asp Arg Gly Pro Arg Gly Glu Arg Gly Pro Pro Gly
35 40 45
Pro Pro Gly Arg Asp Gly Glu Asp Gly Pro Thr Gly Pro Pro Gly Pro
50 55 60
Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala Ala Gln
65 70 75 80
Tyr Asp Gly Lys Gly Val Gly Leu Gly Pro Gly Pro Met Gly Leu Met
85 90 95
Gly Pro Arg Gly Pro Pro Gly Ala Ala Gly Ala Pro Gly Pro Gln Gly
100 105 110
Phe Gln Gly Pro Ala Gly Glu Pro Gly Glu Pro Gly Gln Thr Gly Pro
115 120 125
Ala Gly Ala Arg Gly Pro Ala Gly Pro Pro Gly Lys Ala Gly Glu Asp
130 135 140
Gly His Pro Gly Lys Pro Gly Arg Pro Gly Glu Arg Gly Val Val Gly
145 150 155 160
Pro Gln Gly Ala Arg Gly Phe Pro Gly Thr Pro Gly Leu Pro Gly Phe
165 170 175
Lys Gly Ile Arg Gly His Asn Gly Leu Asp Gly Leu Lys Gly Gln Pro
180 185 190
Gly Ala Pro Gly Val Lys Gly Glu Pro Gly Ala Pro Gly Glu Asn Gly
195 200 205
Thr Pro Gly Gln Thr Gly Ala Arg Gly Leu Pro Gly Glu Arg Gly Arg
210 215 220
Val Gly Ala Pro Gly Pro Ala Gly Ala Arg Gly Ser Asp Gly Ser Val
225 230 235 240
Gly Pro Val Gly Pro Ala Gly Pro Ile Gly Ser Ala Gly Pro Pro Gly
245 250 255
Phe Pro Gly Ala Pro Gly Pro Lys Gly Glu Ile Gly Ala Val Gly Asn
260 265 270
Ala Gly Pro Ala Gly Pro Ala Gly Pro Arg Gly Glu Val Gly Leu Pro
275 280 285
Gly Leu Ser Gly Pro Val Gly Pro Pro Gly Asn Pro Gly Ala Asn Gly
290 295 300
Leu Thr Gly Ala Lys Gly Ala Ala Gly Leu Pro Gly Val Ala Gly Ala
305 310 315 320
Pro Gly Leu Pro Gly Pro Arg Gly Ile Pro Gly Pro Val Gly Ala Ala
325 330 335
Gly Ala Thr Gly Ala Arg Gly Leu Val Gly Glu Pro Gly Pro Ala Gly
340 345 350
Ser Lys Gly Glu Ser Gly Asn Lys Gly Glu Pro Gly Ser Ala Gly Pro
355 360 365

Gln Gly Pro Pro Gly Pro Ser Gly Glu Glu Gly Lys Arg Gly Pro Asn
370 375 380
Gly Glu Ala Gly Ser Ala Gly Pro Pro Gly Pro Pro Gly Leu Arg Gly
385 390 395 400
Ser Pro Gly Ser Arg Gly Leu Pro Gly Ala Asp Gly Arg Ala Gly Val
405 410 415
Met Gly Pro Pro Gly Ser Arg Gly Ala Ser Gly Pro Ala Gly Val Arg
420 425 430
Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly
435 440 445
Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys
450 455 460
Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile
465 470 475 480
Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly
485 490 495
Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His
500 505 510
Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn
515 520 525
Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly
530 535 540
Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro
545 550 555 560
Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His
565 570 575
Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly
580 585 590
Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser
595 600 605
Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro
610 615 620
Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly
625 630 635 640
Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu
645 650 655
Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp
660 665 670
Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly
675 680 685
Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro
690 695 700
Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala
705 710 715 720
Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly
725 730 735
Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val
740 745 750
Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn
755 760 765
Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly
770 775 780
Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro
785 790 795 800
Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu
805 810 815
Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly
820 825 830
Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro
835 840 845
Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln

850 855 860
Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly
865 870 875 880
Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro
885 890 895
Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val
900 905 910
Gly Ser Pro Gly Val Asn Gly Ala Pro Gly Glu Ala Gly Arg Asp Gly
915 920 925
Asn Pro Gly Asn Asp Gly Pro Pro Gly Arg Asp Gly Gln Pro Gly His
930 935 940
Lys Gly Glu Arg Gly Tyr Pro Gly Asn Ile Gly Pro Val Gly Ala Ala
945 950 955 960
Gly Ala Pro Gly Pro His Gly Pro Val Gly Pro Ala Gly Lys His Gly
965 970 975
Asn Arg Gly Glu Thr Gly Pro Ser Gly Pro Val Gly Pro Ala Gly Ala
980 985 990
Val Gly Pro Arg Gly Pro Ser Gly Pro Gln Gly Ile Arg Gly Asp Lys
995 1000 1005
Gly Glu Pro Gly Glu Lys Gly Pro Arg Gly Leu Pro Gly Leu Lys Gly
1010 1015 1020
His Asn Gly Leu Gln Gly Leu Pro Gly Ile Ala Gly His His Gly Asp
1025 1030 1035 1040
Gln Gly Ala Pro Gly Ser Val Gly Pro Ala Gly Pro Arg Gly Pro Ala
1045 1050 1055
Gly Pro Ser Gly Pro Ala Gly Lys Asp Gly Arg Thr Gly His Pro Gly
1060 1065 1070
Thr Val Gly Pro Ala Gly Ile Arg Gly Pro Gln Gly His Gln Gly Pro
1075 1080 1085
Ala Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Val Ser
1090 1095 1100
Gly Gly Gly Tyr Asp Phe Gly Tyr Asp Gly Asp Phe Tyr Arg Ala Asp
1105 1110 1115 1120
Gln Pro Arg Ser Ala Pro Ser Leu Arg Pro Lys Asp Tyr Glu Val Asp
1125 1130 1135
Ala Thr Leu Lys Ser Leu Asn Asn Gln Ile Glu Thr Leu Leu Thr Pro
1140 1145 1150
Glu Gly Ser Arg Lys Asn Pro Ala Arg Thr Cys Arg Asp Leu Arg Leu
1155 1160 1165
Ser His Pro Glu Trp Ser Ser Gly Tyr Tyr Trp Ile Asp Pro Asn Gln
1170 1175 1180
Gly Cys Thr Met Asp Ala Ile Lys Val Tyr Cys Asp Phe Ser Thr Gly
1185 1190 1195 1200
Glu Thr Cys Ile Arg Ala Gln Pro Glu Asn Ile Pro Ala Lys Asn Trp
1205 1210 1215
Tyr Arg Ser Ser Lys Asp Lys Lys His Val Trp Leu Gly Glu Thr Ile
1220 1225 1230
Asn Ala Gly Ser Gln Phe Glu Tyr Asn Val Glu Gly Val Thr Ser Lys
1235 1240 1245
Glu Met Ala Thr Gln Leu Ala Phe Met Arg Leu Leu Ala Asn Tyr Ala
1250 1255 1260
Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Ile Ala Tyr Met Asp
1265 1270 1275 1280
Glu Glu Thr Gly Asn Leu Lys Lys Ala Val Ile Leu Gln Gly Ser Asn
1285 1290 1295
Asp Val Glu Leu Val Ala Glu Gly Asn Ser Arg Phe Thr Tyr Thr Val
1300 1305 1310
Leu Val Asp Gly Cys Ser Lys Lys Thr Asn Glu Trp Gly Lys Thr Ile
1315 1320 1325
Ile Glu Tyr Lys Thr Asn Lys Pro Ser Arg Leu Pro Phe Leu Asp Ile
1330 1335 1340

Ala Pro Leu Asp Ile Gly Gly Ala Asp His Glu Phe Phe Val Asp Ile
1345 1350 1355 1360
Gly Pro Val Cys Phe Lys
1365

<210> 266
<211> 2028
<212> DNA
<213> Homo sapiens

<400> 266
atggcatatg caaaagccct gaggctgcag tggagagagc cattgaaagg gaagggcaat 60
aaggagcggt tcaagggaga gtatcaactc acatgggcct tgaaggccac gcactgccta 120
gcagcaactc actggagccc ctcttgcccc ccgcaacagg tgtttgggga cctggaccag 180
gtgaggatga cctcggaggg ctccgactgc cgttgcaagt gcatcatgcg gcccctgagc 240
aaggacgcgt gtagccgagt gcgcagtggg cgggcacgcg tggaggactt ctacacggtg 300
gagactgtga gctcgggcac tgactgccgc tgctcctgta ccgcacctcc ctcctctctc 360
aacccctgtg agaacgagtg gaagatggag aaactcaaaa agcaggcgcc cgagctcctc 420
aagctgcagt ccatggtgga tctcctggag ggcaccctgt acagcatgga cttgatgaag 480
gtgcacgcct acgtccacaa ggtggcctcc cagatgaaca cactggaaga gagcatcaag 540
gccaacctga gccgggagaa tgaggtggtg aaggacagcg tgcgccacct cagtgagcag 600
ttgaggcact atgagaatca ctctgccatc atgctgggca tcaagaagga gctgtcccgc 660
ctgggcctcc agctgctgca gaaggatgcc gccgccgccc ctgccacccc tgccacgggc 720
actggtagca aggcccagga cacagctaga ggaaaaggca aggacatcag caagtatggc 780
agtgtgcaga aaagctttgc agacagaggc ctcccaaaac ctcccaagga gaagctgctt 840
caggtggaga agctgagaaa ggagagcggc aagggcagtt tcctccagcc cacagccaag 900
ccccgcgccc tggcccagca gcaggctgtg atccggggct tcacctacta caaggcaggc 960
aagcaggagg tgaccgaggc ggtggcagac aacaccctcc agggcacttc ctggctggag 1020
caactgccgc ccaaggtgga gggcaggtcc aactccgcag agcccaactc cgcagagcag 1080
gatgaggctg agcccaggtc ctccgagcga gtggacctgg cttctggcac ccccacttca 1140
atccctgcca ccaccaccac cgccaccacc accccaaccc ccaccaccag tctcctgccc 1200
accgagccac cttcaggtcc agaagtctcc agccaaggca gagaggcgag ctgtgagggc 1260
accctccggg ctgtggaccc ccctgtgagg caccacagct atgggcgcca cgagggagcc 1320
tggatgaagg accctgcagc tcgagacgac aggatctatg tcaccaacta ctactatgga 1380
aacagcctgg tggagttccg caacctggaa aacttcaagc aaggccgctg gagtaacatg 1440
tacaagctac cctacaactg gatcggcaca ggccacgtgg tgtaccaggg cgccttctac 1500
tacaaccgcg ccttcaccaa gaacatcatc aagtacgacc tacggcagcg cttcgtggcc 1560
tcctgggcgc tgctgcccga cgtggtatat gaggacacca caccttggaa gtggcgcgga 1620
cactcggaca ttgactttgc cgtggacgag agcggcctgt gggtcatcta ccccgccgtg 1680
gacgaccgcg atgaggccca gcccgaggtg atcgtcctga gtcgcttgga ccccggcgat 1740
ctctccgtgc accgggagac cacgtggaag acacggctgc ggcggaactc ctacgggaac 1800
tgcttcctgg tgtgcggcat cctgtatgcc gtggacacgt acaaccagca ggaaggccag 1860
gtcgcctacg ctttcgacac gcacacgggc accgacgcac gcccccagct gccgttcctc 1920
aacgagcacg cctacaccac ccagatcgac tacaacccca aggagcgggt gctgtacgcc 1980
tgggacaatg gccaccagct cacctacacc ctccacttcg tggtctga 2028

<210> 267
<211> 675
<212> PRT
<213> Homo sapiens

<400> 267
Met Ala Tyr Ala Lys Ala Leu Arg Leu Gln Trp Arg Glu Pro Leu Lys
1 5 10 15
Gly Lys Gly Asn Lys Glu Arg Phe Lys Gly Glu Tyr Gln Leu Thr Trp
20 25 30
Ala Leu Lys Ala Thr His Cys Leu Ala Ala Thr His Trp Ser Pro Ser
35 40 45
Cys Pro Pro Gln Gln Val Phe Gly Asp Leu Asp Gln Val Arg Met Thr
50 55 60
Ser Glu Gly Ser Asp Cys Arg Cys Lys Cys Ile Met Arg Pro Leu Ser

65 70 75 80
Lys Asp Ala Cys Ser Arg Val Arg Ser Gly Arg Ala Arg Val Glu Asp
85 90 95
Phe Tyr Thr Val Glu Thr Val Ser Ser Gly Thr Asp Cys Arg Cys Ser
100 105 110
Cys Thr Ala Pro Pro Ser Ser Leu Asn Pro Cys Glu Asn Glu Trp Lys
115 120 125
Met Glu Lys Leu Lys Lys Gln Ala Pro Glu Leu Leu Lys Leu Gln Ser
130 135 140
Met Val Asp Leu Leu Glu Gly Thr Leu Tyr Ser Met Asp Leu Met Lys
145 150 155 160
Val His Ala Tyr Val His Lys Val Ala Ser Gln Met Asn Thr Leu Glu
165 170 175
Glu Ser Ile Lys Ala Asn Leu Ser Arg Glu Asn Glu Val Val Lys Asp
180 185 190
Ser Val Arg His Leu Ser Glu Gln Leu Arg His Tyr Glu Asn His Ser
195 200 205
Ala Ile Met Leu Gly Ile Lys Lys Glu Leu Ser Arg Leu Gly Leu Gln
210 215 220
Leu Leu Gln Lys Asp Ala Ala Ala Ala Pro Ala Thr Pro Ala Thr Gly
225 230 235 240
Thr Gly Ser Lys Ala Gln Asp Thr Ala Arg Gly Lys Gly Lys Asp Ile
245 250 255
Ser Lys Tyr Gly Ser Val Gln Lys Ser Phe Ala Asp Arg Gly Leu Pro
260 265 270
Lys Pro Pro Lys Glu Lys Leu Leu Gln Val Glu Lys Leu Arg Lys Glu
275 280 285
Ser Gly Lys Gly Ser Phe Leu Gln Pro Thr Ala Lys Pro Arg Ala Leu
290 295 300
Ala Gln Gln Gln Ala Val Ile Arg Gly Phe Thr Tyr Tyr Lys Ala Gly
305 310 315 320
Lys Gln Glu Val Thr Glu Ala Val Ala Asp Asn Thr Leu Gln Gly Thr
325 330 335
Ser Trp Leu Glu Gln Leu Pro Pro Lys Val Glu Gly Arg Ser Asn Ser
340 345 350
Ala Glu Pro Asn Ser Ala Glu Gln Asp Glu Ala Glu Pro Arg Ser Ser
355 360 365
Glu Arg Val Asp Leu Ala Ser Gly Thr Pro Thr Ser Ile Pro Ala Thr
370 375 380
Thr Thr Thr Ala Thr Thr Thr Pro Thr Pro Thr Thr Ser Leu Leu Pro
385 390 395 400
Thr Glu Pro Pro Ser Gly Pro Glu Val Ser Ser Gln Gly Arg Glu Ala
405 410 415
Ser Cys Glu Gly Thr Leu Arg Ala Val Asp Pro Pro Val Arg His His
420 425 430
Ser Tyr Gly Arg His Glu Gly Ala Trp Met Lys Asp Pro Ala Ala Arg
435 440 445
Asp Asp Arg Ile Tyr Val Thr Asn Tyr Tyr Tyr Gly Asn Ser Leu Val
450 455 460
Glu Phe Arg Asn Leu Glu Asn Phe Lys Gln Gly Arg Trp Ser Asn Met
465 470 475 480
Tyr Lys Leu Pro Tyr Asn Trp Ile Gly Thr Gly His Val Val Tyr Gln
485 490 495
Gly Ala Phe Tyr Tyr Asn Arg Ala Phe Thr Lys Asn Ile Ile Lys Tyr
500 505 510
Asp Leu Arg Gln Arg Phe Val Ala Ser Trp Ala Leu Leu Pro Asp Val
515 520 525
Val Tyr Glu Asp Thr Thr Pro Trp Lys Trp Arg Gly His Ser Asp Ile
530 535 540
Asp Phe Ala Val Asp Glu Ser Gly Leu Trp Val Ile Tyr Pro Ala Val
545 550 555 560

Asp Asp Arg Asp Glu Ala Gln Pro Glu Val Ile Val Leu Ser Arg Leu
565 570 575
Asp Pro Gly Asp Leu Ser Val His Arg Glu Thr Thr Trp Lys Thr Arg
580 585 590
Leu Arg Arg Asn Ser Tyr Gly Asn Cys Phe Leu Val Cys Gly Ile Leu
595 600 605
Tyr Ala Val Asp Thr Tyr Asn Gln Gln Glu Gly Gln Val Ala Tyr Ala
610 615 620
Phe Asp Thr His Thr Gly Thr Asp Ala Arg Pro Gln Leu Pro Phe Leu
625 630 635 640
Asn Glu His Ala Tyr Thr Thr Gln Ile Asp Tyr Asn Pro Lys Glu Arg
645 650 655
Val Leu Tyr Ala Trp Asp Asn Gly His Gln Leu Thr Tyr Thr Leu His
660 665 670
Phe Val Val
675

<210> 268
<211> 1909
<212> DNA
<213> Homo sapiens

<400> 268
gacacctttt aaaatgcaga actaactgag gcatttcagt aactttgctt tcaaatcaat 60
aaagtcaaat gtatggaaac attttgtgcc ctactctcca taccctgtgt actcaaattc 120
tctactgtat gaattatgct ttaagtagaa ttcagtgcca aggagaactt ggtgaaataa 180
attattttaa tttttttttt atcctttaca aagccatgga ttttatttgg ttgatgtgtg 240
ctctgtacac aagccatttc aataggatgg agctgttaat tattttccaa agagtaatag 300
acatgcaaaa gtttcaataa aaactgggcc attaacaaat aaattaataa actaataagc 360
attcccttct aggtttttgc caaactgcct atccaataac aaatttgaga atcgttgaaa 420
aagctagtta tatttcagag aaatgatttt cattattgaa actgttctcc ctagcaggcc 480
attttccctt tttcctggga gtttagcaag tttaggagag aatagtcatg aaaagaaagg 540
gaagaaaggg gagaagggaa gaggttaaaa agtaagtgct cagacctatg aacgtaatcc 600
ctttgctaga aatatttaag agcagctcag cttggttgaa actgagtttt gtcatcttcc 660
atatttgcag gaaggtattt tctgacttgc aatgcagcta gatgtaaaat tttattttat 720
catcctagaa agccttgact agaaaaatga ataaatattg agggtttcct gtccatatct 780
ggcttgcatg tgccagaaag cagagaatag aaaatgtaat ctccaacatc caagcatcga 840
aacccaaggg gtaggcaatt ctatgtaggt tttggacatg aagtttggtg catcttggtt 900
tatgctggct caactgctat taaacctctc tggcttatag tctcttcatt ctattagaca 960
agcacgtatc gaacacttgc ttcgcacaag gctctttagt taacaattta gcagctactg 1020
tttgtgttaa acacactttt caccaaatag gttctgaggc aaacgagagc aatgactatt 1080
taaagaaagg ctttcccagc atcacttaca catcccaaaa ctaaaaagat caactcttcc 1140
aactgagaaa agactcctgg ctttgaatgg aaacttacag cagagagtca caggccacgg 1200
caacaacaac gacaacaaca aacatttgga atattattct caactcacgt tttaataata 1260
catcttaatt atttttctag tagagaaact acaaatcagc ctcttcaaca tttatataca 1320
gtttaataag cctcttgcaa gttacttgtt ctctcacctg aggtattttt ttcctcccca 1380
ccttgcccct gttcctccct tcctcttctc cctttgcaag aggaaatatt taacatattt 1440
gggtccaact tcaataatgt aataattaat acattaaaag catttaactt cctttctaga 1500
aaaatgcaca ggctaaggca tagacaaaac aaagagaaat gctgagaaat ttgccactgg 1560
agacaagcaa tctgaataaa tatttgccaa aagttctttt tatgtcatat agtgtcagga 1620
tttgaaggag ctattttttt taatgttgca actagcaact catcttcgga agacacagcc 1680
aggagaatga agtagaagtg aaaggtttat aaatccattt gtaagcattt atcccatata 1740
ttttaaattc aagaaaaatt gtgtttatct ttagaatttt gtattcaata ctttatgtac 1800
tatgtgactc atgcttctgg ataaataaag caccaaatat gtatctgtaa ccacaatcac 1860
acatattata ttaaatatat atctatataa caaaaaaaaa aaaaaaaaa 1909

<210> 269
<211> 83
<212> PRT
<213> Homo sapiens

<400> 269
Met Tyr Gly Asn Ile Leu Cys Pro Thr Leu His Thr Leu Cys Thr Gln
1 5 10 15
Ile Leu Tyr Cys Met Asn Tyr Ala Leu Ser Arg Ile Gln Cys Gln Gly
20 25 30
Glu Leu Gly Glu Ile Asn Tyr Phe Asn Phe Phe Phe Ile Leu Tyr Lys
35 40 45
Ala Met Asp Phe Ile Trp Leu Met Cys Ala Leu Tyr Thr Ser His Phe
50 55 60
Asn Arg Met Glu Leu Leu Ile Ile Phe Gln Arg Val Ile Asp Met Gln
65 70 75 80
Lys Phe Gln

<210> 270
<211> 1720
<212> DNA
<213> Homo sapiens

<400> 270
gactgcagat gaaattagta actggtgggg tcgtggggtg tgaatggtgg gcgggagcag 60
ctatgtcagt tggtgtgttt ctgcttatgt tagggtaatt gggcacggcc tttgtgtaac 120
tggtgaatat ctctgaacct gggcatgaaa cagagagatg tcctaactct gggtgagagg 180
aatcctcatt tttctctgcc ctctcactgt ggcatcctaa gaaaaaagtt ttgggttcct 240
gcagcatgaa ggagagctct gctcccagaa tttgggagct ccagatttct tccagggtgt 300
ggaggcatca atatatcagt ctgggaaagg ggttcctggg ccactccagg agctgagttg 360
ggtggaaggt gctgagagtg tgggtggggg ccacttctga gcacccatgt ggcacccact 420
gctggtccct gtttgtggct gggcactcag gaaaatgttt ttggtgctaa gagtaaaaag 480
ccaaccaaca aacacatctc tttttctgt ctattcactg gaaagtaaaa gcagtctggg 540
cgcaggctgg ggacccagat ggaattcaaa cttatgcctg ctctcaaggt gctcacggtt 600
gctgataaac agctggataa aatgaagagt ctatgagtga gggatgcaga gccagggaag 660
gctggtggag tgatgccacc agcacagggg tatgagtttg cagctgccaa ggggccaagg 720
gatgagctgg ggccctcctt cccaatggca tctcccccctg gtctggaact gaagacactg 780
agcaatggtc cccaagcccc aaggagatca gctcccctgg gcccagtggc cccaaccagg 840
gagggtgtgg agaatgcctg cttctcctca gaggagcatg agacccattt ccagaaccct 900
gggaacacga gactgggcag ctcacccagt cccccctgggg gtgtctcctc actgccccga 960
tcccagcggg atgatctgtc ccttcattca gaggaggggc cagccctgga gcccgtgagc 1020
cgccccggtgg attatggctt tgtttccgcc ctcgttttcc tggtgagtgg gattcttctg 1080
gtggtgacag catacgccat cccccgtgag gctcgagtca atccggacac agtgacagcg 1140
cgggagatgg aacgactgga gatgtactac gcccgcctag gctcccacct ggacaggtgc 1200
atcatcgcag gcctcgggct gctcacggtg ggcggcatgc tcttgtcggt gctgctcatg 1260
gtctccctgt gcaagggcga gctgtaccgc cggaggacct tcgtccccgg caagggctcc 1320
aggaagacct acggctccat taacctgcgc atgagacagc tcaatgggga tgggggccag 1380
gccctggtgg agaatgaagt tgtccaggtc tcagagacta gccacaccct ccagaggtct 1440
taagaactag cccaccttat ctggctgctt tagctccagt gctacaaggt ccacccccctg 1500
ctcccgccca cctgacccct gccaaggccc tggggtttta aactgagctc acatagggcc 1560
ttgtggaaga agtactgggt gctggaggga gagctcgggg cccagcccat gccccacacg 1620
ggcaagcagc ccactgatct gttttgtagc tgaggttttg catacggttt tgtttggagg 1680
atggcttctg ctgctaaaaa tacaaaagtt tggaaaccgc 1720

<210> 271
<211> 256
<212> PRT
<213> Homo sapiens

<400> 271
Met Pro Pro Ala Gln Gly Tyr Glu Phe Ala Ala Ala Lys Gly Pro Arg
1 5 10 15
Asp Glu Leu Gly Pro Ser Phe Pro Met Ala Ser Pro Pro Gly Leu Glu
20 25 30
Leu Lys Thr Leu Ser Asn Gly Pro Gln Ala Pro Arg Arg Ser Ala Pro

```
        35                  40                  45
Leu Gly Pro Val Ala Pro Thr Arg Glu Gly Val Glu Asn Ala Cys Phe
    50                  55                  60
Ser Ser Glu Glu His Glu Thr His Phe Gln Asn Pro Gly Asn Thr Arg
65                  70                  75                  80
Leu Gly Ser Ser Pro Ser Pro Pro Gly Gly Val Ser Ser Leu Pro Arg
                85                  90                  95
Ser Gln Arg Asp Asp Leu Ser Leu His Ser Glu Glu Gly Pro Ala Leu
            100                 105                 110
Glu Pro Val Ser Arg Pro Val Asp Tyr Gly Phe Val Ser Ala Leu Val
        115                 120                 125
Phe Leu Val Ser Gly Ile Leu Leu Val Val Thr Ala Tyr Ala Ile Pro
    130                 135                 140
Arg Glu Ala Arg Val Asn Pro Asp Thr Val Thr Ala Arg Glu Met Glu
145                 150                 155                 160
Arg Leu Glu Met Tyr Tyr Ala Arg Leu Gly Ser His Leu Asp Arg Cys
                165                 170                 175
Ile Ile Ala Gly Leu Gly Leu Leu Thr Val Gly Gly Met Leu Leu Ser
            180                 185                 190
Val Leu Leu Met Val Ser Leu Cys Lys Gly Glu Leu Tyr Arg Arg Arg
        195                 200                 205
Thr Phe Val Pro Gly Lys Gly Ser Arg Lys Thr Tyr Gly Ser Ile Asn
    210                 215                 220
Leu Arg Met Arg Gln Leu Asn Gly Asp Gly Gly Gln Ala Leu Val Glu
225                 230                 235                 240
Asn Glu Val Val Gln Val Ser Glu Thr Ser His Thr Leu Gln Arg Ser
                245                 250                 255
```

<210> 272
<211> 1111
<212> DNA
<213> Homo sapiens

<400> 272

```
ccgcgcgctc gccccgccgc tcctgctgca gccccaggcc cctcgccgcc gccaccatgg      60
acgccatcaa gaagaagatg cagatgctga agctcgacaa ggagaacgcc ttggatcgag     120
ctgagcaggc ggaggccgac aagaaggcgg cggaagacag gagcaagcag ctggaagatg     180
agctggtgtc actgcaaaag aaactcaagg gcaccgaaga tgaactggac aaatactctg     240
aggctctcaa agatgcccag gagaagctgg agctggcaga gaaaaaggcc accgatgctg     300
aagccgacgt agcttctctg aacagacgca tccagctggt tgaggaagag ttggatcgtg     360
cccaggagcg tctggcaaca gctttgcaga agctggagga agctgagaag gcagcagatg     420
agagtgagag aggcatgaaa gtcattgaga gtcgagccca aaaagatgaa gaaaaaatgg     480
aaattcagga gatccaactg aaagaggcca agcacattgc tgaagatgcc gaccgcaaat     540
acgaagaggt ggcccgtaag ctggtcatca ttgagagcga cctggaacgt gcagaggagc     600
gggctgagct ctcagaaggc aaatgtgccg agcttgaaga agaattgaaa actgtgacga     660
acaacttgaa gtcactggag gctcaggctg agaagtactc gcagaaggaa gacagatatg     720
aggaagagat caaggtcctt tccgacaagc tgaaggaggc tgagactcgg gctgagtttg     780
cggagaggtc agtaactaaa ttggagaaaa gcattgatga cttagaagac gagctgtacg     840
ctcagaaact gaagtacaaa gccatcagcg aggagctgga ccacgctctc aacgatatga     900
cttccatata agtttctttg cttcacttct cccaagactc cctcgtcgag ctggatgtcc     960
cacctctctg agctctgcat ttgtctattc tccagctgac cctggttctc tctcttagca    1020
tcctgcctta gagccaggca cacactgtgc tttctattgt acagaagctc ttcgtttcag    1080
tgtcaaataa acactgtgta agctaaaaaa a                                   1111
```

<210> 273
<211> 284
<212> PRT
<213> Homo sapiens

<400> 273

```
Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
```

1 5 10 15
Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
20 25 30
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
35 40 45
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
50 55 60
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
65 70 75 80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
85 90 95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys
100 105 110
Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys
115 120 125
Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln
130 135 140
Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg
145 150 155 160
Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu
165 170 175
Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu
180 185 190
Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu
195 200 205
Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu
210 215 220
Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu
225 230 235 240
Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu
245 250 255
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu
260 265 270
Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile
275 280

<210> 274
<211> 2032
<212> DNA
<213> Homo sapiens

<400> 274
caccccgcag cccggcctcg gcctccgccg cttgttgtcg cgccccgccc gcgagcccgc 60
cccgcacgtc ccccgccggc ggccaccatg agcacaggcc tgcggtacaa gagcaagctg 120
gcgaccccag aggacaagca ggacattgac aagcagtacg tgggcttcgc cacactgccc 180
aaccaggtgc accgcaagtc ggtgaagaaa ggctttgact tcacactcat ggtggctggt 240
gagtcaggcc tggggaagtc cacactggtc cacagcctct tcctgacaga cttgtacaag 300
gaccggaagc tgctcagtgc tgaggagcgc atcagccaga cggtagagat tctaaaacac 360
acggtggaca ttgaggagaa gggagtcaag ctgaagctca ccatcgtgga cacgccggga 420
ttcggggacg ctgtcaacaa caccgagtgc tggaagccca tcaccgacta tgtggaccag 480
cagtttgagc agtacttccg tgatgagagc ggcctcaacc gaaagaacat ccaagacaac 540
cgagtgcact gctgcctata cttcatctcc cccttcgggc atgggctgcg gccagtggat 600
gtgggtttca tgaaggcatt gcatgagaag gtcaacatcg tgcctctcat cgccaaagct 660
gactgtcttg tccccagtga gatccggaag ctgaaggagc ggatccggga ggagattgac 720
aagtttggga tccatgtata ccagttccct gagtgtgact cggacgagga tgaggacttc 780
aagcagcagg accgggaact gaaggagagc gcgcccttcg ccgttatagg cagcaacacg 840
gtggtggagg ccaaggggca gcgggtccgg ggccgactgt acccctgggg gatcgtggag 900
gtggagaacc aggcgcattg cgacttcgtg aagctgcgca acatgctcat ccgcacgcat 960
atgcacgacc tcaaggacgt gacgtgcgac gtgcactacg agaactaccg cgcgcactgc 1020
atccagcaga tgaccagcaa actgacccag gacagccgca tggagagccc catccccgatc 1080
ctgccgctgc ccaccccgga cgccgagact gagaagctta tcaggatgaa ggatgaggaa 1140

```
ctgaggcgca tgcaggagat gctgcagagg atgaagcagc agatgcagga ccagtgacgc      1200
tcgccgcgga cacaccgtcc gtctccggga cgccctcgca cccctggaca ccagaccgga      1260
ctgttcccga cccggagacg cggggccaca gcccccagct gaccctaatt tattctcagc      1320
accacccccct cccaggtcat tgtgtctgtt tccgaggggc ctggaccgta gcccccgccc     1380
agctggccct ctctgacctt gggggatcag gagcgaagtt gggcgggact tcagagatcc      1440
gcctcccttg cccttccccc gcccccggac ggtcacagca cccaaaccgc aggccctgct      1500
ctggcaggca ggcaaagcta ggcagaagag gattcccagg atcctgggtc tgttccctgc      1560
cccagtgctg cagaacggac ttgggagccc tcctttgcct gctcccgcgg gtcacccagc      1620
gagtgctgag accccatttt ctgtcgaggc gggccgagtc ttcccttatc cccagacgcc      1680
tagcgggcag ggttgggctg aatcaaatgg gagccctcca gacataagga ggccagaggc      1740
tgcaaggagc ggggtcgtga ccgcttacac cccttctcca cagcccggcc cgacctggag      1800
ggcccccggg gcactgggcg gtgagccacc tcctggcaac tctcggtgcc gtcccctgcc      1860
ctcgctcgag gcctcttctc cccagcaccg ctgtggtgtg ccgggatcct gagcctaggc      1920
ctcccgatgt tcccaccccgc atgatccctt cccgccacac gatgctccgt tttcttccgt     1980
tgtgaatgcc gcgtcctgtc ctggtgacag gagaacaatg ttggtgaacg tc              2032
```

<210> 275
<211> 369
<212> PRT
<213> Homo sapiens

<400> 275

```
Met Ser Thr Gly Leu Arg Tyr Lys Ser Lys Leu Ala Thr Pro Glu Asp
1               5                   10                  15
Lys Gln Asp Ile Asp Lys Gln Tyr Val Gly Phe Ala Thr Leu Pro Asn
            20                  25                  30
Gln Val His Arg Lys Ser Val Lys Lys Gly Phe Asp Phe Thr Leu Met
        35                  40                  45
Val Ala Gly Glu Ser Gly Leu Gly Lys Ser Thr Leu Val His Ser Leu
    50                  55                  60
Phe Leu Thr Asp Leu Tyr Lys Asp Arg Lys Leu Leu Ser Ala Glu Glu
65                  70                  75                  80
Arg Ile Ser Gln Thr Val Glu Ile Leu Lys His Thr Val Asp Ile Glu
                85                  90                  95
Glu Lys Gly Val Lys Leu Lys Leu Thr Ile Val Asp Thr Pro Gly Phe
            100                 105                 110
Gly Asp Ala Val Asn Asn Thr Glu Cys Trp Lys Pro Ile Thr Asp Tyr
        115                 120                 125
Val Asp Gln Gln Phe Glu Gln Tyr Phe Arg Asp Glu Ser Gly Leu Asn
    130                 135                 140
Arg Lys Asn Ile Gln Asp Asn Arg Val His Cys Cys Leu Tyr Phe Ile
145                 150                 155                 160
Ser Pro Phe Gly His Gly Leu Arg Pro Val Asp Val Gly Phe Met Lys
                165                 170                 175
Ala Leu His Glu Lys Val Asn Ile Val Pro Leu Ile Ala Lys Ala Asp
            180                 185                 190
Cys Leu Val Pro Ser Glu Ile Arg Lys Leu Lys Glu Arg Ile Arg Glu
        195                 200                 205
Glu Ile Asp Lys Phe Gly Ile His Val Tyr Gln Phe Pro Glu Cys Asp
    210                 215                 220
Ser Asp Glu Asp Glu Asp Phe Lys Gln Gln Asp Arg Glu Leu Lys Glu
225                 230                 235                 240
Ser Ala Pro Phe Ala Val Ile Gly Ser Asn Thr Val Val Glu Ala Lys
                245                 250                 255
Gly Gln Arg Val Arg Gly Arg Leu Tyr Pro Trp Gly Ile Val Glu Val
            260                 265                 270
Glu Asn Gln Ala His Cys Asp Phe Val Lys Leu Arg Asn Met Leu Ile
        275                 280                 285
Arg Thr His Met His Asp Leu Lys Asp Val Thr Cys Asp Val His Tyr
    290                 295                 300
Glu Asn Tyr Arg Ala His Cys Ile Gln Gln Met Thr Ser Lys Leu Thr
```

305 310 315 320
Gln Asp Ser Arg Met Glu Ser Pro Ile Pro Ile Leu Pro Leu Pro Thr
325 330 335
Pro Asp Ala Glu Thr Glu Lys Leu Ile Arg Met Lys Asp Glu Glu Leu
340 345 350
Arg Arg Met Gln Glu Met Leu Gln Arg Met Lys Gln Gln Met Gln Asp
355 360 365
Gln

<210> 276
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 276
tgcagactga tatggattca ccactgctaa cacctcctgg ttggaactac aggaatagaa 60
ctggaaaggg aaaaaaggca gcattcacca catcccaatc ctgaatccaa gagtctaaga 120
tagtccccca ctcctatctc aggcttagag gattagatta atctcctgga gggaagactc 180
ttccttgaaa catttttttt tatctgcctg tagctattgg gataattcgg gaaatccaca 240
gggacagttc aagtcatctt tgtcctctac tttctgttgc actctcagcc ttgttctctt 300
tttagaaact gcatggtaac tattatatag ctaaagaaga gcattctgac ctctgccctg 360
ggacttcctg gatcctcctc ttcttataaa tacaagggca gagctggtat cccggggagc 420
caggaagcag tgagcccagg agtcctcggc cagccctgcc tgcccaccag gaggatgaag 480
gtctccgtgg ctgccctctc ctgcctcatg cttgttgctg tccttggatc ccaggcccag 540
ttcacaaatg atgcagagac agagttaatg atgtcaaagc ttccactgga aaatccagta 600
gttctgaaca gctttcactt tgctgctgac tgctgcacct cctacatctc acaaagcatc 660
ccgtgttcac tcatgaaaag ttattttgaa acgagcagcg agtgctccaa gccaggtgtc 720
atattcctca ccaagaaggg gcggcaagtc tgtgccaaac ccagtggtcc gggagttcag 780
gattgcatga aaaagctgaa gccctactca atataataat aaagagacaa aagaggccag 840
ccacccacct ccaacacctc ctgagcctct gaagctccca ccaggccagc tctcctccca 900
caacagcttc ccacagcatg aagatctccg tggctgccat tcccttcttc ctcctcatca 960
ccatcgccct agggaccaag actgaatcct cctcacgggg accttaccac ccctcagagt 1020
gctgcttcac ctacactacc tacaagatcc cgcgtcagcg gattatggat tactatgaga 1080
ccaacagcca gtgctccaag cccggaattg tcttcatcac caaaaggggc cattccgtct 1140
gtaccaaccc cagtgacaag tgggtccagg actatatcaa ggacatgaag gagaactgag 1200
tgacccagaa ggggtggcga aggcacagct cagagacata aagagaagat gccaaggccc 1260
cctcctccac ccaccgctaa ctctcagccc cagtcacccct cttggagctt ccctgctttg 1320
aattaaagac cactcatgct cttc 1344

<210> 277
<211> 93
<212> PRT
<213> Homo sapiens

<400> 277
Met Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile
1 5 10 15
Ala Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro
20 25 30
Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg
35 40 45
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
50 55 60
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp
65 70 75 80
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
85 90

<210> 278
<211> 1344

<212> DNA
<213> Homo sapiens

<400> 278
tgcagactga tatggattca ccactgctaa cacctcctgg ttggaactac aggaatagaa 60
ctggaaaggg aaaaaaggca gcattcacca catcccaatc ctgaatccaa gagtctaaga 120
tagtccccca ctcctatctc aggcttagag gattagatta atctcctgga gggaagactc 180
ttccttgaaa cattttttttt tatctgcctg tagctattgg gataattcgg gaaatccaca 240
gggacagttc aagtcatctt tgtcctctac tttctgttgc actctcagcc ttgttctctt 300
tttagaaact gcatggtaac tattatatag ctaaagaaga gcattctgac ctctgccctg 360
ggacttcctg gatcctcctc ttcttataaa tacaagggca gagctggtat cccggggagc 420
caggaagcag tgagcccagg agtcctcggc cagccctgcc tgcccaccag gaggatgaag 480
gtctccgtgg ctgccctctc ctgcctcatg cttgttgctg tccttggatc ccaggcccag 540
ttcacaaatg atgcagagac agagttaatg atgtcaaagc ttccactgga aaatccagta 600
gttctgaaca gctttcactt tgctgctgac tgctgcacct cctacatctc acaaagcatc 660
ccgtgttcac tcatgaaaag ttattttgaa acgagcagcg agtgctccaa gccaggtgtc 720
atattcctca ccaagaaggg gcggcaagtc tgtgccaaac ccagtggtcc gggagttcag 780
gattgcatga aaaagctgaa gccctactca atataataat aaagagacaa aagaggccag 840
ccacccacct ccaacacctc ctgagcctct gaagctccca ccaggccagc tctcctccca 900
caacagcttc ccacagcatg aagatctccg tggctgccat tcccttcttc ctcctcatca 960
ccatcgccct agggaccaag actgaatcct cctcacgggg accttaccac ccctcagagt 1020
gctgcttcac ctacactacc tacaagatcc cgcgtcagcg gattatggat tactatgaga 1080
ccaacagcca gtgctccaag cccggaattg tcttcatcac caaaagggc cattccgtct 1140
gtaccaaccc cagtgacaag tgggtccagg actatatcaa ggacatgaag gagaactgag 1200
tgacccagaa ggggtggcga aggcacagct cagagacata aagagaagat gccaaggccc 1260
cctcctccac ccaccgctaa ctctcagccc cagtcaccct cttggagctt ccctgctttg 1320
aattaaagac cactcatgct cttc 1344

<210> 279
<211> 93
<212> PRT
<213> Homo sapiens

<400> 279
Met Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile
1 5 10 15
Ala Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro
20 25 30
Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg
35 40 45
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
50 55 60
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp
65 70 75 80
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
85 90

<210> 280
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 280
tgcagactga tatggattca ccactgctaa cacctcctgg ttggaactac aggaatagaa 60
ctggaaaggg aaaaaaggca gcattcacca catcccaatc ctgaatccaa gagtctaaga 120
tagtccccca ctcctatctc aggcttagag gattagatta atctcctgga gggaagactc 180
ttccttgaaa cattttttttt tatctgcctg tagctattgg gataattcgg gaaatccaca 240
gggacagttc aagtcatctt tgtcctctac tttctgttgc actctcagcc ttgttctctt 300
tttagaaact gcatggtaac tattatatag ctaaagaaga gcattctgac ctctgccctg 360
ggacttcctg gatcctcctc ttcttataaa tacaagggca gagctggtat cccggggagc 420
caggaagcag tgagcccagg agtcctcggc cagccctgcc tgcccaccag gaggatgaag 480

```
gtctccgtgg ctgccctctc ctgcctcatg cttgttgctg tccttggatc ccaggcccag    540
ttcacaaatg atgcagagac agagttaatg atgtcaaagc ttccactgga aaatccagta    600
gttctgaaca gctttcactt tgctgctgac tgctgcacct cctacatctc acaaagcatc    660
ccgtgttcac tcatgaaaag ttattttgaa acgagcagcg agtgctccaa gccaggtgtc    720
atattcctca ccaagaaggg gcggcaagtc tgtgccaaac ccagtggtcc gggagttcag    780
gattgcatga aaaagctgaa gccctactca atataataat aaagagacaa aagaggccag    840
ccacccacct ccaacacctc ctgagcctct gaagctccca ccaggccagc tctcctccca    900
caacagcttc ccacagcatg aagatctccg tggctgccat tcccttcttc ctcctcatca    960
ccatcgccct agggaccaag actgaatcct cctcacgggg accttaccac ccctcagagt   1020
gctgcttcac ctacactacc tacaagatcc cgcgtcagcg gattatggat tactatgaga   1080
ccaacagcca gtgctccaag cccggaattg tcttcatcac caaaaggggc cattccgtct   1140
gtaccaaccc cagtgacaag tgggtccagg actatatcaa ggacatgaag gagaactgag   1200
tgacccagaa ggggtggcga aggcacagct cagagacata aagagaagat gccaaggccc   1260
cctcctccac ccaccgctaa ctctcagccc cagtcaccct cttggagctt ccctgctttg   1320
aattaaagac cactcatgct cttc                                          1344
```

<210> 281
<211> 93
<212> PRT
<213> Homo sapiens

<400> 281

```
Met Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile
1               5                   10                  15
Ala Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro
            20                  25                  30
Ser Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg
        35                  40                  45
Ile Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile
    50                  55                  60
Val Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp
65                  70                  75                  80
Lys Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
                85                  90
```

<210> 282
<211> 2750
<212> DNA
<213> Homo sapiens

<400> 282

```
tacgatggca acacctcccg caaggccccc aatgagttcc tgacctcggt ggtggagctc     60
atcggcgccg ccaaggccct gctggcgtgg ctggaccgat tgctatttta tgtgtcactt    120
gagagaaaac agttaaataa aaactaattt aatacaaaat ttagctgggc ttggtggcac    180
atgcctgtaa tcccagctac tcgggaggct gaagcaggag agttgcttga acctgggagg    240
cgtagattgc agtgagccaa gatcatccca ctgcactcca gcctgggcga cagagtgaga    300
cacagtctca aacaaaacaa aacaaaaagg aatttagagt agcccatggg gtagctatgc    360
ttaccaacat ccagtgggat ccccgtggat tctccctacc cctttttaag aggattgttg    420
ctaccttcta gggctccgtt tacagggatc actgatttct cagtcacgaa gaacaaaatt    480
atccagcttt gcttggacct gaccactaca gtccagaagg attgctttgt agcggaaatg    540
gaggataaag ttttaactgt ggtcaaggtt ttaaatggca tctgtgacaa aacaatccga    600
tctaccacag atcctgtgat gagccagtgt gcatgtctgg aggaagttca cttaccaaac    660
attaaacctg gggaaggcct gggcatgtac atcaaatcaa cctatgatgg gttacacgtg    720
attactggaa ccacagaaaa ttctcctgca gacagatctc agaagattca tgctggtgac    780
gaagtcattc aagttaatca gcaaactgtg gtgggatggc agctgaaaaa tctggtgaag    840
aaattgagag agaatcccac cggagttgtg ttactgctta agaagcgccc caccgggtct    900
ttcaacttta ctcctgctcc cctgaaaaac ctacggtgga agccacctct tgtacagacc    960
tcacctccac ccgcgacaac ccagtcccct gaaagcacta tggatacctc actgaagaag   1020
gagaagtcag ccatcctgga tctttatatt cctcctccgc ctgctgttcc ctactctccc   1080
cgggatgaga atggcagttt tgtttatgga gggtccagta agtgcaaaca accattgcct   1140
ggtcctaagg gttcagagtc cccgaattcc ttcttggacc aggaaagccg gagacgaaga   1200
```

```
ttcaccattg cagactcgga tcagttgcct gggtactcgg tggaaaccaa cattctgccc    1260
acaaaaatga gagagaaaac accatcttat grcaagccac ggcctttgtc catgcctgct    1320
gatgggaact ggatggggat tgtggaccct tttgccagac ctcgaggtca tggcaggaaa    1380
ggggaggatg cccttgccg gtatttcagt aacgagcgga ttcctccgat cattgaagag    1440
agctcctctc cccataccg gttctccaga cccacgaccg agcggcatct ggtccggggt    1500
gcggactaca tccgaggaag caggtgctac atcaactcag atctccacag cagcgccacg    1560
attccattcc aggaggaagg gaccaaaaag aaatctggct cctcagctac gaagtcctcg    1620
tccacagaac cgtccctcct ggtcagctgg tttacgcgcc tcaaactgtt gactcactga    1680
gagggaccct gctcaggcca cctgcctggc tcctgcccca agtgccttgc ttttacagtg    1740
gacagcctct tctcgtttcg gcctcagtat tatgtaggga ccttatgcaa tttctttttc    1800
ttttgaaaag ttatctactg cccttcttgg aagtttgcag gattggatgg gaacaaattc    1860
agaggatctt aggtgctggc ttgtggagac aaaaggaggg aaatgggtag agcctgtttg    1920
tcttgcttcc ccagagatag aatgtgaaga cacgcgctag aaatcgcagt cctggccaga    1980
gacgttatgg tcattgtgag ggactggtgg cattgttcct ttttgagggg ctggggggac    2040
tcaaattggt ggctgttttc acacagatgt gttggtttgt ggtccaactt ctttatctga    2100
aaaagccagt gagaaaacat ttttgatttg atttttctaa actatctacc atattttaag    2160
tgtagcagct ttgactttgc aataacgtgg caagtatctg atttctcctt tgaggcagag    2220
gtttaagtgt aggcctgtta cacttgtttg ataccttttt catgacagtc tcagtataga    2280
tcagttggta cagaaataca tgaacacatt ttgatagggc ttatttcaca caaagaagtt    2340
tatggttatt tgtgtggggt ggtgttgtta tatattattg tctttaaggg aaaagaagct    2400
ataagattcg ctgacagcca aagtatcatt tagaaaagtg aagaacaaga tttaggttga    2460
tgaaagatac atgagtttgc atttgacct gttcagtgtc tgtcttccag cacggtgtgt    2520
acacttcttc aaaattgtac acagtttgct aattagaaat atcttggaaa gcctcatggt    2580
cactaatttt caactagcat caggtatttt gaaaacgtgt gtctggatat taactcttgt    2640
ttaaactgaa tgtatgatat tttgttagaa tggaaaagta ctatcttgtt aatttaagta    2700
ttttaaatat agttgtatat ttttcttact cttaaaaaaa aaaaaaaaaa               2750
```

<210> 283
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(380)
<223> Xaa = Any Amino Acid

<400> 283

```
Met Glu Asp Lys Val Leu Thr Val Val Lys Val Leu Asn Gly Ile Cys
 1               5                  10                  15
Asp Lys Thr Ile Arg Ser Thr Thr Asp Pro Val Met Ser Gln Cys Ala
            20                  25                  30
Cys Leu Glu Glu Val His Leu Pro Asn Ile Lys Pro Gly Glu Gly Leu
        35                  40                  45
Gly Met Tyr Ile Lys Ser Thr Tyr Asp Gly Leu His Val Ile Thr Gly
    50                  55                  60
Thr Thr Glu Asn Ser Pro Ala Asp Arg Ser Gln Lys Ile His Ala Gly
65                  70                  75                  80
Asp Glu Val Ile Gln Val Asn Gln Gln Thr Val Val Gly Trp Gln Leu
                85                  90                  95
Lys Asn Leu Val Lys Lys Leu Arg Glu Asn Pro Thr Gly Val Val Leu
            100                 105                 110
Leu Leu Lys Lys Arg Pro Thr Gly Ser Phe Asn Phe Thr Pro Ala Pro
        115                 120                 125
Leu Lys Asn Leu Arg Trp Lys Pro Pro Leu Val Gln Thr Ser Pro Pro
    130                 135                 140
Pro Ala Thr Thr Gln Ser Pro Glu Ser Thr Met Asp Thr Ser Leu Lys
145                 150                 155                 160
Lys Glu Lys Ser Ala Ile Leu Asp Leu Tyr Ile Pro Pro Pro Pro Ala
                165                 170                 175
Val Pro Tyr Ser Pro Arg Asp Glu Asn Gly Ser Phe Val Tyr Gly Gly
```

```
                180                     185                     190
Ser Ser Lys Cys Lys Gln Pro Leu Pro Gly Pro Lys Gly Ser Glu Ser
            195                     200                     205
Pro Asn Ser Phe Leu Asp Gln Glu Ser Arg Arg Arg Arg Phe Thr Ile
        210                     215                     220
Ala Asp Ser Asp Gln Leu Pro Gly Tyr Ser Val Glu Thr Asn Ile Leu
225                     230                     235                     240
Pro Thr Lys Met Arg Glu Lys Thr Pro Ser Tyr Xaa Lys Pro Arg Pro
                245                     250                     255
Leu Ser Met Pro Ala Asp Gly Asn Trp Met Gly Ile Val Asp Pro Phe
                260                     265                     270
Ala Arg Pro Arg Gly His Gly Arg Lys Gly Glu Asp Ala Leu Cys Arg
            275                     280                     285
Tyr Phe Ser Asn Glu Arg Ile Pro Pro Ile Ile Glu Glu Ser Ser Ser
        290                     295                     300
Pro Pro Tyr Arg Phe Ser Arg Pro Thr Thr Glu Arg His Leu Val Arg
305                     310                     315                     320
Gly Ala Asp Tyr Ile Arg Gly Ser Arg Cys Tyr Ile Asn Ser Asp Leu
                325                     330                     335
His Ser Ser Ala Thr Ile Pro Phe Gln Glu Glu Gly Thr Lys Lys Lys
                340                     345                     350
Ser Gly Ser Ser Ala Thr Lys Ser Ser Ser Thr Glu Pro Ser Leu Leu
            355                     360                     365
Val Ser Trp Phe Thr Arg Leu Lys Leu Leu Thr His
        370                     375                     380
```

<210> 284
<211> 1789
<212> DNA
<213> Homo sapiens

<400> 284

```
ggttcaggaa cctgctggtt ctgatacata aatcagacag cctctgctgc atgacacgaa      60
gcttgcttct gcctggcatc tgtgagcagc tgccaggctc cggccaggat cccttccttc     120
tcctcattgg ctgatggatc ccaaggggct cctctccttg accttcgtgc tgtttctctc     180
cctggctttt ggggcaagct acggaacagg tgggcgcatg atgaactgcc caaagattct     240
ccggcagttg ggaagcaaag tgctgctgcc cctgacatat gaaaggataa ataagagcat     300
gaacaaaagc atccacattg tcgtcacaat ggcaaaatca ctggagaaca gtgtcgagaa     360
caaaatagtg tctcttgatc catccgaagc aggccctcca cgttatctag gagatcgcta     420
caagttttat ctggagaatc tcaccctggg gatacgggaa agcaggaagg aggatgaggg     480
atggtacctt atgaccctgg agaaaaatgt ttcagttcag cgcttttgcc tgcagttgag     540
gctttatgag caggtctcca ctccagaaat taaagtttta aacaagaccc aggagaacgg     600
gacctgcacc ttgatactgg gctgcacagt ggagaagggg gaccatgtgg cttacagctg     660
gagtgaaaag gcgggcaccc acccactgaa cccagccaac agctcccacc tcctgtccct     720
caccctcggc ccccagcatg ctgacaatat ctacatctgc accgtgagca accctatcag     780
caacaattcc cagaccttca gcccgtggcc cggatgcagg acagacccct cagaaacaaa     840
accatgggca gtgtatgctg ggctgttagg gggtgtcatc atgattctca tcatggtggt     900
aatactacag ttgagaagaa gaggtaaaac gaaccattac cagacaacag tggaaaaaaa     960
aagccttacg atctatgccc aagtccagaa accaggtcct cttcagaaga aacttgactc    1020
cttcccagct caggaccctt gcaccaccat atatgttgct gccacagagc ctgtcccaga    1080
gtctgtccag gaaacaaatt ccatcacagt ctatgctagt gtgacacttc cagagagctg    1140
acaccagaga ccaacaaagg gactttctga aggaaaatgg aaaaaccaaa atgaacactg    1200
aacttggcca caggcccaag tttcctctgg cagacatgct gcacgtctgt acccttctca    1260
gatcaactcc ctggtgatgt ttcttccaca tacatctgtg aaatgaacaa ggaagtgagg    1320
cttcccaaga atttagcttg ctgtgcagtg gctgcaggcg cagaacagag cgttacttga    1380
taacagcgtt ccatctttgt gttgtagcag atgaaatgga cagtaatgtg agttcagact    1440
ttgggcatct tgctcttggc tggaactgat aataaaaatc agactgaaag ccaggacatc    1500
tgagtaccta tctcacacac tgaccaccag tcacaaagtc tggaaaagtt tacattttgg    1560
ctatctttac tttgttctgg gagctgatca tgataacctg cagacctgat caagcctctg    1620
tgcctcagtt tctctctcag gataaagagt gaatagaggc cgaagggtga atttcttatt    1680
atacataaaa cactctgata ttattgtata aaggaagcta agaatattat tttatttgca    1740
```

aaacccagaa gctaaaaagt caataaacag aaagaatgat tttgagaaa

<210> 285
<211> 335
<212> PRT
<213> Homo sapiens

<400> 285
Met Asp Pro Lys Gly Leu Leu Ser Leu Thr Phe Val Leu Phe Leu Ser
1 5 10 15
Leu Ala Phe Gly Ala Ser Tyr Gly Thr Gly Gly Arg Met Met Asn Cys
20 25 30
Pro Lys Ile Leu Arg Gln Leu Gly Ser Lys Val Leu Leu Pro Leu Thr
35 40 45
Tyr Glu Arg Ile Asn Lys Ser Met Asn Lys Ser Ile His Ile Val Val
50 55 60
Thr Met Ala Lys Ser Leu Glu Asn Ser Val Glu Asn Lys Ile Val Ser
65 70 75 80
Leu Asp Pro Ser Glu Ala Gly Pro Pro Arg Tyr Leu Gly Asp Arg Tyr
85 90 95
Lys Phe Tyr Leu Glu Asn Leu Thr Leu Gly Ile Arg Glu Ser Arg Lys
100 105 110
Glu Asp Glu Gly Trp Tyr Leu Met Thr Leu Glu Lys Asn Val Ser Val
115 120 125
Gln Arg Phe Cys Leu Gln Leu Arg Leu Tyr Glu Gln Val Ser Thr Pro
130 135 140
Glu Ile Lys Val Leu Asn Lys Thr Gln Glu Asn Gly Thr Cys Thr Leu
145 150 155 160
Ile Leu Gly Cys Thr Val Glu Lys Gly Asp His Val Ala Tyr Ser Trp
165 170 175
Ser Glu Lys Ala Gly Thr His Pro Leu Asn Pro Ala Asn Ser Ser His
180 185 190
Leu Leu Ser Leu Thr Leu Gly Pro Gln His Ala Asp Asn Ile Tyr Ile
195 200 205
Cys Thr Val Ser Asn Pro Ile Ser Asn Asn Ser Gln Thr Phe Ser Pro
210 215 220
Trp Pro Gly Cys Arg Thr Asp Pro Ser Glu Thr Lys Pro Trp Ala Val
225 230 235 240
Tyr Ala Gly Leu Leu Gly Gly Val Ile Met Ile Leu Ile Met Val Val
245 250 255
Ile Leu Gln Leu Arg Arg Arg Gly Lys Thr Asn His Tyr Gln Thr Thr
260 265 270
Val Glu Lys Lys Ser Leu Thr Ile Tyr Ala Gln Val Gln Lys Pro Gly
275 280 285
Pro Leu Gln Lys Lys Leu Asp Ser Phe Pro Ala Gln Asp Pro Cys Thr
290 295 300
Thr Ile Tyr Val Ala Ala Thr Glu Pro Val Pro Glu Ser Val Gln Glu
305 310 315 320
Thr Asn Ser Ile Thr Val Tyr Ala Ser Val Thr Leu Pro Glu Ser
325 330 335

<210> 286
<211> 305
<212> PRT
<213> Homo sapiens

<400> 286
Met Asp Pro Lys Gly Leu Leu Ser Leu Thr Phe Val Leu Phe Leu Ser
1 5 10 15
Leu Ala Phe Gly Ala Ser Tyr Gly Thr Gly Gly Arg Met Met Asn Cys
20 25 30

Pro Lys Ile Leu Arg Gln Leu Gly Ser Lys Val Leu Leu Pro Leu Thr
35 40 45
Tyr Glu Arg Ile Asn Lys Ser Met Asn Lys Ser Ile His Ile Val Val
50 55 60
Thr Met Ala Lys Ser Leu Glu Asn Ser Val Glu Asn Lys Ile Val Ser
65 70 75 80
Leu Asp Pro Ser Glu Ala Gly Pro Pro Arg Tyr Leu Gly Asp Arg Tyr
85 90 95
Lys Phe Tyr Leu Glu Asn Leu Thr Leu Gly Ile Arg Glu Ser Arg Lys
100 105 110
Glu Asp Glu Gly Trp Tyr Leu Met Thr Leu Glu Lys Asn Val Ser Val
115 120 125
Gln Arg Phe Cys Leu Gln Leu Arg Leu Tyr Glu Gln Val Ser Thr Pro
130 135 140
Glu Ile Lys Val Leu Asn Lys Thr Gln Glu Asn Gly Thr Cys Thr Leu
145 150 155 160
Ile Leu Gly Cys Thr Val Glu Lys Gly Asp His Val Ala Tyr Ser Trp
165 170 175
Ser Glu Lys Ala Gly Thr His Pro Leu Asn Pro Ala Asn Ser Ser His
180 185 190
Leu Leu Ser Leu Thr Leu Gly Pro Gln His Ala Asp Asn Ile Tyr Ile
195 200 205
Cys Thr Val Ser Asn Pro Ile Ser Asn Asn Ser Gln Thr Phe Ser Pro
210 215 220
Trp Pro Gly Cys Arg Thr Asp Pro Ser Gly Lys Thr Asn His Tyr Gln
225 230 235 240
Thr Thr Val Glu Lys Lys Ser Leu Thr Ile Tyr Ala Gln Val Gln Lys
245 250 255
Pro Gly Pro Leu Gln Lys Lys Leu Asp Ser Phe Pro Ala Gln Asp Pro
260 265 270
Cys Thr Thr Ile Tyr Val Ala Ala Thr Glu Pro Val Pro Glu Ser Val
275 280 285
Gln Glu Thr Asn Ser Ile Thr Val Tyr Ala Ser Val Thr Leu Pro Glu
290 295 300
Ser
305

<210> 287
<211> 298
<212> PRT
<213> Homo sapiens

<400> 287
Met Asp Pro Lys Gly Leu Leu Ser Leu Thr Phe Val Leu Phe Leu Ser
1 5 10 15
Leu Ala Phe Gly Ala Ser Tyr Gly Thr Gly Gly Arg Met Met Asn Cys
20 25 30
Pro Lys Ile Leu Arg Gln Leu Gly Ser Lys Val Leu Leu Pro Leu Thr
35 40 45
Tyr Glu Arg Ile Asn Lys Ser Met Asn Lys Ser Ile His Ile Val Val
50 55 60
Thr Met Ala Lys Ser Leu Glu Asn Ser Val Glu Asn Lys Ile Val Ser
65 70 75 80
Leu Asp Pro Ser Glu Ala Gly Pro Pro Arg Tyr Leu Gly Asp Arg Tyr
85 90 95
Lys Phe Tyr Leu Glu Asn Leu Thr Leu Gly Ile Arg Glu Ser Arg Lys
100 105 110
Glu Asp Glu Gly Trp Tyr Leu Met Thr Leu Glu Lys Asn Val Ser Val
115 120 125
Gln Arg Phe Cys Leu Gln Leu Arg Leu Tyr Glu Gln Val Ser Thr Pro
130 135 140

Glu Ile Lys Val Leu Asn Lys Thr Gln Glu Asn Gly Thr Cys Thr Leu
145 150 155 160
Ile Leu Gly Cys Thr Val Glu Lys Gly Asp His Val Ala Tyr Ser Trp
165 170 175
Ser Glu Lys Ala Gly Thr His Pro Leu Asn Pro Ala Asn Ser Ser His
180 185 190
Leu Leu Ser Leu Thr Leu Gly Pro Gln His Ala Asp Asn Ile Tyr Ile
195 200 205
Cys Thr Val Ser Asn Pro Ile Ser Asn Asn Ser Gln Thr Phe Ser Pro
210 215 220
Trp Pro Gly Cys Arg Thr Asp Pro Ser Glu Thr Lys Pro Trp Ala Val
225 230 235 240
Tyr Ala Gly Leu Leu Gly Gly Val Ile Met Ile Leu Ile Met Val Val
245 250 255
Ile Leu Gln Leu Arg Arg Arg Gly Lys Thr Asn His Tyr Gln Thr Thr
260 265 270
Val Glu Lys Lys Ser Leu Thr Ile Tyr Ala Gln Val Gln Lys Pro Gly
275 280 285
Asp Thr His His Gln Thr Ser Asp Leu Phe
290 295

<210> 288
<211> 3640
<212> DNA
<213> Homo sapiens

<400> 288
aggacgggac ggagccgggg cagccagaag aggtgggaaa agcggaggag gacgcccagg 60
aggaggcggc ggcggcggcc gggaagtgaa aggtctcgca aagttcagcg gcggctgcgg 120
gcgccgagcc ccgggctagc ggcagacgag cccgcagggc cgctccgcgg ggcagcgcag 180
ccaggccggc tatggtcccg gggctcccgc cgcccccag gtgcccggga cccgccaggc 240
cggtgcgcga gggtcacccc acctccccgc gcggtcccgg cccctggctc ccagctgccg 300
gcgaccgctg accgagcccg gcgccccagg aggaggaaga aaccagggcc ccgttccctc 360
ccgaggacgg cggcgcttca tcccgcagcc cagaggtctc ggctccctcc ggcacccgcc 420
cggcccggct gctcccggct cctcccggcc atggggagct gcgcgcggct gctgctgctc 480
tggggctgca cggtggtggc cgcaggactg agtggagtag ctggagtgag ttcccgctgt 540
gaaaaagcct gcaaccctcg gatgggaaat ttggctttgg ggcgaaaact ctgggcagac 600
accacctgcg gtcagaatgc taccgaactg tactgcttct acagtgagaa cacggatctg 660
acttgtcggc agcccaaatg tgacaagtgc aatgctgcct atcctcacct ggctcacctg 720
ccatctgcca tggcagactc atccttccgg tttcctcgca catggtggca gtctgcggag 780
gatgtgcaca gagaaaagat ccagttagac ctggaagctg aattctactt cactcaccta 840
attgtgatgt tcaagtcccc caggccggct gccatggtgc tggaccgctc ccaggacttt 900
gggaaaacat ggaagcctta taagtacttt gcgactaact gctccgctac atttggcctg 960
gaagatgatg ttgtcaagaa gggcgctatt tgtacttcta aatactccag tccttttcca 1020
tgcactggag gagaggttat tttcaaagct ttgtcaccac catacgatac agagaaccct 1080
tacagtgcca aagttcagga gcagctgaag atcaccaacc ttcgcgtgca gctgctgaaa 1140
cgacagtctt gtccctgtca gagaaatgac ctgaacgaag agcctcaaca ttttacacac 1200
tatgcaatct atgatttcat tgtcaagggc agctgcttct gcaatggcca cgctgatcaa 1260
tgcatacctg ttcatggctt cagacctgtc aaggccccag gaacattcca catggtccat 1320
gggaagtgta tgtgtaagca caacacagca ggcagccact gccagcactg tgccccgtta 1380
tacaatgacc ggccatggga ggcagctgat ggcaaaacgg gggctcccaa cgagtgcaga 1440
acctgcaagt gtaatgggca tgctgatacc tgtcacttcg acgttaatgt gtgggaggca 1500
tcagggaatc gtagtggtgg tgtctgtgat gactgtcagc acaacacaga aggacagtat 1560
tgccagaggt gcaagccagg cttctatcgt gacctgcgga gacccttctc agctccagat 1620
gcttgcaaac cgtgttcctg ccatccagta ggatcagctg tccttcctgc caactcagtg 1680
accttctgcg accccagcaa tggtgactgc ccttgcaagc ctggggtggc agggcgacgt 1740
tgtgacaggt gcatggtggg atactggggc ttcggagact atggctgtcg accatgtgac 1800
tgtgcgggga gctgtgaccc tatcaccgga gactgcatca gcagccacac agacatagac 1860
tggtatcatg aagttcctga cttccgtccc gtgcacaata agagcgaacc agcctgggag 1920
tgggaggatg cgcaggggtt ttctgcactt ctacactcag gtaaatgcga atgtaaggaa 1980
cagacattag gaaatgccaa ggcattctgt ggaatgaaat attcatatgt gctaaaaata 2040

aagattttat cagctcatga taaaggtact catgttgagg tcaatgtgaa gattaaaaag 2100
gtcttaaaat ctaccaaact gaagatttc cgaggaaagc gaacattata tccagaatca 2160
tggacggaca gaggatgcac ttgtccaatc ctcaatcctg gtttggaata ccttgtagca 2220
ggacatgagg atataagaac aggcaaacta attgtgaata tgaaaagctt tgtccagcac 2280
tggaaacctt ctcttggaag aaaagtcatg gatattttaa aaagagagtg caagtagcat 2340
taagatggat agcacataat ggcacttgtc tatgtacaaa acacaaactt tagagcaaga 2400
agacctcaga caggaaactg gaatttttta aagtgccaaa acatatagaa atgtttgaat 2460
gcatgggtct tatctaactt atctcttctg gacccatgtt taaatacagt tttatttcat 2520
gaagagaaat gaaaacccct acactgatat ctgttttcta tgggactgat tctgaaattc 2580
ttaactatta agaatatttt aatagcagca tgacatttag cagtaatcca ttaagggcag 2640
tacctctaac aaggacgcct tccagcttca gcgatgttac ttacgtttga tgctacttaa 2700
agtaatgaat gacgttttaa ggaatcccta accctactat cagaaaaggt gtttgttaaa 2760
gagccttctc ttgtgtgtta cgcatgaact ttggtctgta ggtgttaaat ggaacctctc 2820
catgtgtata tagtatttcc ttgtataaag cactttacta cctaccactt gtgttgtgaa 2880
cgtttggtga ctgctgttga aagaaggaaa agggtgtgtg agaaagccta ctgaagcagc 2940
agcactgcca ctacatgtgg acaaaagtga ccatataaaa gaagttgtgc tatttaactc 3000
tgaatacttg gagaaactag gtgaagatgc aaccagaaag gagaatatgt atgcgtgaag 3060
tctcagcttt gagctggagg ctagattcca agatgacagc catgatgaaa ctttttaaaa 3120
aactaaacca gaagagactt taaaataaga gaaagaaatc ataaatgtag acatatgctt 3180
ggctaaaggg gaaatggact ttaaatttta aagagctcat ttgcaatgca cttgtataca 3240
cttcaaaaat tattgtagac acagaatttg ttatattttt gtgcttagta tttaaacctg 3300
aacattgaaa cagttttcct ccttgtcttt cttaacagta atagtcatta tatttacctg 3360
ttttttaaca caatgtatgt gatagtcaaa aaatcacagt ttttcattat tattcatctt 3420
ctgtacccac gcataaccac tatacatagt ttcttttgta cttgaatata caaaacatga 3480
acacagtgcc atatgaataa tttcacatac agaacctttt tttctctgaa gtcctgtgga 3540
cttgcaaata tatatatata ttgctttgtt aatttgtttt tatatttcat atatgtaata 3600
aaggaatatg atctgaaaaa aaaaaaaaaa aaaaaaaaaa 3640

<210> 289
<211> 628
<212> PRT
<213> Homo sapiens

<400> 289

Met Gly Ser Cys Ala Arg Leu Leu Leu Leu Trp Gly Cys Thr Val Val
1   5   10   15
Ala Ala Gly Leu Ser Gly Val Ala Gly Val Ser Ser Arg Cys Glu Lys
            20   25   30
Ala Cys Asn Pro Arg Met Gly Asn Leu Ala Leu Gly Arg Lys Leu Trp
        35   40   45
Ala Asp Thr Thr Cys Gly Gln Asn Ala Thr Glu Leu Tyr Cys Phe Tyr
    50   55   60
Ser Glu Asn Thr Asp Leu Thr Cys Arg Gln Pro Lys Cys Asp Lys Cys
65   70   75   80
Asn Ala Ala Tyr Pro His Leu Ala His Leu Pro Ser Ala Met Ala Asp
                85   90   95
Ser Ser Phe Arg Phe Pro Arg Thr Trp Trp Gln Ser Ala Glu Asp Val
            100   105   110
His Arg Glu Lys Ile Gln Leu Asp Leu Glu Ala Glu Phe Tyr Phe Thr
        115   120   125
His Leu Ile Val Met Phe Lys Ser Pro Arg Pro Ala Ala Met Val Leu
    130   135   140
Asp Arg Ser Gln Asp Phe Gly Lys Thr Trp Lys Pro Tyr Lys Tyr Phe
145   150   155   160
Ala Thr Asn Cys Ser Ala Thr Phe Gly Leu Glu Asp Asp Val Val Lys
                165   170   175
Lys Gly Ala Ile Cys Thr Ser Lys Tyr Ser Ser Pro Phe Pro Cys Thr
            180   185   190
Gly Gly Glu Val Ile Phe Lys Ala Leu Ser Pro Pro Tyr Asp Thr Glu
        195   200   205
Asn Pro Tyr Ser Ala Lys Val Gln Glu Gln Leu Lys Ile Thr Asn Leu

210 215 220
Arg Val Gln Leu Leu Lys Arg Gln Ser Cys Pro Cys Gln Arg Asn Asp
225 230 235 240
Leu Asn Glu Glu Pro Gln His Phe Thr His Tyr Ala Ile Tyr Asp Phe
245 250 255
Ile Val Lys Gly Ser Cys Phe Cys Asn Gly His Ala Asp Gln Cys Ile
260 265 270
Pro Val His Gly Phe Arg Pro Val Lys Ala Pro Gly Thr Phe His Met
275 280 285
Val His Gly Lys Cys Met Cys Lys His Asn Thr Ala Gly Ser His Cys
290 295 300
Gln His Cys Ala Pro Leu Tyr Asn Asp Arg Pro Trp Glu Ala Ala Asp
305 310 315 320
Gly Lys Thr Gly Ala Pro Asn Glu Cys Arg Thr Cys Lys Cys Asn Gly
325 330 335
His Ala Asp Thr Cys His Phe Asp Val Asn Val Trp Glu Ala Ser Gly
340 345 350
Asn Arg Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Glu Gly
355 360 365
Gln Tyr Cys Gln Arg Cys Lys Pro Gly Phe Tyr Arg Asp Leu Arg Arg
370 375 380
Pro Phe Ser Ala Pro Asp Ala Cys Lys Pro Cys Ser Cys His Pro Val
385 390 395 400
Gly Ser Ala Val Leu Pro Ala Asn Ser Val Thr Phe Cys Asp Pro Ser
405 410 415
Asn Gly Asp Cys Pro Cys Lys Pro Gly Val Ala Gly Arg Arg Cys Asp
420 425 430
Arg Cys Met Val Gly Tyr Trp Gly Phe Gly Asp Tyr Gly Cys Arg Pro
435 440 445
Cys Asp Cys Ala Gly Ser Cys Asp Pro Ile Thr Gly Asp Cys Ile Ser
450 455 460
Ser His Thr Asp Ile Asp Trp Tyr His Glu Val Pro Asp Phe Arg Pro
465 470 475 480
Val His Asn Lys Ser Glu Pro Ala Trp Glu Trp Glu Asp Ala Gln Gly
485 490 495
Phe Ser Ala Leu Leu His Ser Gly Lys Cys Glu Cys Lys Glu Gln Thr
500 505 510
Leu Gly Asn Ala Lys Ala Phe Cys Gly Met Lys Tyr Ser Tyr Val Leu
515 520 525
Lys Ile Lys Ile Leu Ser Ala His Asp Lys Gly Thr His Val Glu Val
530 535 540
Asn Val Lys Ile Lys Lys Val Leu Lys Ser Thr Lys Leu Lys Ile Phe
545 550 555 560
Arg Gly Lys Arg Thr Leu Tyr Pro Glu Ser Trp Thr Asp Arg Gly Cys
565 570 575
Thr Cys Pro Ile Leu Asn Pro Gly Leu Glu Tyr Leu Val Ala Gly His
580 585 590
Glu Asp Ile Arg Thr Gly Lys Leu Ile Val Asn Met Lys Ser Phe Val
595 600 605
Gln His Trp Lys Pro Ser Leu Gly Arg Lys Val Met Asp Ile Leu Lys
610 615 620
Arg Glu Cys Lys
625

<210> 290
<211> 2540
<212> DNA
<213> Mouse

<400> 290
gtcgcgatgc tgctgcgcct gctgctggcc tgggtggccg cggtgcccgc actgggccag 60

gtcccctgga cgccggagcc tcgagccgcg tgcggcccca gcagctgcta cgcgctcttt 120
ccccggcgcc gcacattcct ggaagcttgg cgggcgtgcc gcgaattggg gggcaacctg 180
gccacaccgc ggaccccaga ggaggcccag cgtgtggaca gcctggtggg ggtcgggccg 240
gccaacgggc tgctatggat tgggttgcag cggcaggcta ggcaatgcca gccgcagcgc 300
ccactgcggg gcttcatatg gaccacggga gaccaggaca ccgccttcac caactgggcc 360
cagccggcta cggaaggacc ctgcccagcc cagcgctgtg cagcccttga ggccagcgga 420
gagcatcgct ggctcgaagg ctcgtgcaca ctggctgtcg atggctacct ctgccagttt 480
ggttttgagg gtgcctgccc tgccttgccg cttgaggtgg gtcaggccgg tcccgctgtc 540
tacaccacac ccttcaacct ggtttccagc gagttcgaat ggctgccctt tggctccgtg 600
gcagctgtgc agtgccaagc tggcagggga gcttctctgc tgtgcgtgaa acagccttca 660
ggtggcgtgg gctggtccca gactggcccg ctgtgcccag ggactggctg tggtcctgac 720
aatgggggtt gcgaacatga gtgtgtggaa gaggtggacg gtgctgtgtc ctgccgctgc 780
agtgaaggct tccgtctagc agcagatggg cacagttgtg aagacccctg tgcccaggcc 840
ccctgtgagc agcagtgtga acctggaggg ccacaaggct atagctgcca ctgtcgcctt 900
ggcttccggc cagctgagga tgatccacac cgctgcgtgg acacggatga gtgccagatt 960
gctggtgtgt gccagcagat gtgtgtcaac tatgttggtg gctttgagtg ttactgcagc 1020
gagggtcacg agcttgaggc agatggtatc agctgtagcc ctgcaggagc catgggtgcc 1080
caggcttccc aggatctcag agatgagttg ctggatgatg gagaagaagg ggaggatgaa 1140
gaggagccct gggaggactt tgatggcacc tggacagagg aacaggggat cctatggctg 1200
gcacctacac atccacctga ctttggcctg ccctataggc ccaacttccc acaggatgga 1260
gagcctcaga gattgcacct ggagcctacc tggccacccc cacttagtgc cccccagggc 1320
ccctaccact cctcagtggt gtctgccaca cggcccatgg tgatctctgc cactcgaccc 1380
acactacctt ctgcccacaa gacctctgtt atttcagcta cacgcccacc cctgagccct 1440
gtccacccac ctgccatggc ccctgccaca cctccagctg tgttctctga gcaccagatc 1500
cccaaaatca aggccaatta tccagacctg ccttttggcc acaagcctgg gataacctcg 1560
gccactcacc cagcacggtc tcctccgtac cagccccccca ttatctcaac caactatccc 1620
caagtcttcc ctccccacca ggcccctatg tctccagata cccacactat cacttatttg 1680
cctccagtcc cccctcacct tgatcctggg gataccactt ctaaagccca tcaacaccct 1740
ttgctcccag atgctccagg tatcagaacc caggcccccc agctttctgt ctcagctctc 1800
cagccccctc ttcctaccaa ctccaggtct tctgtccatg aaactcctgt gcctgctgcc 1860
aaccagcccc cagccttccc ttcttctccc ctcccccctc agaggcccac taaccagacc 1920
tcatctatca gccctacaca ttcctattcc agagcccctc tagtcccaag ggaaggagtt 1980
cccagtccca aatcagtgcc acagctgccc tcggtgccct ccacagcagc tccaacagcc 2040
ctggcagagt caggtcttgc aggccaaagc caaagggatg accgctggct gctggtggca 2100
ctcctggtgc caacatgtgt cttcttggtg gtgctgcttg ccctgggcat tgtgtactgc 2160
actcgctgtg gctcccacgc acccaacaag cggatcacgg actgctatcg ctgggtcaca 2220
catgctggga acaagagctc aacagaaccc atgcccccca gaggcagcct tacaggggta 2280
cagacctgta gaaccagtgt gtgatggggt gcagatgccc ctttgtggga tagaagaaaa 2340
ggacttgctt tggacacatg gctgagacca caccaaggac ttatgggggc tgcccagctg 2400
acagaggagg ttctgttctt tgagcccagc atccatggca aaggacacac caggactcca 2460
ggacctcaag ggtgggtgc tgggatcttc tccaataaat ggggtgccaa cctcacccaa 2520
aaaaaaaaaa aaaaaaaaaa 2540

<210> 291
<211> 765
<212> PRT
<213> Mouse

<400> 291
Met Leu Leu Arg Leu Leu Leu Ala Trp Val Ala Ala Val Pro Ala Leu
1 5 10 15
Gly Gln Val Pro Trp Thr Pro Glu Pro Arg Ala Ala Cys Gly Pro Ser
20 25 30
Ser Cys Tyr Ala Leu Phe Pro Arg Arg Arg Thr Phe Leu Glu Ala Trp
35 40 45
Arg Ala Cys Arg Glu Leu Gly Gly Asn Leu Ala Thr Pro Arg Thr Pro
50 55 60
Glu Glu Ala Gln Arg Val Asp Ser Leu Val Gly Val Gly Pro Ala Asn
65 70 75 80
Gly Leu Leu Trp Ile Gly Leu Gln Arg Gln Ala Arg Gln Cys Gln Pro
85 90 95

Gln Arg Pro Leu Arg Gly Phe Ile Trp Thr Thr Gly Asp Gln Asp Thr
100 105 110
Ala Phe Thr Asn Trp Ala Gln Pro Ala Thr Glu Gly Pro Cys Pro Ala
115 120 125
Gln Arg Cys Ala Ala Leu Glu Ala Ser Gly Glu His Arg Trp Leu Glu
130 135 140
Gly Ser Cys Thr Leu Ala Val Asp Gly Tyr Leu Cys Gln Phe Gly Phe
145 150 155 160
Glu Gly Ala Cys Pro Ala Leu Pro Leu Glu Val Gly Gln Ala Gly Pro
165 170 175
Ala Val Tyr Thr Thr Pro Phe Asn Leu Val Ser Ser Glu Phe Glu Trp
180 185 190
Leu Pro Phe Gly Ser Val Ala Ala Val Gln Cys Gln Ala Gly Arg Gly
195 200 205
Ala Ser Leu Leu Cys Val Lys Gln Pro Ser Gly Gly Val Gly Trp Ser
210 215 220
Gln Thr Gly Pro Leu Cys Pro Gly Thr Gly Cys Gly Pro Asp Asn Gly
225 230 235 240
Gly Cys Glu His Glu Cys Val Glu Glu Val Asp Gly Ala Val Ser Cys
245 250 255
Arg Cys Ser Glu Gly Phe Arg Leu Ala Ala Asp Gly His Ser Cys Glu
260 265 270
Asp Pro Cys Ala Gln Ala Pro Cys Glu Gln Gln Cys Glu Pro Gly Gly
275 280 285
Pro Gln Gly Tyr Ser Cys His Cys Arg Leu Gly Phe Arg Pro Ala Glu
290 295 300
Asp Asp Pro His Arg Cys Val Asp Thr Asp Glu Cys Gln Ile Ala Gly
305 310 315 320
Val Cys Gln Gln Met Cys Val Asn Tyr Val Gly Gly Phe Glu Cys Tyr
325 330 335
Cys Ser Glu Gly His Glu Leu Glu Ala Asp Gly Ile Ser Cys Ser Pro
340 345 350
Ala Gly Ala Met Gly Ala Gln Ala Ser Gln Asp Leu Arg Asp Glu Leu
355 360 365
Leu Asp Asp Gly Glu Glu Gly Glu Asp Glu Glu Glu Pro Trp Glu Asp
370 375 380
Phe Asp Gly Thr Trp Thr Glu Glu Gln Gly Ile Leu Trp Leu Ala Pro
385 390 395 400
Thr His Pro Pro Asp Phe Gly Leu Pro Tyr Arg Pro Asn Phe Pro Gln
405 410 415
Asp Gly Glu Pro Gln Arg Leu His Leu Glu Pro Thr Trp Pro Pro Pro
420 425 430
Leu Ser Ala Pro Arg Gly Pro Tyr His Ser Ser Val Val Ser Ala Thr
435 440 445
Arg Pro Met Val Ile Ser Ala Thr Arg Pro Thr Leu Pro Ser Ala His
450 455 460
Lys Thr Ser Val Ile Ser Ala Thr Arg Pro Pro Leu Ser Pro Val His
465 470 475 480
Pro Pro Ala Met Ala Pro Ala Thr Pro Pro Ala Val Phe Ser Glu His
485 490 495
Gln Ile Pro Lys Ile Lys Ala Asn Tyr Pro Asp Leu Pro Phe Gly His
500 505 510
Lys Pro Gly Ile Thr Ser Ala Thr His Pro Ala Arg Ser Pro Pro Tyr
515 520 525
Gln Pro Pro Ile Ile Ser Thr Asn Tyr Pro Gln Val Phe Pro Pro His
530 535 540
Gln Ala Pro Met Ser Pro Asp Thr His Thr Ile Thr Tyr Leu Pro Pro
545 550 555 560
Val Pro Pro His Leu Asp Pro Gly Asp Thr Thr Ser Lys Ala His Gln
565 570 575
His Pro Leu Leu Pro Asp Ala Pro Gly Ile Arg Thr Gln Ala Pro Gln

580 585 590
Leu Ser Val Ser Ala Leu Gln Pro Pro Leu Pro Thr Asn Ser Arg Ser
595 600 605
Ser Val His Glu Thr Pro Val Pro Ala Ala Asn Gln Pro Pro Ala Phe
610 615 620
Pro Ser Ser Pro Leu Pro Pro Gln Arg Pro Thr Asn Gln Thr Ser Ser
625 630 635 640
Ile Ser Pro Thr His Ser Tyr Ser Arg Ala Pro Leu Val Pro Arg Glu
645 650 655
Gly Val Pro Ser Pro Lys Ser Val Pro Gln Leu Pro Ser Val Pro Ser
660 665 670
Thr Ala Ala Pro Thr Ala Leu Ala Glu Ser Gly Leu Ala Gly Gln Ser
675 680 685
Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu Leu Val Pro Thr Cys
690 695 700
Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile Val Tyr Cys Thr Arg
705 710 715 720
Cys Gly Ser His Ala Pro Asn Lys Arg Ile Thr Asp Cys Tyr Arg Trp
725 730 735
Val Thr His Ala Gly Asn Lys Ser Ser Thr Glu Pro Met Pro Pro Arg
740 745 750
Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr Ser Val
755 760 765

<210> 292
<211> 3020
<212> DNA
<213> Mouse

<400> 292
atgtttcctt gctaccatgg tttcctgaac tcaagtggcc agtgtgtggg gcctctgagc 60
cacactctct tgcccacctc tgccaccagt ccacgaagga tgaggaaggg tattggattg 120
tcctggacct cctggaagct agactagggt ctggagcaac gaccggcttt ggactctctg 180
attcaggttc ctcctaagcc tcagagggac aaaaaagagt ccctgcaagt cgtccacggg 240
gctgggagca gccgggtggc tcatgactac tcagagagtc tgcccaaaga aaagagtctt 300
gtattggaaa ggtttctggg tacctgaccg tgttgcgttt gtttctaccc aacgtttaac 360
agagagccca gagccatgat gaagaccttg tccagtggga actgcacact caatgtgcct 420
gctaagaact cctaccgcat ggtggtgctg ggtgcctccc gagtgggcaa gagctccatt 480
gtctcccgct tcctcaatgg ccgctttgag gaccagtaca cgcccactat cgaggacttt 540
catcgcaagg tgtacaacat ccacggggac atgtaccagc tggatatcct ggacacctct 600
ggcaaccacc cattccctgc catgcgccgg ctctccatcc tcacaggaga tgtcttcatc 660
ctggtgttca gcctggatag ccgggagtcc tttgatgagg tcaagcgcct ccagaaacag 720
atcctggagg tcaagtcctg cctgaagaat aaaaccaagg aggcagcaga gctgcccatg 780
gtgatctgtg ggaacaagaa tgaccacagt gagctgtgcc gccaggtccc tgccatggag 840
gctgagctgc tggtgtctgg tgatgaaaac tgcgcctatt tcgaggtgtc agccaagaag 900
aacactaatg tgaacgagat gttctatgtg ctgttcagca tggccaagct gccccatgag 960
atgagccctg cactgcacca taagatctcc gtgcagtacg gcgatgcttt tcacccccgg 1020
cccttctgca tgcgtcgcac taaggtcgca ggtgcctatg gcatggtctc accctttgcc 1080
cgacgcccca gtgtcaacag tgacctcaag tacatcaagg ccaaggtcct acgggagggc 1140
caggcccgag agagggacaa gtgtagcatc cagtgagagg cagggacatc ggggaggggg 1200
cttgggcagt gccttaaggg aggtggctga ggattcccac tgcgcacatc ccacagaggg 1260
ccctaggtgt gtaccctgtg cccattctct tgtttcctgg acacctcctg tgagccgtga 1320
gtgtggttcc tttgtgggag gacggagaca tgtctaggga catgacagca ctcatgccga 1380
gacaagcttt ccgtgggagg gatgcaaaaa ggccaggagt cctgcatcaa agcaagatgc 1440
tcagtacaag tcacaggatg agaacatctt agccagatgc cccagccagg ttccctggtg 1500
gcctctgctc cctctgttca gaccagcttg gtctcagtgt ccctggagaa accaccatct 1560
tgggtcttca gctcctgccg tctggcccag ctgtgtacac tgccccccaa tttagcccct 1620
ggggccatca tgaccttgag tggaggggag agagagagag agagagagag agagagagag 1680
agagagagag agagagacct gtgtccccca gatcactgcc ttttggctcc actcccaggc 1740
tcctccatac gatatttctc tttgttttga agtgtctttc ctgttctgtt tgcagtagac 1800
atgaagtcct tgtactgtaa gaggccaatg ctttgtcttt gaccgggctt cccaattcaa 1860

```
atccattgct ttggccgggg tctccctccc tgctcccagg caggctgtat tctgcccagt    1920
gtccatcggc ctacaaagag cccacagtgc cacagtcaca gcagtaatct cctgccctct    1980
ggagaggatg actgggcttt gagagagtga ttctaacccc ctccgcactc ctaactagtt    2040
caggacagag ctctgactag atgcagcttt cttctgcttt agttccttaa acatctgcca    2100
agcacctacc tgatactggt cccttgtgtg ctaggcaaca gagagcgagg ggtcctgtgt    2160
gtccccagct ccggcctctg ccctcccatg gtgccctttc tgcgcacaca gctgttggag    2220
gaagtggagc agttgagagc cagagccgag tccaggaaag gttggaagga catattgcag    2280
gacttaccct agtgttcagg ctatgctagg tacacaggag tgggggtgac cctgaaaacc    2340
aaaggtcctg ttcaccacct cttaatgcat ctgtgcttta gtcttattag tactgcagct    2400
ggcccatttg agatgactct ggataaagac acctgctgcc aagctttcaa cctgagtttg    2460
gtcccagggt tccatgtggt ggaaggagag aagtcatcca ttgacctcca cacatccatc    2520
atggtacccc tacccccccc cccccccatg aattattgaa gctgatgatt atcagaaacc    2580
acagcaatct aatagtgcat tctctcaagg cccaggtcac tccctgcaag ctgggtcggc    2640
catgggcctt ccatacacac cacgtcatac cctgtctcct tggagctccc agtagccggg    2700
atttggatca tgttacatat gccttcctca gagcaatcac tgaggctatc tgtggatact    2760
gtgcacattg tcacccttgc tctgcacacc aggcccagcc cagactccat acacacacct    2820
gctgctcagc acaattgctt cagcacctgc ttctgtccta caatgactcc agccccagtc    2880
ctgagtatac caggtacttg tccaggcaag tctatggcct ggtccatccg gtcaagctct    2940
actgcctgga cctctgtgta cactatcaat taaagttggt ttgttagctg tgaaaaaaaa    3000
aaaaaaaaaa aaaaaaaaaa                                                3020
```

<210> 293
<211> 266
<212> PRT
<213> Mouse

<400> 293

```
Met Met Lys Thr Leu Ser Ser Gly Asn Cys Thr Leu Asn Val Pro Ala
1               5                   10                  15
Lys Asn Ser Tyr Arg Met Val Val Leu Gly Ala Ser Arg Val Gly Lys
            20                  25                  30
Ser Ser Ile Val Ser Arg Phe Leu Asn Gly Arg Phe Glu Asp Gln Tyr
        35                  40                  45
Thr Pro Thr Ile Glu Asp Phe His Arg Lys Val Tyr Asn Ile His Gly
    50                  55                  60
Asp Met Tyr Gln Leu Asp Ile Leu Asp Thr Ser Gly Asn His Pro Phe
65                  70                  75                  80
Pro Ala Met Arg Arg Leu Ser Ile Leu Thr Gly Asp Val Phe Ile Leu
                85                  90                  95
Val Phe Ser Leu Asp Ser Arg Glu Ser Phe Asp Glu Val Lys Arg Leu
            100                 105                 110
Gln Lys Gln Ile Leu Glu Val Lys Ser Cys Leu Lys Asn Lys Thr Lys
        115                 120                 125
Glu Ala Ala Glu Leu Pro Met Val Ile Cys Gly Asn Lys Asn Asp His
    130                 135                 140
Ser Glu Leu Cys Arg Gln Val Pro Ala Met Glu Ala Glu Leu Leu Val
145                 150                 155                 160
Ser Gly Asp Glu Asn Cys Ala Tyr Phe Glu Val Ser Ala Lys Lys Asn
                165                 170                 175
Thr Asn Val Asn Glu Met Phe Tyr Val Leu Phe Ser Met Ala Lys Leu
            180                 185                 190
Pro His Glu Met Ser Pro Ala Leu His His Lys Ile Ser Val Gln Tyr
        195                 200                 205
Gly Asp Ala Phe His Pro Arg Pro Phe Cys Met Arg Arg Thr Lys Val
    210                 215                 220
Ala Gly Ala Tyr Gly Met Val Ser Pro Phe Ala Arg Arg Pro Ser Val
225                 230                 235                 240
Asn Ser Asp Leu Lys Tyr Ile Lys Ala Lys Val Leu Arg Glu Gly Gln
                245                 250                 255
Ala Arg Glu Arg Asp Lys Cys Ser Ile Gln
            260                 265
```

<210> 294
<211> 5520
<212> DNA
<213> Mouse

<400> 294
gggcgcccgg gactcccgct gagcactcct cccgcacgcc cgggtccctc cggccggcga 60
gccgtccggc ccctgcgctg taggtccccg cggggcgatg ggttgatggg cgcgggggga 120
cgcaggatgc cggtgcctcc cgcgcgtttg ctgctgctgc cgctgctgcc ttgtcttctg 180
ctcctggctc ctggaactcg gggtgcgcct ggctgcccgg tccctatccg cggttgcaag 240
tgctctgggg agcggcccaa gggactaagt ggcggcgccc acaacccggc tcgaaggagg 300
gtggtgtgcg gcggtgggga tctccccgaa cctccagatc ccggccttct gccaaacggc 360
accatcacct tgctcttgag caacaacaag attactgggc tccgcaatgg atccttcttg 420
ggactgtccc tgttggagaa gttggacctg aggagcaatg tcatcagcac tgtgcagcct 480
ggagccttcc taggtctggg agagctaaaa cgcttagatc tctccaacaa tcggattggc 540
tgtctcacct ctgagacatt tcaagggctc cctagacttc tcagactaaa catatctgga 600
aacatctact ctagtctgca acctggggtc tttgatgagc tgccagccct taagattgtg 660
gactttggta ctgagtttct gacctgtgac tgccgcctgc gctggctgct gccctgggcc 720
cggaatcact ccctgcagct gtctgagcgc acactctgtg cctaccccag tgccctgcac 780
gcccatgccc tgagcagcct ccaggagtcc cagcttcgct gtgaaggggc cctggaactg 840
cacacccact acctcatccc atcccttcgc caagtggtgt tccagggtga ccgcctgccc 900
ttccagtgct cagccagcta cttgggcaac gatacccgga tccactggta ccacaatggg 960
gctcctatgg agagcgatga gcaggccggc atcgtccttg ctgaaaacct tatccatgat 1020
tgcaccttca tcaccagtga gctgaccctg tctcacattg gtgtgtgggc ctctggtgaa 1080
tgggagtgct ccgtgtccac agtccaaggc aacaccagca agaaggtgga gatagtagtg 1140
ctggagacct ctgcctccta ctgccctgca gagcgggtga ccaacaaccg tggggacttc 1200
aggtggcccc gaaccttggc tggcatcacg gcttaccagt cctgtttaca gtacccccttc 1260
acctctgtgc ccttgagtgg gggagccccg ggtacccgag cctcacgcag gtgtgaccga 1320
gctggccgct gggagccagg ggactactcg cactgtctgt acaccaatga catcactcgg 1380
gtgctctaca cctttgtgct gatgcccatc aacgcctcca atgcattgac gttggcccac 1440
cagctgcgag tgtataccgc agaggccgcc agcttctcag acatgatgga cgtggtctat 1500
gtggctcaga tgatccagaa gtttttgggt tacgttgacc agatcaagga gctggtggag 1560
gtgatggtgg acatggccag caacctgatg ctggtggatg agcaccttct gtggctggcc 1620
cagagagaag acaaagcctg cagtggcatt gtgggtgccc tggagcgaat cggaggagct 1680
gctcttagcc cccatgccca gcacatctct gtgaattcaa gaaatgtggc actggaggcc 1740
tacctcatca agcctcacag ctacgtgggt ctgacttgca cggctttcca gaggagggag 1800
gtaggagtgt cgggtgcaca gccaagcagc gtcggccagg atgccccagt ggagcccgaa 1860
cccctagctg atcagcagct taggttccgc tgcaccactg ggaggcccaa catttctctg 1920
tcatccttcc acatcaagaa tagcgtggcc ctggcctcca tccagctgcc ccccagcctg 1980
ttctcaaccc ttccggctgc cctggctccc ccagtccctc cagattgcac cctgcaactg 2040
ctggtcttca gaaatggccg tcttttccgc agccacggca acaacacttc ccgtcctgga 2100
gcagctgggc ctggcaagag gcgtggtgtg gccaccccag tcatatttgc aggaaccagt 2160
ggctgtggtg tgggaaactt gacggagccc gtggctgtgt cactgaggca ctgggctgaa 2220
ggagctgacc ccatggcagc ttggtggaac caggacgggc ctggaggctg gagttctgaa 2280
ggctgcaggc tccgctacag ccagcccaac gtcagctccc tgtactgcca gcacttgggc 2340
aatgtggccg tgcttatgga gctgaatgca ttcccgcggg aggcaggagg ctctggggct 2400
gggttgcatc ccgtcgtgta cccctgcacg gctttgctgc tactctgtct cttctccacc 2460
atcatcacgt acatcctcaa ccacagctcc atccacgtgt cccggaaggg ttggcacatg 2520
ctgctgaacc tttgtttcca tatggccatg acctctgctg tcttcgtggg gggcgtcacg 2580
ctcaccaact accaaatggt ttgtcaagcg gtgggcatca ctctgcacta ctcttccttg 2640
tcgtcactgc tctggatggg ggtcaaggct cgagtcctcc acaaggagct tagttggagg 2700
gcacccccctc tggaagaagg ggaagcagct ccgcctggtc ctcgccccat gctccggttc 2760
tacttgattg ctggagggat ccccctcata atctgcggca tcaccgctgc ggtcaacatc 2820
cacaactacc gggaccacag tccctattgt tggctggtgt ggcgtccaag ccttggtgcc 2880
ttctacatac cggtggcgtt gattctgcct atcacctgga tctacttctt gtgtgcaggc 2940
cttcacttac ggagccatgt ggcccagaat ccaaagcagg gtaacaggat ctctctggag 3000
ccaggggaag agctgagggg ttccaccagg ctcaggagta gtggcgtcct cctgaatgac 3060
tctggttctc ttttggctac agttagcgca ggagtaggga cacctgcgcc cccagaggat 3120
ggtgatggcg tatattctcc tggagtccag ctgggggcgc tgatgaccac gcatttcctg 3180
tacctggcta tgtgggcttg tggtgccttg gcggtgtctc agcgctggct gccccgagtg 3240

gtgtgtagct gtctgtacgg cgtggcagct tcagctcttg gtctgtttgt cttcactcac 3300
cactgtgcca gacgtagaga tgtccgggct tcctggcgcg cctgctgccc tcctgcttcg 3360
ccctcggcct cccatgtccc agcccgggcc ctgccgactg ctacagagga tggatcccca 3420
gtgttggggg agggaccagc ctctctcaag tcctccccaa gtggcagcag tggccgcgcg 3480
ccgccacccc cctgcaaact caccaatctg caggtggccc agagtcaggt gtgcgaggca 3540
agcgtggccg cccgcggaga tggagagcca gagcccaccg gctcccgtgg cagcctagct 3600
ccccggcacc ataacaacct gcatcatggg cgccgagtac acaagagtcg ggccaagggg 3660
caccgagccg gagagactgg tggtaagagc cggctcaagg cgttgcgcgc gggcacgtcc 3720
ccaggagctc ccgagctgtt gtccagtgag agcggcagtt tgcacaacag cccgtctgac 3780
agctacccgg gcagcagccg caacagtcca ggcgacggtc ttccactcga gggtgagccc 3840
atgcttacgc cgtcggaggg cagtgacaca agcgccgcgc caatcgctga gacggggcgc 3900
cccgggcagc gccgcagcgc cagccgtgac aacctcaagg gcagcggcag cgcgctggag 3960
agggagagca agcgccgctc ctatccgctc aacactacca gtcttaacgg tgcccccaaa 4020
gggggcaagt atgaggatgc cagtgtaact ggtgcagagg ccatagcggg aggctccatg 4080
aagactggcc tctggaaaag cgagaccacc gtctaggtcc agatttagga tgggcgggtc 4140
acgcgggctt gtttactccc aaatcctctt gggcggtcca agccgtctac tgatgtgtat 4200
gtaggtttaa ggcggccatg ctgatgctgc ccttgagtcc accatcatta gttacccagg 4260
ctagggaaag gggagggagg cagatgcttg cccctactgt ggactatccc tcagcagtag 4320
cgacagacaa tcccagacca gttttggtgg ccaagttctt ggtatcctgc caggtaggca 4380
taaaacatcc atcggtccct agggtaaccc ataaactgag ttgaagagcc cagcccaggt 4440
aggctcagga aatgagaggg agaccgggga actgggttct ccacaccagc ccggcaaggt 4500
atcctgtgac tgccaagatc ccaggcctct ctcccagttt tggcttggga aaccatccca 4560
gcaggtgagc caggggggcgt aacaggtgct gcctttcaga ttaactatgc aaggggggatg 4620
ggggtgggag gggtagggca gtgtggtggg cagctctaga gatgagcttg tccctcagga 4680
ggcaggcagg tgggaaaagg tgcattaggg agacagaatc cctaactatg ggagtggtac 4740
acagtttttc cagcagagtt cacagcaaac cctgaacccc cacacacctg ggaagtgata 4800
ctgccagcag gtgccttaag actcaagggg agggagctga tatgtggatc tcacaaccta 4860
tacagtggtc tgcaagtggc tccacttagc tgcttaatta taatacccac tgtctgttcc 4920
cagccctcca actccggggg actgagggga aatgcctcca tgaggctcct gtggcaaagc 4980
catgctaata atctgacttc taacctcagt tagaaaccca aaatgccaaa ccacctccta 5040
actcgctgaa acccaaccac actctgaggc agcgcctggg tccaggctgc tcaagagcct 5100
atgcttccag cccccatttt cctcaactca agatgccttt taatacagaa ctacatggaa 5160
gtagaggaac ccttgggcac tgggaagtag cagggatccc agctctgatc aagtgagagg 5220
acagagcagg gaagacgcca tactcgctga gatgggtccc attatttatg ctttgctgca 5280
cagacactat tagaggaaaa gctttgtatt actctcccac gtgagctgct gctgtttacc 5340
ctgccaatgc cttagcactg gagagctttt tgcaatatgc tggggaaagg ggagggaggg 5400
gatgaagtgc caaagaaaac acattttaaa agctctggtt ttatacaata gaatgttttc 5460
cagcagatgc ctctttgttt taatatatta aaatcttgca aaaaaaaaaa aaaaaaaaaa 5520

<210> 295
<211> 1329
<212> PRT
<213> Mouse

<400> 295
Met Pro Val Pro Pro Ala Arg Leu Leu Leu Leu Pro Leu Leu Pro Cys
1 5 10 15
Leu Leu Leu Leu Ala Pro Gly Thr Arg Gly Ala Pro Gly Cys Pro Val
20 25 30
Pro Ile Arg Gly Cys Lys Cys Ser Gly Glu Arg Pro Lys Gly Leu Ser
35 40 45
Gly Gly Ala His Asn Pro Ala Arg Arg Arg Val Val Cys Gly Gly Gly
50 55 60
Asp Leu Pro Glu Pro Pro Asp Pro Gly Leu Leu Pro Asn Gly Thr Ile
65 70 75 80
Thr Leu Leu Leu Ser Asn Asn Lys Ile Thr Gly Leu Arg Asn Gly Ser
85 90 95
Phe Leu Gly Leu Ser Leu Leu Glu Lys Leu Asp Leu Arg Ser Asn Val

100 105 110
Ile Ser Thr Val Gln Pro Gly Ala Phe Leu Gly Leu Gly Glu Leu Lys
115 120 125
Arg Leu Asp Leu Ser Asn Asn Arg Ile Gly Cys Leu Thr Ser Glu Thr
130 135 140
Phe Gln Gly Leu Pro Arg Leu Leu Arg Leu Asn Ile Ser Gly Asn Ile
145 150 155 160
Tyr Ser Ser Leu Gln Pro Gly Val Phe Asp Glu Leu Pro Ala Leu Lys
165 170 175
Ile Val Asp Phe Gly Thr Glu Phe Leu Thr Cys Asp Cys Arg Leu Arg
180 185 190
Trp Leu Leu Pro Trp Ala Arg Asn His Ser Leu Gln Leu Ser Glu Arg
195 200 205
Thr Leu Cys Ala Tyr Pro Ser Ala Leu His Ala His Ala Leu Ser Ser
210 215 220
Leu Gln Glu Ser Gln Leu Arg Cys Glu Gly Ala Leu Glu Leu His Thr
225 230 235 240
His Tyr Leu Ile Pro Ser Leu Arg Gln Val Val Phe Gln Gly Asp Arg
245 250 255
Leu Pro Phe Gln Cys Ser Ala Ser Tyr Leu Gly Asn Asp Thr Arg Ile
260 265 270
His Trp Tyr His Asn Gly Ala Pro Met Glu Ser Asp Glu Gln Ala Gly
275 280 285
Ile Val Leu Ala Glu Asn Leu Ile His Asp Cys Thr Phe Ile Thr Ser
290 295 300
Glu Leu Thr Leu Ser His Ile Gly Val Trp Ala Ser Gly Glu Trp Glu
305 310 315 320
Cys Ser Val Ser Thr Val Gln Gly Asn Thr Ser Lys Lys Val Glu Ile
325 330 335
Val Val Leu Glu Thr Ser Ala Ser Tyr Cys Pro Ala Glu Arg Val Thr
340 345 350
Asn Asn Arg Gly Asp Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr
355 360 365
Ala Tyr Gln Ser Cys Leu Gln Tyr Pro Phe Thr Ser Val Pro Leu Ser
370 375 380
Gly Gly Ala Pro Gly Thr Arg Ala Ser Arg Arg Cys Asp Arg Ala Gly
385 390 395 400
Arg Trp Glu Pro Gly Asp Tyr Ser His Cys Leu Tyr Thr Asn Asp Ile
405 410 415
Thr Arg Val Leu Tyr Thr Phe Val Leu Met Pro Ile Asn Ala Ser Asn
420 425 430
Ala Leu Thr Leu Ala His Gln Leu Arg Val Tyr Thr Ala Glu Ala Ala
435 440 445
Ser Phe Ser Asp Met Met Asp Val Val Tyr Val Ala Gln Met Ile Gln
450 455 460
Lys Phe Leu Gly Tyr Val Asp Gln Ile Lys Glu Leu Val Glu Val Met
465 470 475 480
Val Asp Met Ala Ser Asn Leu Met Leu Val Asp Glu His Leu Leu Trp
485 490 495
Leu Ala Gln Arg Glu Asp Lys Ala Cys Ser Gly Ile Val Gly Ala Leu
500 505 510
Glu Arg Ile Gly Gly Ala Ala Leu Ser Pro His Ala Gln His Ile Ser
515 520 525
Val Asn Ser Arg Asn Val Ala Leu Glu Ala Tyr Leu Ile Lys Pro His
530 535 540
Ser Tyr Val Gly Leu Thr Cys Thr Ala Phe Gln Arg Arg Glu Val Gly
545 550 555 560
Val Ser Gly Ala Gln Pro Ser Ser Val Gly Gln Asp Ala Pro Val Glu
565 570 575
Pro Glu Pro Leu Ala Asp Gln Gln Leu Arg Phe Arg Cys Thr Thr Gly
580 585 590

Arg Pro Asn Ile Ser Leu Ser Ser Phe His Ile Lys Asn Ser Val Ala
595 600 605
Leu Ala Ser Ile Gln Leu Pro Pro Ser Leu Phe Ser Thr Leu Pro Ala
610 615 620
Ala Leu Ala Pro Pro Val Pro Pro Asp Cys Thr Leu Gln Leu Leu Val
625 630 635 640
Phe Arg Asn Gly Arg Leu Phe Arg Ser His Gly Asn Asn Thr Ser Arg
645 650 655
Pro Gly Ala Ala Gly Pro Gly Lys Arg Arg Gly Val Ala Thr Pro Val
660 665 670
Ile Phe Ala Gly Thr Ser Gly Cys Gly Val Gly Asn Leu Thr Glu Pro
675 680 685
Val Ala Val Ser Leu Arg His Trp Ala Glu Gly Ala Asp Pro Met Ala
690 695 700
Ala Trp Trp Asn Gln Asp Gly Pro Gly Gly Trp Ser Ser Glu Gly Cys
705 710 715 720
Arg Leu Arg Tyr Ser Gln Pro Asn Val Ser Ser Leu Tyr Cys Gln His
725 730 735
Leu Gly Asn Val Ala Val Leu Met Glu Leu Asn Ala Phe Pro Arg Glu
740 745 750
Ala Gly Gly Ser Gly Ala Gly Leu His Pro Val Val Tyr Pro Cys Thr
755 760 765
Ala Leu Leu Leu Leu Cys Leu Phe Ser Thr Ile Ile Thr Tyr Ile Leu
770 775 780
Asn His Ser Ser Ile His Val Ser Arg Lys Gly Trp His Met Leu Leu
785 790 795 800
Asn Leu Cys Phe His Met Ala Met Thr Ser Ala Val Phe Val Gly Gly
805 810 815
Val Thr Leu Thr Asn Tyr Gln Met Val Cys Gln Ala Val Gly Ile Thr
820 825 830
Leu His Tyr Ser Ser Leu Ser Ser Leu Leu Trp Met Gly Val Lys Ala
835 840 845
Arg Val Leu His Lys Glu Leu Ser Trp Arg Ala Pro Pro Leu Glu Glu
850 855 860
Gly Glu Ala Ala Pro Pro Gly Pro Arg Pro Met Leu Arg Phe Tyr Leu
865 870 875 880
Ile Ala Gly Gly Ile Pro Leu Ile Ile Cys Gly Ile Thr Ala Ala Val
885 890 895
Asn Ile His Asn Tyr Arg Asp His Ser Pro Tyr Cys Trp Leu Val Trp
900 905 910
Arg Pro Ser Leu Gly Ala Phe Tyr Ile Pro Val Ala Leu Ile Leu Pro
915 920 925
Ile Thr Trp Ile Tyr Phe Leu Cys Ala Gly Leu His Leu Arg Ser His
930 935 940
Val Ala Gln Asn Pro Lys Gln Gly Asn Arg Ile Ser Leu Glu Pro Gly
945 950 955 960
Glu Glu Leu Arg Gly Ser Thr Arg Leu Arg Ser Ser Gly Val Leu Leu
965 970 975
Asn Asp Ser Gly Ser Leu Leu Ala Thr Val Ser Ala Gly Val Gly Thr
980 985 990
Pro Ala Pro Pro Glu Asp Gly Asp Gly Val Tyr Ser Pro Gly Val Gln
995 1000 1005
Leu Gly Ala Leu Met Thr Thr His Phe Leu Tyr Leu Ala Met Trp Ala
1010 1015 1020
Cys Gly Ala Leu Ala Val Ser Gln Arg Trp Leu Pro Arg Val Val Cys
1025 1030 1035 1040
Ser Cys Leu Tyr Gly Val Ala Ala Ser Ala Leu Gly Leu Phe Val Phe
1045 1050 1055
Thr His His Cys Ala Arg Arg Arg Asp Val Arg Ala Ser Trp Arg Ala
1060 1065 1070
Cys Cys Pro Pro Ala Ser Pro Ser Ala Ser His Val Pro Ala Arg Ala

1075 1080 1085
Leu Pro Thr Ala Thr Glu Asp Gly Ser Pro Val Leu Gly Glu Gly Pro
1090 1095 1100
Ala Ser Leu Lys Ser Ser Pro Ser Gly Ser Ser Gly Arg Ala Pro Pro
1105 1110 1115 1120
Pro Pro Cys Lys Leu Thr Asn Leu Gln Val Ala Gln Ser Gln Val Cys
1125 1130 1135
Glu Ala Ser Val Ala Ala Arg Gly Asp Gly Glu Pro Glu Pro Thr Gly
1140 1145 1150
Ser Arg Gly Ser Leu Ala Pro Arg His His Asn Asn Leu His His Gly
1155 1160 1165
Arg Arg Val His Lys Ser Arg Ala Lys Gly His Arg Ala Gly Glu Thr
1170 1175 1180
Gly Gly Lys Ser Arg Leu Lys Ala Leu Arg Ala Gly Thr Ser Pro Gly
1185 1190 1195 1200
Ala Pro Glu Leu Leu Ser Ser Glu Ser Gly Ser Leu His Asn Ser Pro
1205 1210 1215
Ser Asp Ser Tyr Pro Gly Ser Ser Arg Asn Ser Pro Gly Asp Gly Leu
1220 1225 1230
Pro Leu Glu Gly Glu Pro Met Leu Thr Pro Ser Glu Gly Ser Asp Thr
1235 1240 1245
Ser Ala Ala Pro Ile Ala Glu Thr Gly Arg Pro Gly Gln Arg Arg Ser
1250 1255 1260
Ala Ser Arg Asp Asn Leu Lys Gly Ser Gly Ser Ala Leu Glu Arg Glu
1265 1270 1275 1280
Ser Lys Arg Arg Ser Tyr Pro Leu Asn Thr Thr Ser Leu Asn Gly Ala
1285 1290 1295
Pro Lys Gly Gly Lys Tyr Glu Asp Ala Ser Val Thr Gly Ala Glu Ala
1300 1305 1310
Ile Ala Gly Gly Ser Met Lys Thr Gly Leu Trp Lys Ser Glu Thr Thr
1315 1320 1325
Val

<210> 296
<211> 2840
<212> DNA
<213> Mouse

<400> 296
cggggctgct ccctctgcag ccgccgccgc cgccgcgcag acccggaggt cgtccgcgcc 60
caccatgcga gctcagctct ggttgctgca gttgctgcta ctccgcgggg ccgcgcgcgc 120
gctcagtccc gcaacacccg caggtcacaa tgaaggtcaa gactctgcat ggactgccaa 180
gaggaccagg caaggctgga gtcggagacc ccgagagagc cccgcgcagg tgttgaagcc 240
aggcaagacc cagctaagcc aggacttggg tgggggctcc ctggccatcg acacacttcc 300
ggacaacagg actcgggtgg tggaggacaa ccataactac tacgtgtccc gtgtctacgg 360
ccctggtgag aaacaaagcc aggatctgtg ggtggacctg gctgtggcca accggagtca 420
tgtgaagatc cacaggatcc tctccagttc tcaccgacag gcttcaagag tggtcttgtc 480
ctttgatttc cctttctatg ggcatcctct gcggcagatc accatagcaa ccggaggctt 540
catcttcatg gggcacatgc tccaccggat gctcacagct acgcagtatg tggcacccct 600
gatggccaac ttcaaccccg gctactctga caactccacg gttgcttact ttgacaatgg 660
gaccgttttt gtggttcagt gggatcatgt ttacctccag gaccgggagg acaggggcag 720
cttcaccttc caggcggccc tacaccgaga tggccgcatt gtcttcggct acaaagagat 780
ccccatggct gtcctggata tcagctctgc ccagcacccct gtcaaggcag gcctgtccga 840
cgctttcatg attctcaatt catccccaga ggtgccagag tctcagagac ggaccatttt 900
cgaataccac cgtgtggaac tggactccag caagatcacc accacctcgg ccgtggagtt 960
caccccgttg ccaacctgcc tccagcatca gagttgcgac acctgcgtgt cctcgaatct 1020
aaccttcaac tgcagctggt gccatgtcct gcagaggtgt tccagtggct ttgaccgata 1080
ccgccaagaa tggctgacct acggctgtgc ccaggaggca gaaggcaaga catgcgagga 1140
cttccaggat gatagccact actcagcctc ccctgacagc tccttcagcc cctttaatgg 1200
cgactccact acctcttcct ccctcttcat tgacagcctc accacagaag atgacaccaa 1260

gttgaatccc tacgcagaag gagacggcct tccggaccac tcatctccga agtccaaggg 1320
tcctcccgtg cacctgggca ccatcgtggg tatcgtgctt gctgtactcc tggtagcggc 1380
catcatcctg gctgggattt acatcagtgg ccaccctaat tccaatgctg cactcttctt 1440
catcgagcgg agacctcacc actggccagc catgaagttc cataaccacc ccaaccactc 1500
tacctacacc gaggtagagc cctccgggca cgagaaggaa ggcttcgtgg aggccgagca 1560
gtgctgagag agcatcgggc cagagacctg gagatggcat gaaagacaag tcacagcaca 1620
gagaagtgat tttttttcct ggcttcctcg gagctggccc tgggccagga agacaagaca 1680
acagcttgtg gtgccaacac tacagtttgg tctgcacacc ccatttaaag gggctcagt 1740
aatacaactg cgaaggctcc ttggggaaca ctgacctcaa gagttccctg tttcaatggg 1800
aggaggcttc gtttggggtc tctcagtggt ctgcagctat ggcggagccc ctgcccactg 1860
gagacagcct cctgtgttcc tcctgctcac tgaagcccac actgggccat tgcattccgg 1920
ggtctataga ttcaagagct ggtcttgcta gctatggagt cagtgccctt ggctccaaac 1980
tttgtggctt agaagcctga agaagggat cccttccctc cgagagcgct taaccctgag 2040
atgcgctaac agagagaaaa gtaaccttgg ggaacttgca tttttctggc cttggtcctt 2100
tgcttcattg tttttttgc agaggccggg gccaacatcc gagcactgta gcctgcagct 2160
cattctgtac cctgccctgc cctgcccctc agcctccacc ctgcaagctg gtcttgcatg 2220
gctgccagta atgagtgggg cccttactgt gccatgtgtc tggtgcctgc attactcgtt 2280
aacctgttct gttatcaacg gcagtagttt ccttcaaaga gggggacaat ttacctggct 2340
cctgttttaa cttggctgac cagagtcgag ttcttgtaac cattaaaaac aactaggggg 2400
ccgggtgtgg tggtgctcac actcaggagg ctgagctctg agatcaaggc cagcctggtc 2460
tacagagaga gcctgtcttg aagaaacaag acaaatgggg ggctagaggt ttccctgaga 2520
cacccctgcc ttagcaaggg gctccagttg gatcccgttg aagcacggtg gccgcgaagg 2580
tagggcagag aaatctggta tgggagggag agaccttgac ctggaaagcg gcctccatct 2640
ctccagctct gcaaagagct ttgggaactg ggagttgacg ttcccacact cagcctggtt 2700
ttaagggact tctgtccccg tggtggacca ggacggcttc taaaggacaa tgaaaaccta 2760
gagctcacct tcatcccaaa gaagcgtcat cagcaaataa ataaggtata gccctcaaaa 2820
aaaaaaaaaa aaaaaaaaaa 2840

<210> 297
<211> 500
<212> PRT
<213> Mouse

<400> 297
Met Arg Ala Gln Leu Trp Leu Leu Gln Leu Leu Leu Leu Arg Gly Ala
1 5 10 15
Ala Arg Ala Leu Ser Pro Ala Thr Pro Ala Gly His Asn Glu Gly Gln
20 25 30
Asp Ser Ala Trp Thr Ala Lys Arg Thr Arg Gln Gly Trp Ser Arg Arg
35 40 45
Pro Arg Glu Ser Pro Ala Gln Val Leu Lys Pro Gly Lys Thr Gln Leu
50 55 60
Ser Gln Asp Leu Gly Gly Gly Ser Leu Ala Ile Asp Thr Leu Pro Asp
65 70 75 80
Asn Arg Thr Arg Val Val Glu Asp Asn His Asn Tyr Tyr Val Ser Arg
85 90 95
Val Tyr Gly Pro Gly Glu Lys Gln Ser Gln Asp Leu Trp Val Asp Leu
100 105 110
Ala Val Ala Asn Arg Ser His Val Lys Ile His Arg Ile Leu Ser Ser
115 120 125
Ser His Arg Gln Ala Ser Arg Val Val Leu Ser Phe Asp Phe Pro Phe
130 135 140
Tyr Gly His Pro Leu Arg Gln Ile Thr Ile Ala Thr Gly Gly Phe Ile
145 150 155 160
Phe Met Gly Asp Met Leu His Arg Met Leu Thr Ala Thr Gln Tyr Val
165 170 175
Ala Pro Leu Met Ala Asn Phe Asn Pro Gly Tyr Ser Asp Asn Ser Thr
180 185 190
Val Ala Tyr Phe Asp Asn Gly Thr Val Phe Val Val Gln Trp Asp His
195 200 205
Val Tyr Leu Gln Asp Arg Glu Asp Arg Gly Ser Phe Thr Phe Gln Ala

```
    210                 215                 220
Ala Leu His Arg Asp Gly Arg Ile Val Phe Gly Tyr Lys Glu Ile Pro
225                 230                 235                 240
Met Ala Val Leu Asp Ile Ser Ser Ala Gln His Pro Val Lys Ala Gly
                245                 250                 255
Leu Ser Asp Ala Phe Met Ile Leu Asn Ser Ser Pro Glu Val Pro Glu
            260                 265                 270
Ser Gln Arg Arg Thr Ile Phe Glu Tyr His Arg Val Glu Leu Asp Ser
        275                 280                 285
Ser Lys Ile Thr Thr Thr Ser Ala Val Glu Phe Thr Pro Leu Pro Thr
    290                 295                 300
Cys Leu Gln His Gln Ser Cys Asp Thr Cys Val Ser Ser Asn Leu Thr
305                 310                 315                 320
Phe Asn Cys Ser Trp Cys His Val Leu Gln Arg Cys Ser Ser Gly Phe
                325                 330                 335
Asp Arg Tyr Arg Gln Glu Trp Leu Thr Tyr Gly Cys Ala Gln Glu Ala
            340                 345                 350
Glu Gly Lys Thr Cys Glu Asp Phe Gln Asp Asp Ser His Tyr Ser Ala
        355                 360                 365
Ser Pro Asp Ser Ser Phe Ser Pro Phe Asn Gly Asp Ser Thr Thr Ser
    370                 375                 380
Ser Ser Leu Phe Ile Asp Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu
385                 390                 395                 400
Asn Pro Tyr Ala Glu Gly Asp Gly Leu Pro Asp His Ser Ser Pro Lys
                405                 410                 415
Ser Lys Gly Pro Pro Val His Leu Gly Thr Ile Val Gly Ile Val Leu
            420                 425                 430
Ala Val Leu Leu Val Ala Ala Ile Ile Leu Ala Gly Ile Tyr Ile Ser
        435                 440                 445
Gly His Pro Asn Ser Asn Ala Ala Leu Phe Phe Ile Glu Arg Arg Pro
    450                 455                 460
His His Trp Pro Ala Met Lys Phe His Asn His Pro Asn His Ser Thr
465                 470                 475                 480
Tyr Thr Glu Val Glu Pro Ser Gly His Glu Lys Glu Gly Phe Val Glu
                485                 490                 495
Ala Glu Gln Cys
            500
```

<210> 298
<211> 2010
<212> DNA
<213> Mouse

<400> 298

```
gagagaggtc gcggcagcgg catggcaagg ttccggaggg ccgacctggc cgcagcagga      60
gttatgttac tttgtcactt tttaacagac cggttccact tcgcccacgg ggagcctgga     120
caccatacca atgattggat ttatgaagtt acaaacgctt ttccttggaa tgaagagggg     180
gtagaagtgg actctcaagc atacaaccac aggtggaaaa gaaatgtgga ccctttttaag    240
gcagtagaca caaacagagc cagcatgggc caagcctctc cagagtccaa agggttcact     300
gacctgctac tggatgacgg acaggacaat aacacccaga tagaggagga cacggatcac     360
aattactaca tttctcggat atatggtcca gcggattctg ccagccggga tctgtgggtt     420
aacatagacc aaatggaaaa agacaaagtg aagattcacg ggatactttc caacactcat     480
cggcaagctg caagagtgaa tctgtccttc gatttccat tttatggtca ttttctaaat      540
gaagtcactg tggcaactgg gggtttcata tatactggag aagttgtaca tcgaatgctc     600
acagctacac agtatatagc tcctttaatg gcaaattttg atcccagtgt atccagaaat     660
tcaactgtca gatattttga taatggcaca gctcttgttg tccagtggga ccatgtccac     720
ctgcaggata attacaacct gggaagcttc acattccagg ccacactcct catggacggg     780
cgcatcatct ttggatacaa agaaatccct gtcttggtca cacagataag ttctaccaac     840
catccagtga aagtcggtt gtctgatgca tttgtcgtgg tccacaggat ccagcaaata      900
cccaatgttc gaagaagaac aatttatgaa tatcaccgag tagaactaca aatgtccaaa     960
attaccaaca tctcagctgt ggagatgact ccacttccca catgtctcca gttcaatggt    1020
```

```
tgtggccctt gtgtgtcctc gcagattggt ttcaactgca gttggtgcag caaacttcaa   1080
agatgctcca gtggatttga tcgccatcgg caggactggg tggacagtgg atgcccggaa   1140
gaggtacagt caaaagagaa gatgtgtgag aagacagagc caggagagac gtctcaaact   1200
accacgacct cccacacgac caccatgcaa ttcagggtcc tgaccaccac caggagagct   1260
gtgacatcgc agatgcctac cagcctgcct acagaagatg acacgaagat agccctacat   1320
ctcaaagaca gtggagcctc cacagatgac agtgcagctg agaagaaagg aggaaccctc   1380
catgcaggcc tcattgttgg aattctcatc ttggtcctca ttatagcagc ggccattctg   1440
gtgacagtgt atatgtatca ccatccaaca tcagcagcca gcatcttctt cattgagaga   1500
cgcccaagca gatggccagc aatgaagttt cgaagaggct caggacaccc tgcctatgca   1560
gaagttgaac cagttggaga gaaagaaggt tttattgtat cagagcagtg ctaaaatttt   1620
aggacagagc agcaccagta ctggcttaca ggtgttaaga ctaaaacttt gcttatgcat   1680
ttaagacaaa cagacacaca acccacaacc acacacaaag gagccctaaa ctgctgtaga   1740
cagaagggcg acgagatttc tggacaagcc cagcccagga acattgaaag gaaaactcag   1800
acttgtacaa gacaccatgt acaatgatta aagaattccc tagtggaatg acatccatgg   1860
ttcacaagga acatctccgg tggacttgcc aggagtgtga cgagatgacg atgctttgg    1920
tttaggtgca gggttgcaaa gaaatcaagg aaaaaaaata tgacaataaa taaagcttta   1980
gttcacaagg gaaaaaaaaa aaaaaaaaaa                                     2010
```

<210> 299
<211> 530
<212> PRT
<213> Mouse

<400> 299

```
Met Ala Arg Phe Arg Arg Ala Asp Leu Ala Ala Ala Gly Val Met Leu
1               5                   10                  15
Leu Cys His Phe Leu Thr Asp Arg Phe His Phe Ala His Gly Glu Pro
            20                  25                  30
Gly His His Thr Asn Asp Trp Ile Tyr Glu Val Thr Asn Ala Phe Pro
        35                  40                  45
Trp Asn Glu Glu Gly Val Glu Val Asp Ser Gln Ala Tyr Asn His Arg
    50                  55                  60
Trp Lys Arg Asn Val Asp Pro Phe Lys Ala Val Asp Thr Asn Arg Ala
65                  70                  75                  80
Ser Met Gly Gln Ala Ser Pro Glu Ser Lys Gly Phe Thr Asp Leu Leu
                85                  90                  95
Leu Asp Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp
            100                 105                 110
His Asn Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ala Asp Ser Ala Ser
        115                 120                 125
Arg Asp Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys
    130                 135                 140
Ile His Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn
145                 150                 155                 160
Leu Ser Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Asn Glu Val Thr
                165                 170                 175
Val Ala Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met
            180                 185                 190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro
        195                 200                 205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala
    210                 215                 220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu
225                 230                 235                 240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile
                245                 250                 255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr
            260                 265                 270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His
        275                 280                 285
Arg Ile Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr
```

290 295 300
His Arg Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val
305 310 315 320
Glu Met Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Gly Cys Gly Pro
325 330 335
Cys Val Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu
340 345 350
Gln Arg Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp
355 360 365
Ser Gly Cys Pro Glu Glu Val Gln Ser Lys Glu Lys Met Cys Glu Lys
370 375 380
Thr Glu Pro Gly Glu Thr Ser Gln Thr Thr Thr Thr Ser His Thr Thr
385 390 395 400
Thr Met Gln Phe Arg Val Leu Thr Thr Thr Arg Arg Ala Val Thr Ser
405 410 415
Gln Met Pro Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu
420 425 430
His Leu Lys Asp Ser Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys
435 440 445
Lys Gly Gly Thr Leu His Ala Gly Leu Ile Val Gly Ile Leu Ile Leu
450 455 460
Val Leu Ile Ile Ala Ala Ala Ile Leu Val Thr Val Tyr Met Tyr His
465 470 475 480
His Pro Thr Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser
485 490 495
Arg Trp Pro Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr
500 505 510
Ala Glu Val Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu
515 520 525
Gln Cys
530

<210> 300
<211> 5220
<212> DNA
<213> Mouse

<400> 300
cggaactgct tcgactgcaa agcttcaagc gcagcctggg agcggcctgg tggccctatc 60
ccggcagctc cacacagcag aacgccctgg gtccctgaaa ctcgaaaccc gggctcagaa 120
ccagcggaaa ccaaagcgaa atccttgaac ttctctgaac aattgcttcc gggcgtttgc 180
tgagagccgg gggacctgac cggagcccag gccgcgtatg gcgcgcccct gatgtcacac 240
ggacgccagc gaggccagcg ctccggctgc agcatggacc gcgcggggcg cctgggtgcg 300
ggcctgcggg gactctgcgt ggctgcactc gtgctcgtgt gcgccggaca cgggggccgc 360
cgcgaggatg gggaccagc ttgctacgga ggattcgacc tctacttcat cctggacaag 420
tcaggaagtg tgctgcacca ctggaatgaa atctactact tcgtggagca gttggctcat 480
agattcatca gcccacagct aaggatgtcc ttcattgtct tctctactcg agggacaact 540
ttaatgaaac taactgagga cagggaacag atccgacaag gcctagaaga gctccagaaa 600
gttctgccag gaggagacac ttacatgcac gaaggattcg agagggccag tgagcagatt 660
tactatgaga acagtcaagg atacaggacg gcgagcgtca tcatcgcgtt gacggatggg 720
gagctgcacg aggacctctt cttctactca gagagggagg ctaaccgatc ccgagacctt 780
ggtgcgattg tttactgcgt tggcgtgaag gatttcaatg aaactcagtt ggctcggatt 840
gcagacagta aggaccacgt gtttcctgtg aacgacggct tccaggctct ccaaggcatt 900
atccactcaa ttttaaagaa atcctgcatc gaaattctgg cggctgaacc atccaccatc 960
tgcgcgggag agtcctttca agtggtcgta agaggaaatg gcttccgaca tgcccgcaat 1020
gtggacaggg tcctctgcag cttcaaaatc aatgactcag tcacgctcaa tgagaagccc 1080
tttgctgtgg aagacactta tttgctgtgc ccagcaccaa tcttgaaaga agttggcatg 1140
aaagctgcac tgcaggtcag catgaacgac ggcctgtcct tcatctccag ttctgtcatc 1200
atcaccacca cacactgttc agacggctcc atcctggcga ttgctctgct ggtcctcttc 1260
ctgctgctgg ccctggcgct gctctggtgg ttctggcccc tctgctgcac agtgatcatc 1320
aaggaggtcc ctccaccccc tgttgaggag agtgaggaag aagacgatga tggtttgcca 1380

aagaagaaat ggcccacagt agatgcctct tattatggtg gacgcggtgt gggaggcatt 1440
aaaagaatgg aggtccgctg gggagaaaag ggctccacag aagaaggggc gaagttagaa 1500
aaggcaaaga atgcacgagt caagatgcca gagcaagaat atgagttccc agaaccccga 1560
aacctcaaca acaacatgcg ccggccttcc tcgcctcgga agtggtactc gcccatcaag 1620
ggaaaactcg atgccttgtg ggttctgctg agaaaaggat atgaccgagt gtctgtgatg 1680
aggccacagc caggagacac gggacgctgt atcaacttca ccagagtgaa gaacagtcag 1740
ccagccaagt atcccctgaa caacacctac caccccagct ccccacctcc cgctcctatc 1800
tacacacccc caccccctgc tccccactgc cctcccccag cccccagtgc ccccactcct 1860
cccattcctt ccccaccatc cactctcccc cctcctcctc aggccccacc ccctaacagg 1920
gcacctcccc cctcccgacc tcctccaagg ccttctgtct agaacccaaa gtccgagctc 1980
tgggctgcct gagcaactcc agcaggaggc ttctctgctg aaagaaagat ctgcccagcc 2040
tatgtggtga gtggcggctg atgtttgcac gatttaaaag caagtcgtga tgggcagaac 2100
aaaatgggca ttttgaactg cctgaagaca gacaatgaga caataacagt cacattatag 2160
cctgtgaccc ctcacctcta gaggaaggtt cccgagatgg ccacattgcc acagtgctct 2220
cagccagatt atgtcccatg aagaccagga agaaagtgac ttccaagaat ggaatgcagc 2280
attggataag aaacacctgg ctgagattct gacctcactg atttgactct tgattcttgg 2340
actgggagcc aggccatctc cacccctggt accacccagc aactctgaaa atgtgcagtg 2400
tccctagtat gcatcgaata ggtatccaac tgggatctgc aggttgcctt ataaagagca 2460
tatgctctat tctctttccc gaacttcctg gtttcccagt gatgagggaa ggggaaaggt 2520
gttgccatgc ttagaagtta gaggacgtca gtgctcagca ctgatggaga agcgttgatg 2580
ggagtgtcca gctcttacat ctagaaatgg ctggcttcag caggcacagt tcctaaacca 2640
acaagccttg tcattgtcaa aggcaaccta ctaatgattc accttaaaca tcaaggttga 2700
ctgtggcata ggtcagagct gatcacacag aaccttcccc atgaaatcgc aaggttcctc 2760
atcttcaaat acccaggacc ccagagattt ctaaatccag ctaagagaca gtagtcctga 2820
cttggcaaga aaaccattcc cagttgtttt actctgaaac aggccgttgt atgtatggta 2880
tatctctcct tggcctttca acctgctcac aagtattacc agttatgaag caaggagaaa 2940
tacatccagt gtgtaataga aaagctctgc ccacaatccc catgtcactc ctctacatta 3000
ttctgaagct gcttggtcag tgagcccttt aacctcatgt agactctgga cactgtcacc 3060
caatcatgaa aacagaggtc attgtcaaag gcagtgtata gcctgtacaa aaatgatgct 3120
tccttcctca gtttccacag gccccaaaat tcctgtctta ggctcctaaa cctctaaact 3180
ttttcctgga acaaaagata taaaacgggc ataagttttt atgttttggg ctgtgatctc 3240
caaagatcct tcaagaactc aagttagcct cattcttcca gcttgtttag aacagaggca 3300
tccaggtgtc atgcactcca tagacaccaa tccttgttcc caaggcagac attattaatc 3360
aatctcagca ctagttctca atttaatcca attatatttt tccacagtac ttcacatctc 3420
ttatgacctg ttggtcatca gttagaattg agagagataa acactgtttg taatccctac 3480
cttagaaaga aaagcagagg agaatggggg aaccaccagc ataaaagtta ttatctgggg 3540
aaaatcgacc tgaaagaacg cccaagtcca agacctatgg tgctgacacc aaagtaacac 3600
tttcccaagt gtaccccaga ccccactctt ctccctgtgg ccaccactcc ctgcttttca 3660
ggagttgtga aaaagatctc cttcaccctt actgtgcccc catattagaa caaggcttgt 3720
ttagtgtagt ccttgttaaa caggtgccag aatgtctcag ccacctgaga tgacattgct 3780
gggccccaga aaaccattcc aaggagaatg ggctccccag gctcagagca tgcaactatg 3840
agcccatggc aactgttttg actgctggca gtacaaaacg ggccacccca cattacagct 3900
gcaggatttg tgcagccata agaaagtatg aaccaagatg ctggtgttgc tgttcaacaa 3960
gcatgggctt cggggaaggc agcagactcc gagagcaggc cttgtgcagt gtcccaaggg 4020
gctgtggtga agtgtctgag gaaaaatgaa tgctgataca tggtgattct gagaagaatt 4080
tgcaaggttt gaccttagaa tttatggaat gtcttccctg gtcattcaga attatggcta 4140
gaagtttcta gaaaccgtca aggttaatac ctttcagagt aggtgattac aggcaggaag 4200
agctttgatg tggtttacaa agcccatcag ttctgtgtca ttccctgtaa gcaacaggag 4260
atggtggttg tgattagcaa actgcatgtg ttatttgttt gactccttgt tattgtcctt 4320
acggaggatt ttttttatat aagccaaatt ttgttgtata tattcatatt ccacgtgaca 4380
gatggaagca cgtcctatca gtgtgaataa aaagaacagt tgtagtaaat tattaaagcc 4440
agtgatttca tggcaggtta ccctaccaag ctgtgcttgt tgatctccca tgaccatact 4500
gcttttacaa tgtacaaata gttcctaggt gacgagaccc tcctttacat aatgccgatg 4560
acagccttgc tgggaactgc ggtccttctg ctgtgacagc cagctcgaaa acaggtcctg 4620
cctggagctt gccatacact ttagggagac ataagagctg tctttcccca gcgtcaggga 4680
caaagctacc ataaagaagt ggaaaagtct tggctctcca gcctgggaca gaggtctctc 4740
tggaacccca aggaagagca gaaatgatcc ttgcctgcca ctgcacacaa tgtgatggtg 4800
gaaaatccat caaggaataa ttgtgagata atgaccgaca gttcaggcgc aaagggaatt 4860
catgctgtgt aaagtgggtg gaattcgttt gcaagctatg caaagcctga tcttactcac 4920
caggaggatg gaaagggttt ttttagttat ctgagctcag ctgagttatc acgcttggag 4980
aaccgattta aaggaattag aatatgattt ctgaatacac ataacattaa actcttctct 5040

```
ttttctatgg taatttagtt atggacgttc agcgtctctg agttattgtt ataaaagact      5100
tgtcatcacc gcactgtgct gtaggagact gggctgaacc tgtacaatgg tataccctgg      5160
aagttgcttt tttaaaaaaa aataataata aacacctaaa atcaaaaaaa aaaaaaaaaa      5220
```

<210> 301
<211> 562
<212> PRT
<213> Mouse

<400> 301

```
Met Asp Arg Ala Gly Arg Leu Gly Ala Gly Leu Arg Gly Leu Cys Val
1               5                   10                  15
Ala Ala Leu Val Leu Val Cys Ala Gly His Gly Gly Arg Arg Glu Asp
            20                  25                  30
Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp
        35                  40                  45
Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val
    50                  55                  60
Glu Gln Leu Ala His Arg Phe Ile Ser Pro Gln Leu Arg Met Ser Phe
65                  70                  75                  80
Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp
                85                  90                  95
Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro
            100                 105                 110
Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln
        115                 120                 125
Ile Tyr Tyr Glu Asn Ser Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile
    130                 135                 140
Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu
145                 150                 155                 160
Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val
                165                 170                 175
Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser
            180                 185                 190
Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly
        195                 200                 205
Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala
    210                 215                 220
Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg
225                 230                 235                 240
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser
                245                 250                 255
Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ala Val
            260                 265                 270
Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly
        275                 280                 285
Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile
    290                 295                 300
Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile
305                 310                 315                 320
Leu Ala Ile Ala Leu Leu Val Leu Phe Leu Leu Leu Ala Leu Ala Leu
                325                 330                 335
Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val
            340                 345                 350
Pro Pro Pro Pro Val Glu Glu Ser Glu Glu Glu Asp Asp Gly Leu
        355                 360                 365
Pro Lys Lys Lys Trp Pro Thr Val Asp Ala Ser Tyr Tyr Gly Gly Arg
    370                 375                 380
```

```
Gly Val Gly Gly Ile Lys Arg Met Glu Val Arg Trp Gly Glu Lys Gly
385                 390                 395                 400
Ser Thr Glu Glu Gly Ala Lys Leu Glu Lys Ala Lys Asn Ala Arg Val
                405                 410                 415
Lys Met Pro Glu Gln Glu Tyr Glu Phe Pro Glu Pro Arg Asn Leu Asn
            420                 425                 430
Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser Pro Ile
        435                 440                 445
Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly Tyr Asp
    450                 455                 460
Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg Cys Ile
465                 470                 475                 480
Asn Phe Thr Arg Val Lys Asn Ser Gln Pro Ala Lys Tyr Pro Leu Asn
                485                 490                 495
Asn Thr Tyr His Pro Ser Ser Pro Pro Pro Ala Pro Ile Tyr Thr Pro
            500                 505                 510
Pro Pro Pro Ala Pro His Cys Pro Pro Pro Ala Pro Ser Ala Pro Thr
        515                 520                 525
Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro Gln Ala
    530                 535                 540
Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro Arg Pro
545                 550                 555                 560
Ser Val
```

<210> 302
<211> 2690
<212> DNA
<213> Mouse

<400> 302

```
agctttcccc accacagaat ccaagtcgga actcttggca ccatgaaccc agccatcagc      60
gtcgctctcc tgctctcagg tactgggcaa gggtcagggc tggcattcta aggaatctgg     120
cttcctccca tcccgggaag tagcctcttt gccatagtct caggggcaca ggtggttggg     180
aggtgcgggg gtggggagtg gggaggagcc tcaacctcac cagtggtggt ctttgacata     240
ttagaaactc cataatggat ctaggaactc ctctgctggg tggtggtggt tgtggtacac     300
acctttaatc tcagcactca ggaggcagag tcaggtggat ctgttagtct gaagccagct     360
ggtctacaga gcaaattcca ggacagccag agctattctc aagatagaga atccctttct     420
tgaaaaaacc atttaaaaac aaaaacaaaa gcaacacact cctttgatct cctgttcttg     480
aaacacattg ttgggaccca gaacttcagt agattgatgg aagttggagt ctgcaagtgg     540
tggaacatcc caccaatacc tcaagggcga gtgcaaaccc cacatccccc cagctcaagc     600
tcacttttcc tgcaggtggg aggcccgggt ctgtgtctcc ccaaattcag agaaggcact     660
gctgtgcagt cttgcaggtg tcccgagggc agaaggtgac cagcctgaca gcctgcctgg     720
tgaaccaaaa ccttcgcctg gactgccgcc atgagaataa caccaaggat aactccatcc     780
agcatgagtt cagcctgacc cgagagaaga ggaagcacgt gctctcaggc acccttggga     840
tacccgagca cacgtaccgc tcccgcgtca ccctctccaa ccagccctat atcaaggtcc     900
ttaccctagc caacttcacc accaaggatg agggcgacta cttttgtgag cttcaagtct     960
cgggcgcgaa tcccatgagc tccaataaaa gtatcagtgt gtatagaggt gagactggtt    1020
cccagaaaga taaaatgtct aggttagcta ggctggggta gccaataaaa aaaaaaaaaa    1080
aaaaaaaaaa aaaaacaggc acctccatta cccttcccct aactgctggt ctcctgggaa    1140
actgctgctg tctatgtgag tggggcaaga ttaggggcca gaaaggggga gcttgtagta    1200
aaagcacagt tgaggaaact aaatgggaaa ggcagtacag tggtgattct tgtggtgtgg    1260
aggttctgtt acagcatccg gtggagccgc taagatgaga aagcgccagc tagctgcctt    1320
gaacagctga cacctgtctt tgcccgcctg agtcctgatc tcccctcctc ccggcacccc    1380
ttctctatcc acagacaagc tggtcaagtg tggcggcata agcctgctgg ttcagaacac    1440
atcctggatg ctgctgctgc tgctttccct ctccctcctc caagccctgg acttcatttc    1500
tctgtgactg gttgggccca aggagaaaca ggggccctcg aggagcccct cgggtccttc    1560
ctctgcagag gtcttgcttc tcccggtcag ctgactccct ccccaagtcc ttccaatatc    1620
tcagaacatg gggagaaacg gggaccttgt ccctcctaag gaaccccagt gctgcatgcc    1680
atcatccccc ccaccctcgc ccccaccccc gccacttctc cctccatgca taccactagc    1740
tgtcattttg tactctgtat ttattctagg gctgcttctg attatttagt ttgttctttc    1800
```

```
cctggagacc tgttagaaca taagggcgta tggtgggtag gggaggcagg atatcagtcc    1860
ctggggcgag ttcctccctg ccaaggaagc cagatgcctg aaagagatat ggatgaggga    1920
agttggactg tgcctgtacc tggtacagtc atactctgtg ggaatcatc ggggaggggg     1980
gggggctca agatgggaga gctctgctag cctttgtgga ccatccaatg aggatgaggg     2040
cttagattct accaggtcat tctcagccac cacacacaag cgctctgcca tcactgaaga    2100
agccccctag ggccttgggc cagggcacac tcagtaaaga tgcaggttca gtcagggaat    2160
gatggggaaa ggggtaggag gtgggggagg gatcaccccc tcctctaaaa cacgagcctg    2220
ctgtctccaa aggcctctgc ctgtagtgag ggtggcagaa gaagacaagg agccagaact    2280
ctgactccag gatctaagtc cgtgcaggaa ggggatccta gaaccatccg gttggaccca    2340
gcttaccaag ggagagcctt tattcttctt tccctctgcc cctctgtgcc agcccctctt    2400
gctgtccctg atccccagac agacgagagt cttgcaaaca gcctgttcca agacctccta    2460
atctcagggg caggcggtgg agctgagatc cggcgtgcac acttttggt tgatagcttt     2520
cccaaggatc ctctcccccca ctggcagctc tgcctgtccc atcaccatgt ataataccac   2580
cactgctaca gcatctcacc gaggaaagaa aaatgcacaa taaaaccaag cctctggagt    2640
gtgtcctggt gtctgtctct tctgtgtcct ggcgtctgtc tcttctgtgt               2690
```

<210> 303
<211> 162
<212> PRT
<213> Mouse

<400> 303

```
Met Asn Pro Ala Ile Ser Val Ala Leu Leu Leu Ser Val Leu Gln Val
1               5                   10                  15
Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asn Gln
            20                  25                  30
Asn Leu Arg Leu Asp Cys Arg His Glu Asn Asn Thr Lys Asp Asn Ser
        35                  40                  45
Ile Gln His Glu Phe Ser Leu Thr Arg Glu Lys Arg Lys His Val Leu
    50                  55                  60
Ser Gly Thr Leu Gly Ile Pro Glu His Thr Tyr Arg Ser Arg Val Thr
65                  70                  75                  80
Leu Ser Asn Gln Pro Tyr Ile Lys Val Leu Thr Leu Ala Asn Phe Thr
                85                  90                  95
Thr Lys Asp Glu Gly Asp Tyr Phe Cys Glu Leu Gln Val Ser Gly Ala
            100                 105                 110
Asn Pro Met Ser Ser Asn Lys Ser Ile Ser Val Tyr Arg Asp Lys Leu
        115                 120                 125
Val Lys Cys Gly Gly Ile Ser Leu Leu Val Gln Asn Thr Ser Trp Met
    130                 135                 140
Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Leu Asp Phe Ile
145                 150                 155                 160
Ser Leu
```

<210> 304
<211> 4588
<212> DNA
<213> Mouse

<400> 304

```
tgcgatcccc tcgccggcgg tcatccgagc acagcgctag ggctgtctct gcacgcagcc    60
ctgccgtgcg ccctccgtac tctcgtcctc cgagcgccgc agggatggta cccatccgac    120
ctgccctcgc gccctggcct cgtcacctgc tgcgctgcgt cttgcttctc gggggactgc    180
gtctcggcca cccggcggac tccgccgccg ccctcctgga gcctgatgtc ttcctcatct    240
tcagccaggg gatgcagggc tgtctggagg cccagggtgt gcaggtccga gtcaccccat    300
tctgcaatgc cagtctccct gcccagcgct ggaagtgggt ctcccggaac cgactcttca    360
acctgggtgc cacacagtgc ctgggtacag gctggccagt caccaacacc acagtttcct    420
tgggcatgta tgagtgtgac agagaggcct tgagtcttcg gatggcagtg tcgtacacta    480
ggggaccagt tgtccctgct tctgggggct cgtgcaagca atgcatccaa gcctggcacc    540
tggagcgcgg tgaccagacc cgcagtggcc attggaacat ctatggcagt gaagaagacc    600
```

tatgtgctcg accttactat gaggtctaca ccatccaggg aaactcacac ggaaagccgt 660
gcactatccc cttcaaatac gacaaccagt ggttccacgg ctgcaccagc actggcagag 720
aagatgggca cctgtggtgt gccaccaccc aggactacgg caaagatgag cgctggggct 780
tctgccccat caagagtaac gactgtgaga ccttctggga caaagaccag ctgactgaca 840
gctgttacca gtttaacttc caatccacac tgtcctggag ggaggcctgg gccagctgcg 900
agcagcaggg tgcagacttg ctgagtatca cggagatcca cgagcagacc tacatcaacg 960
ggctcctcac gggctacagc tccacgctat ggattggcct taatgacctg gataccagtg 1020
gaggctggca gtggtcagac aactcacccc tcaagtacct caactgggag agtgatcagc 1080
cggacaaccc aggtgaggag aactgtggag tgatccggac tgagtcctca ggcggctggc 1140
agaaccatga ctgcagcatc gccctgccct atgtttgcaa gaagaaaccc aacgctacgg 1200
tcgagcccat ccagccagac cggtggacca atgtcaaggt ggaatgtgac cccagctggc 1260
agcccttcca gggccactgc taccgcctgc aggccgagaa gcgcagctgg caggagtcca 1320
agagggcgtg tctgcggggt gggggtgacc tccttagcat ccacagcatg gctgagctgg 1380
agttcatcac caaacagatc aagcaagagg tggaggagct atggattggc ctcaatgatt 1440
tgaaactgca gatgaatttt gagtggtccg acgggagcct cgtgagcttc acccactggc 1500
acccctttga gcccaacaac tttcgtgaca gcctggagga ctgtgtcacc atctgggggc 1560
cggaaggacg ctggaacgac agtccctgta accagtcctt gccatccatt tgcaagaagg 1620
caggccggct gagccagggc gctgcggagg aggaccacga ctgccggaag ggttggacgt 1680
ggcatagccc atcctgctac tggctgggag aggaccaagt gatctacagt gatgcccggc 1740
gcctgtgtac tgaccatggc tctcagctgg tcaccatcac caacaggttt gagcaggcct 1800
tcgtcagcag cctcatctat aactgggagg gcgaatactt ctggacagcc ctgcaagacc 1860
tcaacagtac tggctccttc cgttggctca gtggggatga agtcatatat acccattgga 1920
atcgagacca gcctgggtac agacgtggag gctgtgtggc tctggccact ggcagtgcca 1980
tgggactgtg ggaggtgaag aactgcacat cgttccgggc tcgctacatc tgccgacaga 2040
gcctgggcac accggtcaca ccagagctgc ctgggccaga ccccacgccc agcctcactg 2100
gctcctgtcc ccagggctgg gtctcagacc ccaaactccg acactgctat aaggtgttca 2160
gctcagagcg gctgcaggag aagaagagtt ggatccaggc cctgggggtc tgccgggagt 2220
tgggggccca gctgctgagt ctggccagct atgaggagga gcactttgtg gcccacatgc 2280
tcaacaagat ctttggtgag tcagagcctg agagccatga gcagcactgg ttttggattg 2340
gcctgaaccg cagagaccct agagagggtc acagctggcg ctggagcgac ggtctagggt 2400
tttcctacca caattttgcc cggagccgac atgatgacga tgatatccga ggctgtgcag 2460
tgctggacct ggcctccctg cagtgggtac ccatgcagtg ccagacgcag cttgactgga 2520
tctgcaagat ccctagaggt gtggatgtgc gggaaccaga cattggtcga caaggccgtc 2580
tggagtgggt acgctttcag gaggccgagt acaagttttt tgagcaccac tcctcgtggg 2640
cgcaggcaca gcgcatctgc acctggttcc aggcagatct gacctccgtt cacagccaag 2700
cagaactggg cttcctgggg caaaacctgc agaagctgtc ctcagaccag gagcagcact 2760
ggtggatcgg cctgcacacc ttggagagtg acggacgctt caggtggaca gatggttcta 2820
ttataaactt catctcttgg gcaccgggaa aacctagacc cattggcaag gacaagaagt 2880
gtgtatacat gacagccaga caagaggact gggggggacca gaggtgccat acggctttgc 2940
cctacatctg taagcgcagc aatagctctg gagagactca gccccaagac ttgccacctt 3000
cagccttagg aggctgcccc tccggttgga accagttcct caataagtgt ttccgaatcc 3060
agggccagga cccccaggac agggtgaaat ggtcagaggc acagttctcc tgtgaacagc 3120
aagaagccca gctggtcacc attgcaaacc ccttagagca agcatttatc acagccagcc 3180
tccccaacgt gacctttgac ctttggattg gcctgcatgc ctctcagagg gacttccagt 3240
ggattgaaca agaacccctg ctctatacca actgggcacc aggagagccc tctggcccca 3300
gccctgctcc cagtggcacc aagccgacca gctgtgcggt gatcctgcac agcccctcag 3360
cccacttcac tggccgctgg gatgatcgga gctgcacaga ggagacgcat ggcttcatct 3420
gccagaaggg cacagacccc tcgctaagcc catccccagc agcaacaccc cctgccccgg 3480
gcgctgagct ctcctatctc aaccacacct tccggctgct gcagaagcca ctgcgctgga 3540
aagatgctct cctgctgtgt gagagccgaa atgccagcct ggcacacgtg cccgatccct 3600
acacacaagc cttcctcaca caggctgcac gggggctgca aacaccactg tggatcgggc 3660
tggccagtga ggagggctca cggaggtatt cctggctctc agaggagcct ctgaattatg 3720
tgagctggca agatgaggag ccccagcact cgggaggctg tgcctacgtg gatgtggatg 3780
gaacctggcg caccaccagc tgtgatacca agctgcaggg ggcagtgtgt ggggtgagca 3840
gggggccccc accccgaagg ataaactacc gtggcagctg tcctcagggc ttggctgact 3900
cgtcctggat tcccttcagg gagcattgct attctttcca catggaggtg ctgttgggcc 3960
acaaggaggc gctgcagcgc tgtcagaaag ctggtgggac ggttctgtcc attcttgatg 4020
agatggagaa tgtgtttgtc tgggagcacc tgcagacagc tgaagcccaa agtcgaggtg 4080
cctggttggg catgaacttc aaccccaaag gaggcacgct ggtctggcaa gacaacacag 4140
ctgtgaacta ttctaactgg gggcccccctg gcctgggccc tagcatgcta agccacaaca 4200
gctgctactg gatccagagc agcagcggac tgtggcgccc cggggcttgt accaacatca 4260

ccatgggagt tgtctgcaag ctccctagag tggaagagaa cagcttcttg ccatcagcag 4320
ccctccccga gagcccggtt gccctggtgg tggtgctgac agcggtgctg ctcctcctgg 4380
ccttgatgac ggcagccctc atcctctacc ggcgccgaca gagtgcggag cgtgggtcct 4440
tcgagggggc ccgctacagt cgcagcagcc actctggccc cgcagaggcc accgagaaga 4500
acattctggt gtctgacatg gaaatgaacg aacagcaaga atagagccaa gggcgtggtc 4560
ggggtggagc caaagcgggg gaggcagg 4588

<210> 305
<211> 1479
<212> PRT
<213> Mouse

<400> 305
Met Val Pro Ile Arg Pro Ala Leu Ala Pro Trp Pro Arg His Leu Leu
1 5 10 15
Arg Cys Val Leu Leu Leu Gly Gly Leu Arg Leu Gly His Pro Ala Asp
20 25 30
Ser Ala Ala Ala Leu Leu Glu Pro Asp Val Phe Leu Ile Phe Ser Gln
35 40 45
Gly Met Gln Gly Cys Leu Glu Ala Gln Gly Val Gln Val Arg Val Thr
50 55 60
Pro Phe Cys Asn Ala Ser Leu Pro Ala Gln Arg Trp Lys Trp Val Ser
65 70 75 80
Arg Asn Arg Leu Phe Asn Leu Gly Ala Thr Gln Cys Leu Gly Thr Gly
85 90 95
Trp Pro Val Thr Asn Thr Thr Val Ser Leu Gly Met Tyr Glu Cys Asp
100 105 110
Arg Glu Ala Leu Ser Leu Arg Met Ala Val Ser Tyr Thr Arg Gly Pro
115 120 125
Val Val Pro Ala Ser Gly Gly Ser Cys Lys Gln Cys Ile Gln Ala Trp
130 135 140
His Leu Glu Arg Gly Asp Gln Thr Arg Ser Gly His Trp Asn Ile Tyr
145 150 155 160
Gly Ser Glu Glu Asp Leu Cys Ala Arg Pro Tyr Tyr Glu Val Tyr Thr
165 170 175
Ile Gln Gly Asn Ser His Gly Lys Pro Cys Thr Ile Pro Phe Lys Tyr
180 185 190
Asp Asn Gln Trp Phe His Gly Cys Thr Ser Thr Gly Arg Glu Asp Gly
195 200 205
His Leu Trp Cys Ala Thr Thr Gln Asp Tyr Gly Lys Asp Glu Arg Trp
210 215 220
Gly Phe Cys Pro Ile Lys Ser Asn Asp Cys Glu Thr Phe Trp Asp Lys
225 230 235 240
Asp Gln Leu Thr Asp Ser Cys Tyr Gln Phe Asn Phe Gln Ser Thr Leu
245 250 255
Ser Trp Arg Glu Ala Trp Ala Ser Cys Glu Gln Gln Gly Ala Asp Leu
260 265 270
Leu Ser Ile Thr Glu Ile His Glu Gln Thr Tyr Ile Asn Gly Leu Leu
275 280 285
Thr Gly Tyr Ser Ser Thr Leu Trp Ile Gly Leu Asn Asp Leu Asp Thr
290 295 300
Ser Gly Gly Trp Gln Trp Ser Asp Asn Ser Pro Leu Lys Tyr Leu Asn
305 310 315 320
Trp Glu Ser Asp Gln Pro Asp Asn Pro Gly Glu Glu Asn Cys Gly Val
325 330 335
Ile Arg Thr Glu Ser Ser Gly Gly Trp Gln Asn His Asp Cys Ser Ile
340 345 350
Ala Leu Pro Tyr Val Cys Lys Lys Lys Pro Asn Ala Thr Val Glu Pro
355 360 365
Ile Gln Pro Asp Arg Trp Thr Asn Val Lys Val Glu Cys Asp Pro Ser
370 375 380

Trp Gln Pro Phe Gln Gly His Cys Tyr Arg Leu Gln Ala Glu Lys Arg
385 390 395 400
Ser Trp Gln Glu Ser Lys Arg Ala Cys Leu Arg Gly Gly Gly Asp Leu
405 410 415
Leu Ser Ile His Ser Met Ala Glu Leu Glu Phe Ile Thr Lys Gln Ile
420 425 430
Lys Gln Glu Val Glu Glu Leu Trp Ile Gly Leu Asn Asp Leu Lys Leu
435 440 445
Gln Met Asn Phe Glu Trp Ser Asp Gly Ser Leu Val Ser Phe Thr His
450 455 460
Trp His Pro Phe Glu Pro Asn Asn Phe Arg Asp Ser Leu Glu Asp Cys
465 470 475 480
Val Thr Ile Trp Gly Pro Glu Gly Arg Trp Asn Asp Ser Pro Cys Asn
485 490 495
Gln Ser Leu Pro Ser Ile Cys Lys Lys Ala Gly Arg Leu Ser Gln Gly
500 505 510
Ala Ala Glu Glu Asp His Asp Cys Arg Lys Gly Trp Thr Trp His Ser
515 520 525
Pro Ser Cys Tyr Trp Leu Gly Glu Asp Gln Val Ile Tyr Ser Asp Ala
530 535 540
Arg Arg Leu Cys Thr Asp His Gly Ser Gln Leu Val Thr Ile Thr Asn
545 550 555 560
Arg Phe Glu Gln Ala Phe Val Ser Ser Leu Ile Tyr Asn Trp Glu Gly
565 570 575
Glu Tyr Phe Trp Thr Ala Leu Gln Asp Leu Asn Ser Thr Gly Ser Phe
580 585 590
Arg Trp Leu Ser Gly Asp Glu Val Ile Tyr Thr His Trp Asn Arg Asp
595 600 605
Gln Pro Gly Tyr Arg Arg Gly Gly Cys Val Ala Leu Ala Thr Gly Ser
610 615 620
Ala Met Gly Leu Trp Glu Val Lys Asn Cys Thr Ser Phe Arg Ala Arg
625 630 635 640
Tyr Ile Cys Arg Gln Ser Leu Gly Thr Pro Val Thr Pro Glu Leu Pro
645 650 655
Gly Pro Asp Pro Thr Pro Ser Leu Thr Gly Ser Cys Pro Gln Gly Trp
660 665 670
Val Ser Asp Pro Lys Leu Arg His Cys Tyr Lys Val Phe Ser Ser Glu
675 680 685
Arg Leu Gln Glu Lys Lys Ser Trp Ile Gln Ala Leu Gly Val Cys Arg
690 695 700
Glu Leu Gly Ala Gln Leu Leu Ser Leu Ala Ser Tyr Glu Glu Glu His
705 710 715 720
Phe Val Ala His Met Leu Asn Lys Ile Phe Gly Glu Ser Glu Pro Glu
725 730 735
Ser His Glu Gln His Trp Phe Trp Ile Gly Leu Asn Arg Arg Asp Pro
740 745 750
Arg Glu Gly His Ser Trp Arg Trp Ser Asp Gly Leu Gly Phe Ser Tyr
755 760 765
His Asn Phe Ala Arg Ser Arg His Asp Asp Asp Asp Ile Arg Gly Cys
770 775 780
Ala Val Leu Asp Leu Ala Ser Leu Gln Trp Val Pro Met Gln Cys Gln
785 790 795 800
Thr Gln Leu Asp Trp Ile Cys Lys Ile Pro Arg Gly Val Asp Val Arg
805 810 815
Glu Pro Asp Ile Gly Arg Gln Gly Arg Leu Glu Trp Val Arg Phe Gln
820 825 830
Glu Ala Glu Tyr Lys Phe Phe Glu His His Ser Ser Trp Ala Gln Ala
835 840 845
Gln Arg Ile Cys Thr Trp Phe Gln Ala Asp Leu Thr Ser Val His Ser
850 855 860
Gln Ala Glu Leu Gly Phe Leu Gly Gln Asn Leu Gln Lys Leu Ser Ser

865 870 875 880
Asp Gln Glu Gln His Trp Trp Ile Gly Leu His Thr Leu Glu Ser Asp
885 890 895
Gly Arg Phe Arg Trp Thr Asp Gly Ser Ile Ile Asn Phe Ile Ser Trp
900 905 910
Ala Pro Gly Lys Pro Arg Pro Ile Gly Lys Asp Lys Lys Cys Val Tyr
915 920 925
Met Thr Ala Arg Gln Glu Asp Trp Gly Asp Gln Arg Cys His Thr Ala
930 935 940
Leu Pro Tyr Ile Cys Lys Arg Ser Asn Ser Ser Gly Glu Thr Gln Pro
945 950 955 960
Gln Asp Leu Pro Pro Ser Ala Leu Gly Gly Cys Pro Ser Gly Trp Asn
965 970 975
Gln Phe Leu Asn Lys Cys Phe Arg Ile Gln Gly Gln Asp Pro Gln Asp
980 985 990
Arg Val Lys Trp Ser Glu Ala Gln Phe Ser Cys Glu Gln Gln Glu Ala
995 1000 1005
Gln Leu Val Thr Ile Ala Asn Pro Leu Glu Gln Ala Phe Ile Thr Ala
1010 1015 1020
Ser Leu Pro Asn Val Thr Phe Asp Leu Trp Ile Gly Leu His Ala Ser
1025 1030 1035 1040
Gln Arg Asp Phe Gln Trp Ile Glu Gln Glu Pro Leu Leu Tyr Thr Asn
1045 1050 1055
Trp Ala Pro Gly Glu Pro Ser Gly Pro Ser Pro Ala Pro Ser Gly Thr
1060 1065 1070
Lys Pro Thr Ser Cys Ala Val Ile Leu His Ser Pro Ser Ala His Phe
1075 1080 1085
Thr Gly Arg Trp Asp Asp Arg Ser Cys Thr Glu Glu Thr His Gly Phe
1090 1095 1100
Ile Cys Gln Lys Gly Thr Asp Pro Ser Leu Ser Pro Ser Pro Ala Ala
1105 1110 1115 1120
Thr Pro Pro Ala Pro Gly Ala Glu Leu Ser Tyr Leu Asn His Thr Phe
1125 1130 1135
Arg Leu Leu Gln Lys Pro Leu Arg Trp Lys Asp Ala Leu Leu Leu Cys
1140 1145 1150
Glu Ser Arg Asn Ala Ser Leu Ala His Val Pro Asp Pro Tyr Thr Gln
1155 1160 1165
Ala Phe Leu Thr Gln Ala Ala Arg Gly Leu Gln Thr Pro Leu Trp Ile
1170 1175 1180
Gly Leu Ala Ser Glu Glu Gly Ser Arg Arg Tyr Ser Trp Leu Ser Glu
1185 1190 1195 1200
Glu Pro Leu Asn Tyr Val Ser Trp Gln Asp Glu Glu Pro Gln His Ser
1205 1210 1215
Gly Gly Cys Ala Tyr Val Asp Val Asp Gly Thr Trp Arg Thr Thr Ser
1220 1225 1230
Cys Asp Thr Lys Leu Gln Gly Ala Val Cys Gly Val Ser Arg Gly Pro
1235 1240 1245
Pro Pro Arg Arg Ile Asn Tyr Arg Gly Ser Cys Pro Gln Gly Leu Ala
1250 1255 1260
Asp Ser Ser Trp Ile Pro Phe Arg Glu His Cys Tyr Ser Phe His Met
1265 1270 1275 1280
Glu Val Leu Leu Gly His Lys Glu Ala Leu Gln Arg Cys Gln Lys Ala
1285 1290 1295
Gly Gly Thr Val Leu Ser Ile Leu Asp Glu Met Glu Asn Val Phe Val
1300 1305 1310
Trp Glu His Leu Gln Thr Ala Glu Ala Gln Ser Arg Gly Ala Trp Leu
1315 1320 1325
Gly Met Asn Phe Asn Pro Lys Gly Gly Thr Leu Val Trp Gln Asp Asn
1330 1335 1340
Thr Ala Val Asn Tyr Ser Asn Trp Gly Pro Pro Gly Leu Gly Pro Ser
1345 1350 1355 1360

Met Leu Ser His Asn Ser Cys Tyr Trp Ile Gln Ser Ser Ser Gly Leu
1365 1370 1375
Trp Arg Pro Gly Ala Cys Thr Asn Ile Thr Met Gly Val Val Cys Lys
1380 1385 1390
Leu Pro Arg Val Glu Glu Asn Ser Phe Leu Pro Ser Ala Ala Leu Pro
1395 1400 1405
Glu Ser Pro Val Ala Leu Val Val Val Leu Thr Ala Val Leu Leu Leu
1410 1415 1420
Leu Ala Leu Met Thr Ala Ala Leu Ile Leu Tyr Arg Arg Arg Gln Ser
1425 1430 1435 1440
Ala Glu Arg Gly Ser Phe Glu Gly Ala Arg Tyr Ser Arg Ser Ser His
1445 1450 1455
Ser Gly Pro Ala Glu Ala Thr Glu Lys Asn Ile Leu Val Ser Asp Met
1460 1465 1470
Glu Met Asn Glu Gln Gln Glu
1475

<210> 306
<211> 3987
<212> DNA
<213> Rat

<400> 306
agtatggaga gaaggtcgtt taaaaaggca gatgtccctt taaggtttgc tttgctgctg 60
cccgtggact ttagcctaaa cagggtcccg cgaagttggc tttatttgtc catgtctcgg 120
acacagcctg ggtagctgcc agtgagattt cagggacgga gcgcgcaaag ggggggggaaa 180
tgtggcaatc catctgggat gtgagacgcg tggagagggc ttagcagcat ttgaccaaaa 240
cacaggaaat cactcctcca cagctcctgg gcgcagcagc ggctggggcc actgccggac 300
accctcggag accacacgag tgacccagag cgcaagtcgc cagcgtcccg gttctgcctg 360
ttcctgccag ctcctgccca cgaaccggca cgtagctggt tccagcagcc gctccagcaa 420
tggtccccag gcgtcctgcc agcctagagg tcactgtagc ctgcatatgg cttctcacgg 480
tcatcctagg cttctgcgtc tccttcaatg ttgatgtgaa aaactcaatg agtttcagtg 540
gcccagtaga ggacatgttt ggatacactg ttcaacaata tgaaaacgaa gaaggcaaat 600
gggttcttat tggttctcct ttagttggcc aacccaaagc aagaactgga gatgtctata 660
agtgtccggt tgggagagag agagcaatgc cttgcgtgaa gttggacttg ccagttaaca 720
catcgatccc caatgtcaca gaaataaagg aaaacatgac atttggatca actttagtca 780
ccaacccgaa tggaggattt ctggcatgtg ggcccttgta tgcctataga tgtggacatt 840
tgcattatac aactggaata tgttctgatg tcagtcctac atttcaagtt gtgaactcct 900
ttgcccctgt acaagaatgc agcacccagc tggacatagt catcgtcctg gatggctcca 960
acagcatcta cccctgggaa agtgtcatcg cctttttaaa cgaccttctt aagaggatgg 1020
atattggccc taagcagaca caggtcggga ttgtacagta tggagagaat gtaacccatg 1080
agttcaacct caataagtat tcatccacag aagaggtcct tgtcgcagca aacaaaatag 1140
gccgacaggg aggcctccaa acgatgacag cccttggaat agacacagcc aggaaagagg 1200
cattcactga agctcggggt gccaggaggg gagttaaaaa agtcatggtt attgtgaccg 1260
acggagaatc gcatgacaac tatcgcctga aacaggtcat ccaagactgc gaggacgaaa 1320
acattcagcg attttccata gctatccttg gccactataa caggggggaac ttaagcactg 1380
aaaaatttgt ggaggaaata aaatcgatcg caagcgagcc cacggaaaag cacttcttca 1440
atgtctcgga tgagttggcc ctggtcacta ttgttaaagc tctgggagaa aggatattcg 1500
ctttggaagc gacagctgac cagtcagcag cttcatttga gatggaaatg tctcagactg 1560
gcttcagtgc tcactactcc caggactggg tcatgcttgg agcggtggga gcctatgact 1620
ggaacggaac tgtggtcatg cagaaggcta accagatggt catccctcat aacaccacct 1680
ttcaaactga gcccgccaag atgaacgagc ctctggcttc ttatttaggt tacacagtga 1740
actcggccac catccctgga gatgtgctct acatcgctgg gcagcctcgg tacaatcata 1800
cgggccaggt cgtcatctac aagatggagg atgggaacat caacattctg cagacactcg 1860
gcggagagca gattggttcc tactttggta gtgtcttaac aacaattgac atcgacaaag 1920
attcttatac tgatctgctt ctcgtcgggg cccccatgta catggggaca gagaaagagg 1980
aacagggcaa ggtgtacgtg tacgctgtga atcagacaag gtttgaatat caaatgagcc 2040
tggaaccaat taggcagacc tgctgctcat ccctgaagga taattcatgc acgaaagaaa 2100
acaagaatga gccctgcggg gcccgcttcg gaacagcaat tgctgctgta aaagacctca 2160
acgtggatgg atttaatgac gtcgtgattg gagctccgct ggaagatgac cacgcaggag 2220
ctgtgtacat ttatcatggc agtggcaaga ccataaggga ggcgtatgca caacgcattc 2280

```
catcaggtgg ggatggcaag accctgaaat ttttcggcca gtctatccac ggagagatgg    2340
atttaaatgg tgacggtctg actgacgtga ccattggagg ccttggtgga gcagccctct    2400
tctgggccag agatgtggct gtagttaaag tgaccatgaa ttttgaaccc aataaagtga    2460
atattcaaaa gaaaaactgc cgtgtggagg gcaaagaaac agtgtgcata aatgctacaa    2520
tgtgttttca tgtgaaatta aagtctaaag aggactcaat ttacgaggct gatctgcagt    2580
accgtgtcac ccttgattca ctgaggcaga tatcacggag ctttttttct ggaactcagg    2640
aaaggaagat tcaaagaaat atcaccgttc gagaatcaga atgcatcagg cactccttct    2700
acatgttgga caaacatgac tttcaggact ctgtgagagt gactctggat tttaatctca    2760
ctgatccaga aaatggtcct gtacttgatg acgctctgcc aaactcagtc cacgaacaca    2820
ttcccttttgc caaagactgt ggaaacaagg aaagatgcat ttcagacctc actctgaatg    2880
tgtccaccac agaaaagagc ctgctgatcg tcaagtccca gcatgacaag ttcaacgtta    2940
gcctcaccgt caaaaacaaa ggagacagtg cgtacaacac caggacagtg gtgcagcatt    3000
caccaaatct gatttttteg ggaattgagg agatccaaaa agatagctgt gaatctaatc    3060
aaaatatcac ttgcagagtt ggatatcctt tcctaagagc aggagaaacg gttaccttca    3120
aaataatatt ccagtttaac acatcccatc tctcggaaaa tgcaatcatt cacttaagtg    3180
caacaagtga cagtgaggag cccctggaat ctcttaatga taatgaagta aatatttcca    3240
tcccagtaaa atatgaagtt ggactgcagt tttacagttc tgcgagtgaa catcacattt    3300
cagtcgctgc caatgagacg atccctgagt ttattaactc cactgaggac attgggaatg    3360
aaattaatgt cttctatacg attagaaaga gggggcattt cccaatgcca gaacttcagc    3420
tgtcaatttc attccccaat ttgacggcag atggttatcc tgtactgtac ccaattggat    3480
ggtcatcttc agataatgtg aactgtagac cccggagcct tgaggacccc tttggcatca    3540
actctgggaa gaaaatgaca atatcgaagt ctgaggttct caaaagaggc acaatccagg    3600
actgcagtag tacgtgtgga gttgccacca tcacgtgtag cctccttcct tccgacctga    3660
gtcaagtgaa tgtctcgctc ctcctgtgga aaccgacttt cataagagca cattttcca    3720
gcttaaacct tactctaaga ggagaactta agagtgaaaa ttcatcgctg actttaagta    3780
gcagcaaccg gaagcgagag ctggctattc agatatccaa agacgggctc ccaggcagag    3840
tgccgctgtg ggttatcctc ctgagcgcct tcgcggggct actgctgcta atgctcctta    3900
tattggctct gtggaagatt ggattcttca aaggccact gaagaagaaa atggagaaat    3960
gaaaggtttc atagaaaaaa aaaaaaa                                        3987
```

<210> 307
<211> 1180
<212> PRT
<213> Rat

<400> 307

```
Met Val Pro Arg Arg Pro Ala Ser Leu Glu Val Thr Val Ala Cys Ile
1               5                   10                  15
Trp Leu Leu Thr Val Ile Leu Gly Phe Cys Val Ser Phe Asn Val Asp
            20                  25                  30
Val Lys Asn Ser Met Ser Phe Ser Gly Pro Val Glu Asp Met Phe Gly
        35                  40                  45
Tyr Thr Val Gln Gln Tyr Glu Asn Glu Glu Gly Lys Trp Val Leu Ile
    50                  55                  60
Gly Ser Pro Leu Val Gly Gln Pro Lys Ala Arg Thr Gly Asp Val Tyr
65                  70                  75                  80
Lys Cys Pro Val Gly Arg Glu Arg Ala Met Pro Cys Val Lys Leu Asp
                85                  90                  95
Leu Pro Val Asn Thr Ser Ile Pro Asn Val Thr Glu Ile Lys Glu Asn
            100                 105                 110
Met Thr Phe Gly Ser Thr Leu Val Thr Asn Pro Asn Gly Gly Phe Leu
        115                 120                 125
Ala Cys Gly Pro Leu Tyr Ala Tyr Arg Cys Gly His Leu His Tyr Thr
    130                 135                 140
Thr Gly Ile Cys Ser Asp Val Ser Pro Thr Phe Gln Val Val Asn Ser
145                 150                 155                 160
Phe Ala Pro Val Gln Glu Cys Ser Thr Gln Leu Asp Ile Val Ile Val
                165                 170                 175
Leu Asp Gly Ser Asn Ser Ile Tyr Pro Trp Glu Ser Val Ile Ala Phe
            180                 185                 190
Leu Asn Asp Leu Leu Lys Arg Met Asp Ile Gly Pro Lys Gln Thr Gln
```

195 200 205
Val Gly Ile Val Gln Tyr Gly Glu Asn Val Thr His Glu Phe Asn Leu
210 215 220
Asn Lys Tyr Ser Ser Thr Glu Glu Val Leu Val Ala Ala Asn Lys Ile
225 230 235 240
Gly Arg Gln Gly Gly Leu Gln Thr Met Thr Ala Leu Gly Ile Asp Thr
245 250 255
Ala Arg Lys Glu Ala Phe Thr Glu Ala Arg Gly Ala Arg Arg Gly Val
260 265 270
Lys Lys Val Met Val Ile Val Thr Asp Gly Glu Ser His Asp Asn Tyr
275 280 285
Arg Leu Lys Gln Val Ile Gln Asp Cys Glu Asp Glu Asn Ile Gln Arg
290 295 300
Phe Ser Ile Ala Ile Leu Gly His Tyr Asn Arg Gly Asn Leu Ser Thr
305 310 315 320
Glu Lys Phe Val Glu Glu Ile Lys Ser Ile Ala Ser Glu Pro Thr Glu
325 330 335
Lys His Phe Phe Asn Val Ser Asp Glu Leu Ala Leu Val Thr Ile Val
340 345 350
Lys Ala Leu Gly Glu Arg Ile Phe Ala Leu Glu Ala Thr Ala Asp Gln
355 360 365
Ser Ala Ala Ser Phe Glu Met Glu Met Ser Gln Thr Gly Phe Ser Ala
370 375 380
His Tyr Ser Gln Asp Trp Val Met Leu Gly Ala Val Gly Ala Tyr Asp
385 390 395 400
Trp Asn Gly Thr Val Val Met Gln Lys Ala Asn Gln Met Val Ile Pro
405 410 415
His Asn Thr Thr Phe Gln Thr Glu Pro Ala Lys Met Asn Glu Pro Leu
420 425 430
Ala Ser Tyr Leu Gly Tyr Thr Val Asn Ser Ala Thr Ile Pro Gly Asp
435 440 445
Val Leu Tyr Ile Ala Gly Gln Pro Arg Tyr Asn His Thr Gly Gln Val
450 455 460
Val Ile Tyr Lys Met Glu Asp Gly Asn Ile Asn Ile Leu Gln Thr Leu
465 470 475 480
Gly Gly Glu Gln Ile Gly Ser Tyr Phe Gly Ser Val Leu Thr Thr Ile
485 490 495
Asp Ile Asp Lys Asp Ser Tyr Thr Asp Leu Leu Leu Val Gly Ala Pro
500 505 510
Met Tyr Met Gly Thr Glu Lys Glu Glu Gln Gly Lys Val Tyr Val Tyr
515 520 525
Ala Val Asn Gln Thr Arg Phe Glu Tyr Gln Met Ser Leu Glu Pro Ile
530 535 540
Arg Gln Thr Cys Cys Ser Ser Leu Lys Asp Asn Ser Cys Thr Lys Glu
545 550 555 560
Asn Lys Asn Glu Pro Cys Gly Ala Arg Phe Gly Thr Ala Ile Ala Ala
565 570 575
Val Lys Asp Leu Asn Val Asp Gly Phe Asn Asp Val Val Ile Gly Ala
580 585 590
Pro Leu Glu Asp Asp His Ala Gly Ala Val Tyr Ile Tyr His Gly Ser
595 600 605
Gly Lys Thr Ile Arg Glu Ala Tyr Ala Gln Arg Ile Pro Ser Gly Gly
610 615 620
Asp Gly Lys Thr Leu Lys Phe Phe Gly Gln Ser Ile His Gly Glu Met
625 630 635 640
Asp Leu Asn Gly Asp Gly Leu Thr Asp Val Thr Ile Gly Gly Leu Gly
645 650 655
Gly Ala Ala Leu Phe Trp Ala Arg Asp Val Ala Val Val Lys Val Thr
660 665 670
Met Asn Phe Glu Pro Asn Lys Val Asn Ile Gln Lys Lys Asn Cys Arg
675 680 685

Val Glu Gly Lys Glu Thr Val Cys Ile Asn Ala Thr Met Cys Phe His
690 695 700
Val Lys Leu Lys Ser Lys Glu Asp Ser Ile Tyr Glu Ala Asp Leu Gln
705 710 715 720
Tyr Arg Val Thr Leu Asp Ser Leu Arg Gln Ile Ser Arg Ser Phe Phe
725 730 735
Ser Gly Thr Gln Glu Arg Lys Ile Gln Arg Asn Ile Thr Val Arg Glu
740 745 750
Ser Glu Cys Ile Arg His Ser Phe Tyr Met Leu Asp Lys His Asp Phe
755 760 765
Gln Asp Ser Val Arg Val Thr Leu Asp Phe Asn Leu Thr Asp Pro Glu
770 775 780
Asn Gly Pro Val Leu Asp Asp Ala Leu Pro Asn Ser Val His Glu His
785 790 795 800
Ile Pro Phe Ala Lys Asp Cys Gly Asn Lys Glu Arg Cys Ile Ser Asp
805 810 815
Leu Thr Leu Asn Val Ser Thr Thr Glu Lys Ser Leu Leu Ile Val Lys
820 825 830
Ser Gln His Asp Lys Phe Asn Val Ser Leu Thr Val Lys Asn Lys Gly
835 840 845
Asp Ser Ala Tyr Asn Thr Arg Thr Val Val Gln His Ser Pro Asn Leu
850 855 860
Ile Phe Ser Gly Ile Glu Glu Ile Gln Lys Asp Ser Cys Glu Ser Asn
865 870 875 880
Gln Asn Ile Thr Cys Arg Val Gly Tyr Pro Phe Leu Arg Ala Gly Glu
885 890 895
Thr Val Thr Phe Lys Ile Ile Phe Gln Phe Asn Thr Ser His Leu Ser
900 905 910
Glu Asn Ala Ile Ile His Leu Ser Ala Thr Ser Asp Ser Glu Glu Pro
915 920 925
Leu Glu Ser Leu Asn Asp Asn Glu Val Asn Ile Ser Ile Pro Val Lys
930 935 940
Tyr Glu Val Gly Leu Gln Phe Tyr Ser Ser Ala Ser Glu His His Ile
945 950 955 960
Ser Val Ala Ala Asn Glu Thr Ile Pro Glu Phe Ile Asn Ser Thr Glu
965 970 975
Asp Ile Gly Asn Glu Ile Asn Val Phe Tyr Thr Ile Arg Lys Arg Gly
980 985 990
His Phe Pro Met Pro Glu Leu Gln Leu Ser Ile Ser Phe Pro Asn Leu
995 1000 1005
Thr Ala Asp Gly Tyr Pro Val Leu Tyr Pro Ile Gly Trp Ser Ser Ser
1010 1015 1020
Asp Asn Val Asn Cys Arg Pro Arg Ser Leu Glu Asp Pro Phe Gly Ile
1025 1030 1035 1040
Asn Ser Gly Lys Lys Met Thr Ile Ser Lys Ser Glu Val Leu Lys Arg
1045 1050 1055
Gly Thr Ile Gln Asp Cys Ser Ser Thr Cys Gly Val Ala Thr Ile Thr
1060 1065 1070
Cys Ser Leu Leu Pro Ser Asp Leu Ser Gln Val Asn Val Ser Leu Leu
1075 1080 1085
Leu Trp Lys Pro Thr Phe Ile Arg Ala His Phe Ser Ser Leu Asn Leu
1090 1095 1100
Thr Leu Arg Gly Glu Leu Lys Ser Glu Asn Ser Ser Leu Thr Leu Ser
1105 1110 1115 1120
Ser Ser Asn Arg Lys Arg Glu Leu Ala Ile Gln Ile Ser Lys Asp Gly
1125 1130 1135
Leu Pro Gly Arg Val Pro Leu Trp Val Ile Leu Leu Ser Ala Phe Ala
1140 1145 1150
Gly Leu Leu Leu Leu Met Leu Leu Ile Leu Ala Leu Trp Lys Ile Gly
1155 1160 1165
Phe Phe Lys Arg Pro Leu Lys Lys Lys Met Glu Lys

1170 1175 1180

<210> 308
<211> 10
<212> DNA
<213> Homo sapiens

<400> 308
gatctccgtg 10

<210> 309
<211> 17
<212> DNA
<213> Homo sapiens

<400> 309
ggggctgccc agctgga 17

<210> 310
<211> 17
<212> DNA
<213> Homo sapiens

<400> 310
catttttatc tactgtc 17

<210> 311
<211> 17
<212> DNA
<213> Homo sapiens

<400> 311
ctttctttga gttttaa 17

<210> 312
<211> 17
<212> DNA
<213> Homo sapiens

<400> 312
tattaactct ctttgga 17

<210> 313
<211> 17
<212> DNA
<213> Homo sapiens

<400> 313
tattaactct ctttggg 17

<210> 314
<211> 17
<212> DNA
<213> Homo sapiens

<400> 314
caggagaccc caggccc 17

<210> 315
<211> 17
<212> DNA

<213> Homo sapiens

<400> 315
ggaaatgtca gcaagta 17

<210> 316
<211> 17
<212> DNA
<213> Homo sapiens

<400> 316
cctggttcag tctccac 17

<210> 317
<211> 17
<212> DNA
<213> Homo sapiens

<400> 317
tttttaagaa ctcgggt 17

<210> 318
<211> 17
<212> DNA
<213> Homo sapiens

<400> 318
tttggttttc caaaaaa 17

<210> 319
<211> 17
<212> DNA
<213> Homo sapiens

<400> 319
tttggttttc caaaaga 17

<210> 320
<211> 17
<212> DNA
<213> Homo sapiens

<400> 320
tttggttttc caaaagc 17

<210> 321
<211> 17
<212> DNA
<213> Homo sapiens

<400> 321
attttgtatg attttta 17

<210> 322
<211> 17
<212> DNA
<213> Homo sapiens

<400> 322
actttagatg ggaagcc 17

<210> 323
<211> 17
<212> DNA
<213> Homo sapiens

<400> 323
gagtgagacc caggaga 17

<210> 324
<211> 17
<212> DNA
<213> Homo sapiens

<400> 324
gagtgagacc caggagc 17

<210> 325
<211> 17
<212> DNA
<213> Homo sapiens

<400> 325
gtacacacac ccccacc 17

<210> 326
<211> 17
<212> DNA
<213> Homo sapiens

<400> 326
ccacagggga attcggg 17

<210> 327
<211> 17
<212> DNA
<213> Homo sapiens

<400> 327
ccacagggga ttctcct 17

<210> 328
<211> 17
<212> DNA
<213> Homo sapiens

<400> 328
ttaaaagtca ctgtgca 17

<210> 329
<211> 17
<212> DNA
<213> Homo sapiens

<400> 329
acagactgtt agccaag 17

<210> 330
<211> 17
<212> DNA
<213> Homo sapiens

<400> 330
ctataggaga ctgggca 17

<210> 331
<211> 17
<212> DNA
<213> Homo sapiens

<400> 331
taccacctcc ctttcct 17

<210> 332
<211> 17
<212> DNA
<213> Homo sapiens

<400> 332
taccacctcc gttgtat 17

<210> 333
<211> 17
<212> DNA
<213> Homo sapiens

<400> 333
gccctttctc cgtagtt 17

<210> 334
<211> 17
<212> DNA
<213> Homo sapiens

<400> 334
gccctttctc tgtagtt 17

<210> 335
<211> 17
<212> DNA
<213> Homo sapiens

<400> 335
ttaaatagca cctttag 17

<210> 336
<211> 17
<212> DNA
<213> Homo sapiens

<400> 336
agacatactg acagaat 17

<210> 337
<211> 17
<212> DNA
<213> Homo sapiens

<400> 337
tcccccagga gccacca 17

<210> 338
<211> 17

<212> DNA
<213> Homo sapiens

<400> 338
tcccccagga gccaccg 17

<210> 339
<211> 17
<212> DNA
<213> Homo sapiens

<400> 339
tacaaatcgt tgtcaaa 17

<210> 340
<211> 17
<212> DNA
<213> Homo sapiens

<400> 340
cattatccaa aaacaat 17

<210> 341
<211> 17
<212> DNA
<213> Homo sapiens

<400> 341
agaaaccacg gaaatgg 17

<210> 342
<211> 17
<212> DNA
<213> Homo sapiens

<400> 342
accaaaacca aataggg 17

<210> 343
<211> 17
<212> DNA
<213> Homo sapiens

<400> 343
tgaaataaac ccagttt 17

<210> 344
<211> 17
<212> DNA
<213> Homo sapiens

<400> 344
tgaaataaac tcagtat 17

<210> 345
<211> 17
<212> DNA
<213> Homo sapiens

<400> 345
gtggagacgg actctgt 17

<210> 346
<211> 17
<212> DNA
<213> Homo sapiens

<400> 346
tttgtgttgt atattta 17

<210> 347
<211> 17
<212> DNA
<213> Homo sapiens

<400> 347
ttatgtttaa tagttga 17

<210> 348
<211> 17
<212> DNA
<213> Homo sapiens

<400> 348
tggaaatgac ccaaaaa 17

<210> 349
<211> 17
<212> DNA
<213> Homo sapiens

<400> 349
tggaaatgac ccaacgc 17

<210> 350
<211> 17
<212> DNA
<213> Homo sapiens

<400> 350
tgccacacag tgacttg 17

<210> 351
<211> 17
<212> DNA
<213> Homo sapiens

<400> 351
gatgaggaga ctggcaa 17

<210> 352
<211> 17
<212> DNA
<213> Homo sapiens

<400> 352
atcaaaggtt tgattta 17

<210> 353
<211> 17
<212> DNA
<213> Homo sapiens

<400> 353
agtcacatag tacataa 17

<210> 354
<211> 17
<212> DNA
<213> Homo sapiens

<400> 354
ttcggttggt caaagat 17

<210> 355
<211> 17
<212> DNA
<213> Homo sapiens

<400> 355
ccccacacgg gcaagca 17

<210> 356
<211> 17
<212> DNA
<213> Homo sapiens

<400> 356
ggcttgcctt tttgtat 17

<210> 357
<211> 17
<212> DNA
<213> Homo sapiens

<400> 357
atcccttccc gccacac 17

<210> 358
<211> 69
<212> PRT
<213> Homo sapiens

<400> 358
Ser Leu Gly Asp Arg Val Arg Leu Ser Pro Lys Lys Arg Lys Lys Val
1 5 10 15
Ile Gln Cys Ser Phe Tyr Arg Asp Lys Arg Ser Asn Ser Ser Gly Trp
20 25 30
Val Trp Trp Leu Met Pro Val Ile Pro Thr Leu Trp Glu Ala Lys Ala
35 40 45
Gly Gly Ser His Glu Val Arg Ser Ser Arg Pro Ala Trp Pro Thr Trp
50 55 60
Gln Asn Cys Leu Tyr
65

PEM's
Complete web table #25 (PEM3) + #47 (PEM6) are G1, rest are G3

Table 1. Previously characterized and novel Pan Endothelial Markers. The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 96,694 and 96,588 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUVEC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUVEC SAGE library contained 290,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8x10^6 tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Velculescu et. al. (Nat Genet 1999 Dec;23(4):387-8).

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	CATATCATTAA	247	501	130	87	2	angiomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
2	TGCACTTCAAG	328	141	0	0	0	hevin
3	TTTGCACCTTT	165	84	191	115	4	connective tissue growth factor (CTGF, IGFBP-rP2)
4	CCCTTGTCCG	131	104	1	1	0	ESTs
5	TTGCTGACTTT	73	131	2	14	1	collagen, type VI, alpha 1
6	ACCATTGGATT	102	67	0	0	2	interferon induced transmembrane protein 1 (9-27, Leu 13)
7	ACACTTCTTTC	104	44	60	62	2	guanine nucleotide binding protein 11
8	TTCTGCTCTTG	71	67	118	72	0	von Willebrand factor
9	TCCCTGGCAGA	68	68	3	13	3	cysteine-rich protein 2 (CRP-2, ESP-1, SmLIM)
10	TAATCCTCAAG	26	108	34	16	1	collagen, type XVIII, alpha 1
11	ATGTCTTTTCT	58	65	17	17	3	insulin-like growth factor-binding protein 4
12	GGGATTAAAGC	40	67	30	14	2	CD146 (S-Endo 1, P1H12, Muc18, MCAM, Mel-CAM)
13	TTAGTGTCGTA	38	69	9	13	0	SPARC (osteonectin, BM-40)
14	TTCTCCCAAAT	20	86	16	84	2	collagen, type IV, alpha 2
15	GTGCTAAGCGG	24	74	0	10	2	collagen, type VI, alpha 2
16	GTTTATGGATA	35	58	11	11	1	matrix Gla protein (MGP)
17	CCCTTTCACAC	52	33	0	0	0	ESTs, Weakly similar to HPBRII-7 protein
18	TGTTCTGGAGA	58	27	18	56	2	gap junction protein, alpha 1, 43kD (connexin 43)
19	AAGATCAAGAT	34	50	2	4	1	actin, alpha 1, skeletal muscle / actin, alpha 2, smooth muscle, aorta
20	TCTCTGAGCAT	32	48	0	0	0	aggrecanase 1 (metalloproteinase with thrombospondin type 1 motifs, 4)
21	CAGGTTTCATA	22	56	0	0	0	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
22	GCACAAGTTCT	43	25	6	22	0	calcitonin receptor-like receptor activity modifying protein 2
23	AGCTTGTGGCC	45	23	0	0	0	calcitonin receptor-like receptor activity modifying protein 3
24	CTTCTGGATAA	13	54	12	0	0	cell division cycle 42 (GTP-binding protein, 25kD)
G1 25	CAACAATAATA	42	25	13	6	0	ESTs

26	ACCGGCGCCCG	50	15	0	0	0	tetranectin (plasminogen-binding protein)
27	GGAAGCTAAGT	35	27	0	5	1	osteoblast specific factor 2 (fasciclin I-like)
28	GCAATTTAACC	38	21	0	3	0	solute carrier family 21 (prostaglandin transporter), member 2
29	GATAACTACAT	18	35	4	4	0	angiomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
30	TATGAGGGTAA	19	30	40	2	0	regulator of G-protein signalling 5
31	CCACGGGATTC	10	39	0	0	0	collagen, type III, alpha 1
32	TTTACAAAGAG	28	21	0	1	1	carboxypeptidase E
33	CCCAGTAAGAT	22	25	0	16	1	cysteine and glycine-rich protein 2 (LIM domain only, smooth muscle)
34	ACAAAGCATTT	28	20	0	14	1	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA
35	GCCTGTCCCTC	8	38	22	11	0	ESTs / biglycan
36	TACTTTATAAG	25	21	1	1	0	metalloproteinase with thrombospondin type 1 motifs (ADAMTS1, METH-1)
37	TGTTTAATACA	15	29	2	1	1	ESTs / erythrocyte membrane protein band 4.1-like 2
38	GTCCCTGCCTT	18	25	1	1	0	glutathione S-transferase M2 (muscle)
39	GAGCCATCATA	21	21	2	2	1	ESTs / GTP-binding protein overexpressed in skeletal muscle
40	GGCCCTACAGT	26	13	2	3	0	ESTs / KIAA0821 protein
41	GCTAACCCCTG	7	31	0	1	0	ESTs
42	ATCACACAGCT	19	18	0	0	0	thyroid and eye muscle autoantigen D1 (64kD)
43	ACAAGTACTGT	18	19	38	27	0	cadherin 5, VE-cadherin (vascular epithelium)
44	TCACCGTGGAC	20	17	0	1	0	selectin P (granule membrane protein 140kD, antigen CD62)
45	ACATTCCAAGT	18	18	0	1	1	tissue inhibitor of metalloproteinase 3
46	GAGCCTGGATA	6	28	0	0	0	chondroitin sulfate proteoglycan 4 (melanoma-associated)
47	GGCACTCCTGT	22	13	19	12	0	ESTs
48	TCACAGCCCCC	20	15	8	5	0	ESTs
49	TGCCAGGTGCA	10	23	0	1	0	albumin
50	TGGGAAACCTG	11	22	0	1	1	eukaryotic translation initiation factor 4 gamma, 1
51	TTTCATCCACT	20	13	0	2	0	ESTs, KIAA0362 protein
52	AACAGGGGCCA	15	18	0	0	1	interferon, alpha-inducible protein (clone IFI-6-16)
53	ACTGAAAGAAG	6	26	0	0	1	complement component 1, s subcomponent
54	ACCGTTCTGTA	8	24	10	6	0	transcription factor 4
55	ATACTATAATT	25	6	12	0	0	ESTs
56	TTTGTATAGAA	17	15	4	5	1	hect domain and RLD 2
57	GTAATGACAGA	20	11	1	1	1	stanniocalcin
58	AATAGGGGAAA	13	19	4	1	0	ESTs, KIAA1075 protein
59	GTGCTACTTCT	5	25	2	18	0	collagen, type IV, alpha 1
60	CCGGCCCCTCC	6	24	0	0	1	peanut (Drosophila)-like 2
61	TTGAATTTGTT	19	10	1	1	0	RNA-binding protein gene with multiple splicing
62	CGAGAGTGTGA	22	6	0	0	0	ESTs
63	CCCTGTTCAGC	14	15	38	24	0	tyrosine kinase with IgG and EGF homology domains (Tie)

64	CAGATGGAGGC	18	10	1	9	0	ESTs
65	AGGCTCCTGGC	8	20	0	0	0	ESTs
66	TCTGCTTCTAG	20	8	40	15	0	ESTs
67	GGCTTAGGATG	18	9	10	14	0	ESTs
68	GGTTGTTGCGG	6	21	0	0	1	ESTs
69	ACAAGTACCCA	5	22	4	5	0	P311 protein
70	CTTCTCTTGAG	18	9	1	4	1	basic transcription element binding protein 1
71	GCTAATAATGT	10	17	0	2	0	KIAA1077 protein
72	TGTGCTTTTTT	10	15	1	4	0	KIAA0758 protein / protein kinase, cAMP-dependent, catalytic, alpha
73	CATCACGGATC	17	8	0	1	0	interleukin 1 receptor, type I
74	GCAGCAGCAGC	6	18	0	2	0	T-box 2
75	TGACTGTATTA	13	11	0	0	0	ESTs / amine oxidase, copper containing 3 (vascular adhesion protein 1)
76	GAATGCTCTTG	6	18	0	11	0	gap junction protein, alpha 4, 37kD (connexin 37)
77	GTAGTTCTGGA	18	6	0	5	0	ESTs, clone 23698 mRNA
78	TCCCCTCTCTC	6	17	0	0	0	periodontal ligament fibroblast protein
79	GGGCAGTGGCT	5	18	12	5	0	ESTs, DKFZP686B0621 protein
80	AAATATGTGTT	19	4	13	3	0	ESTs
81	GTCATTTTCTA	11	11	10	2	0	transcription factor 8 (represses interleukin 2 expression)
82	CTCTCCAAACC	14	8	0	0	0	complement component 1 inhibitor (angioedema, hereditary)
83	TTAATGTGTAA	4	18	0	0	0	guanylate cyclase 1, soluble, beta 3
84	TCAAGCAATCA	13	9	0	1	0	ESTs
85	GAAGACACTTG	15	7	1	0	0	ESTs
86	GGGTAGGGTGA	6	15	0	0	1	integrin, alpha 7
87	TGGAACAGTGA	10	10	10	5	0	ESTs
88	GAGTGGCTACC	10	9	0	0	0	ESTs
89	GTCAGGGTCCC	13	7	0	9	0	decidual protein induced by progesterone
90	GTCAGTCACTT	14	6	4	1	0	hairy (Drosophila)-homolog
91	AGCAGAGACAA	14	6	1	10	0	natriuretic peptide receptor A - guanylate cyclase A
92	AGCGATGGAGA	9	10	0	0	0	ESTs
93	CGTGGGGTGTA	9	10	17	3	0	

TEM's complete web table

Table 2. SAGE tags elevated in tumor endothelium. The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. †; multiple tags for this gene are due to alternative polyadenylation sites.

see table 2 from paper for G1, G2 or G3

all G3

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	GGGGCTGCCCA	0	28	0	2	0	ESTs, similarity to thrombomodulin TEM1
2	GATCTCCGTGT	0	25	0	0	0	ESTs, similarity to rat Rhes ras-related protein TEM2
3	CATTTTTATCT	0	23	0	0	0	ESTs
4	CTTTCTTTGAG	0	22	6	20	1	regulated in glioma-like 7-1 (Dkk-3/ REIC)
5	TATTAACTCTC	0	21	1	3	1	ESTs, similarity to JNK interacting protein-3a
6	CAGGAGACCCC	0	16	2	0	0	MMP-11 (stromelysin 3)
7	GGAAATGTCAA	1	31	53	22	1	MMP-2 (gelatinase A, 72kD type IV collagenease)
8	CCTGGTTCAGT	0	15	0	0	0	ESTs
9	TTTTTAAGAAC	0	14	1	4	0	ESTs
10	TTTGGTTTTCC	5	139	0	16	0	collagen, type I, alpha 2, transcript A†
11	ATTTTGTATGA	0	13	4	8	0	nidogen (entactin)
12	ACTTTAGATGG	1	23	0	15	0	collagen, type VI, alpha 3
13	GAGTGAGACCC	3	63	0	0	1	Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	0	ESTs / cystatin S
15	CCACAGGGGAT	2	38	0	2	1	collagen, type III, alpha 1
16	TTAAAAGTCAC	1	19	1	3	1	ESTs
17	ACAGACTGTTA	4	74	0	0	0	ESTs, similarity with sea squirt nidogen TEM7
18	CCACTGCAACC	1	18	0	1	0	
19	CTATAGGAGAC	1	18	1	1	0	ESTs, similarity with homeobox protein DLX-3 TEM8
20	GTTCCACAGAA	0	9	0	3	0	collagen, type I, alpha 2, transcript B†
21	TACCACCTCCC	0	9	4	1	1	ESTs / pregnancy specific beta-1-glycoprotein 1
22	GCCCTTTCTCT	1	17	3	1	2	endo180 lectin
23	TTAAATAGCAC	2	33	0	4	0	collagen, type I, alpha 1
24	AGACATACTGA	1	16	1	0	0	ESTs, DKFZP434G162 protein
25	TCCCCCAGGAG	1	16	0	0	0	bone morphogenetic protein 1 (metalloprotease)
26	AGCCCAAAGTG	0	8	0	0	0	
27	ACTACCATAAC	0	8	0	0	0	slit (Drosophila) homolog 3 (MEGF5)
28	TACAAATCGTT	0	8	0	0	0	KIAA0672 gene product

G3

29	TTGGGTGAAAA	0	8	0	0	0	ESTs
30	CATTATCCAAA	0	8	0	0	0	integrin, alpha 1
31	AGAAACCACGG	0	8	2	7	0	collagen, type IV, alpha 1
32	ACCAAAACCAC	0	8	0	3	0	
33	TGAAATAAAC	0	8	3	1	1	
34	TTTGGTTTCC	1	15	0	0	0	ESTs
35	GTGGAGACGGA	1	15	1	2	1	ESTs
36	TTTGTGTTGTA	1	14	2	0	0	collagen, typeXII, alpha 1
37	TTATGTTTAAT	3	39	0	0	1	lumican
38	TGGAAATGACC	15	179	0	40	0	ESTs / collagen, type I, alpha 1
39	TGCCACACAGT	1	13	0	2	0	transforming growth factor, beta 3
40	GATGAGGAGAC	3	35	0	18	1	collagen, type I, alpha 2, transcript C[†]
41	ATCAAAGGTTT	2	23	0	0	0	ESTs, DKFZp564O222 mRNA
42	AGTCACATAGT	1	11	2	0	0	cell division cycle 42 (GTP-binding protein)
43	TTCGGTTGGTC	4	45	0	19	0	
44	CCCCACACGGG	2	21	0	0	0	ESTs
45	GGCTTGCCTTT	1	10	0	10	1	
46	ATCCCTTCCCG	1	10	1	0	0	peanut-like protein 1

Table 3. Detection of transcripts in various tumor types by RT-PCR and in situ hybridization (ISH). The "+" sign indicates the presence of a robust RT-PCR product or stong positive staining of vessels by in situ hybridization. The "-" sign indicates an undetectable signal by in situ hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number vessels by in situ hybridization.

		TEM1	TEM3	TEM4	TEM5	TEM7	TEM8	TEM9	vWF	Hevin
RT-PCR	Colon Nor.	-	-	-	-	-	-	-	+	ND
	Colon Tum.	+	+	+	+	+	+	+	+	ND
ISH	Colon Nor.	-	-	-	-	-	-	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+	+
	Liver Met.	+	+/-	+	+	+	+	+	+/-	ND
	Lung Tum.	+	ND	+	+	+	+	+	+	+
	Brain Tum.	+	ND	ND	ND	+	ND	ND	+	+*
	Corpus Lut.	+	+	+	+	+	-	+	+	+
	Wound	+	ND	+	ND	+/-	+/-	ND	+	+

* hevin was localized to both endothelial cells and malignant cells in brain tissue.
ND: not determined.

www.sagenet.org\angio\table3.htm (to be posted upon publication)

4

Table 9. SAGE tags elevated in normal endothelium. The top 46 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	TCTCACGTCT	26	0	0	0	0	mucosal vascular addressin cell adhesion molecule 1
2	CTAGCGTTTT	19	0	4	14	0	serum deprivation response (phosphatidylserine-binding protein)
3	GTGGCTGACG	18	0	1	0	0	ESTs / intercellular adhesion molecule 4
4	CTCTTAAAAA	34	1	1	0	0	small inducible cytokine subfamily A (Cys-Cys), member 14
5	TGGGAAGAGG	16	0	3	4	1	ESTs
6	GTTTAAGGAT	16	0	0	0	0	ESTs
7	CTTTGTTTTG	15	0	56	32	1	endothelin 1 / ribosomal protein L27
8	ATTGCCAATC	14	0	0	4	0	TU3A protein
9	TGTTGAAAAA	21	1	1	0	0	selectin E (endothelial adhesion molecule 1)
10	ACAAAAAGGC	21	1	0	6	0	TU3A protein
11	AAGATGCACAC	21	1	1	1	1	phosphodiesterase I - nucleotide pyrophosphatase 2 (autotaxin)
12	GTAGAGGAAA	10	0	0	9	0	platelet/endothelial cell adhesion molecule (CD31 antigen)
13	TTGTTCAAGG	10	0	0	1	0	ESTs
14	CTCTTCAAAAA	19	1	1	0	0	ESTs / small inducible cytokine subfamily A, member 14
15	TATTAAAATA	18	1	8	9	1	transforming growth factor, beta receptor II (70-80kD)
16	GAATTCACCA	9	0	1	14	0	ESTs
17	AAGGAGAACT	9	0	0	0	0	small inducible cytokine subfamily A, member 14
18	AATATCTGAC	9	0	2	2	2	active BCR-related gene
19	TCAGTGACCAG	17	1	4	7	2	protein kinase C eta
20	GCAAAGTGCC	32	2	1	5	0	ESTs
21	TAAATACTTG	8	0	2	0	0	ESTs (2 unigene clusters)
22	GTCACTAATT	8	0	1	0	0	ESTs
23	ATAACCTGCA	8	0	0	0	0	signaling lymphocytic activation molecule
24	TGCATCTGTGC	46	3	1	1	0	ESTs / glycogenin 2
25	TAAAGGCACA	15	1	4	3	0	LIM binding domain 2
26	GACCGCGGCT	73	5	11	7	0	claudin 5
27	ACTCCGGTGT	14	1	0	8	0	ESTs

28	CTTCTCACCT	27	2	3	1	0	GTP-binding protein
29	TCGTGCTTTG	13	1	0	0	0	ESTs
30	GAGCAGTGCT	13	1	4	2	1	feline sarcoma viral (v-fes) - Fujinami avian sarcoma viral (v-fps) homolog
31	CTCTAAAAAA	10	1	0	1	0	ESTs
32	GAAACCCGGT	10	1	0	0	1	phospholipase C, beta 4
33	AACACAGTGC	10	1	7	15	1	ESTs